

Supplementary material

Table S1. The definitions of the  $\alpha$  diversity indexes

Index	Definitions
The Chao1 index	<p>The Chao1 index was used to estimated the total number of species in ecology. The larger the Chao1 index, the more species in the sample. The calculation is as follows: <math>S_{chao1} = S_{obs} + \frac{n_1(n_1-1)}{2(n_2+1)}</math>, and <math>S_{chao1}</math> is the number of estimated OTUs, <math>S_{obs}</math> is number of actual OTUs, <math>n_1</math> is the Number of OTUs with only one sequence, and <math>n_2</math> is the Number of OTUs with only two sequences.</p>
The Ace index	<p>The Ace index was another index used to estimated the number of OTUs, but the algorithm was different from Chao1. The calculation is as follows: <math>S_{ACE} = S_{abund} + S_{rare} / C_{ACE} + n_1 / C_{ACE}</math>. <math>S_{abund}</math> is the number of OTUs with less than 10 sequences, and <math>S_{rare}</math> is the number of OTUs with more than 10 sequences.</p>
The Shannon index	<p>The Shannon index was used to estimated the microbial diversity. The greater the Shannon value, the higher the community diversity. The calculation is as follows:</p> $H_{shannon} = - \sum_{i=1}^{S_{obs}} \frac{n_i}{N} \ln \frac{n_i}{N}$ <p><math>S</math> is the Number of actual OTUs, <math>n_i</math> is the Number of OTUs with <math>i</math> sequences, and <math>N</math> is the Number of sequences.</p>
The Coverage index	<p>The Coverage index could reflect whether the sequencing results represent the actual situation of the sample. The calculation is as follows: <math>C = 1 - n_1/N</math>. <math>n</math> is the Number of OTUs with only one, and <math>N</math> is the Number of sequences.</p>