Supplementary material

Table S1. Analysis of similarities (Anosim)

Groups	R-Value	*p*-Value
NC versus PC	0.3519	0.004**
NC versus A	0.3352	0.033*
NC versus B	0.3796	0.008**
NC versus C	0.2685	0.018*
NC versus D	0.363	0.006**
PC versus A	0.237	0.059
PC versus B	0.3093	0.034*
PC versus C	0.137	0.122
PC versus D	0.4019	0.002**
A versus B	0.1296	0.136
A versus C	0.5759	0.008**
A versus D	0.4333	0.002**
B versus C	0.3537	0.019*
B versus D	0.3722	0.001***
C versus D	0.2519	0.024*

*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$.

Table S2. PCR primer sequences

Name	Pre-primer	Post-primer
IL-1β	GCAACTGTTCCTGAACTCAACT	TCTTTTGGGGTCCGTCAACT
IL-6	CTGCAAGAGACTTCCATCCAG	AGTGGTATAGACAGGTCTGTTGG
TNF-α	AGGCACTCCCCCAAAAGAT	CAGTAGACAGAAGAGCGTGGTG
BDNF	TCATACTTCGGTTGCATGAAGG	AGACCTCTCGAACCTGCCC
CD14	ACTTCTCAGATCCGAAGCCAG	CCGCCGTACAATTCCACAT

Sequencing data analysis, OTU cluster, and species annotation

After sequencing, according to the barcode sequence and PCR primer sequence, each sample data was separated from the overall data. Then, the barcode sequence and primer sequence were cut off, the reads of each sample were merged into raw tags by FLASH (v1.2.7)(1), which were further filtered to obtain high-quality clean tags (2), according to the QIIME(3) quality control process. The tags were compared with a reference database (Silva database) and then the UCHIME algorithm (4) was applied to detect chimera sequences, finally, the effective tags were obtained by removing the chimera sequences (5).

The algorithm of Uparse (6) (v7.0.1001) was used to cluster all effective tags in all samples and sequences with ≥97% identity similarity were assigned to the same OTUs by default. The representative sequence for each OTU was screened for further annotation. For each representative sequence, the Silva Database(7) was used to annotate taxonomic information based on the Mothur algorithm. Multiple sequence alignment was performed by MUSCLE software(8) to study phylogenetic relationships between different OTUs and the differences between the dominant species in different samples or groups. Finally, by taking the sample with the least amount of data as a standard, the data for each sample was normalized, and subsequent analyses of alpha diversity and beta diversity were all based on this normalized data output.

References

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