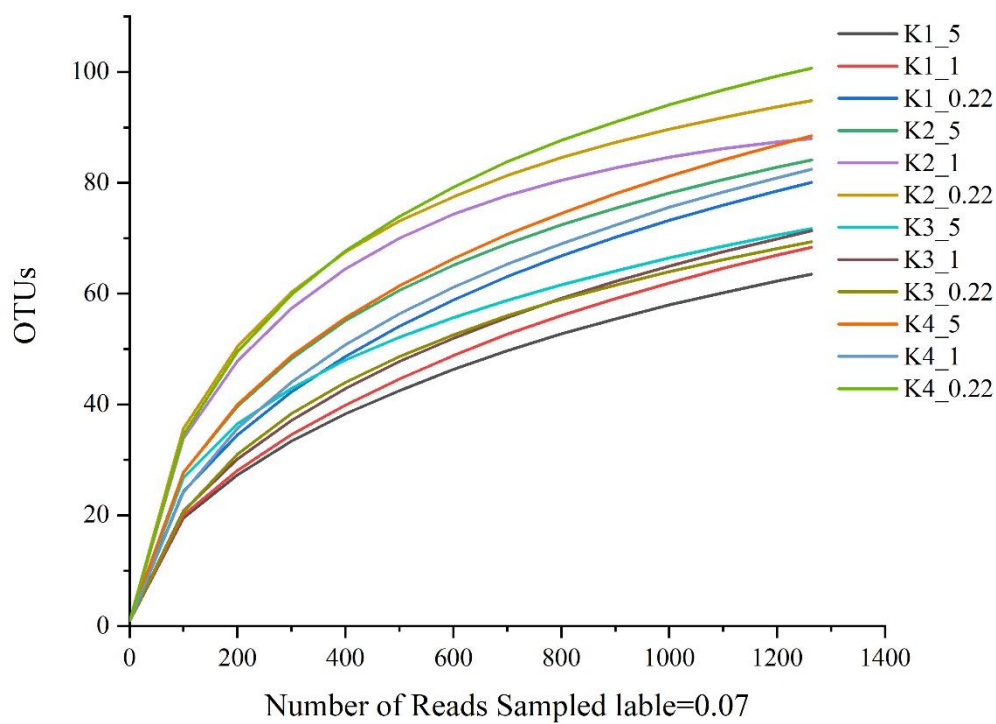


Supplementary material

Supplementary Table S1. Variability between different sites.

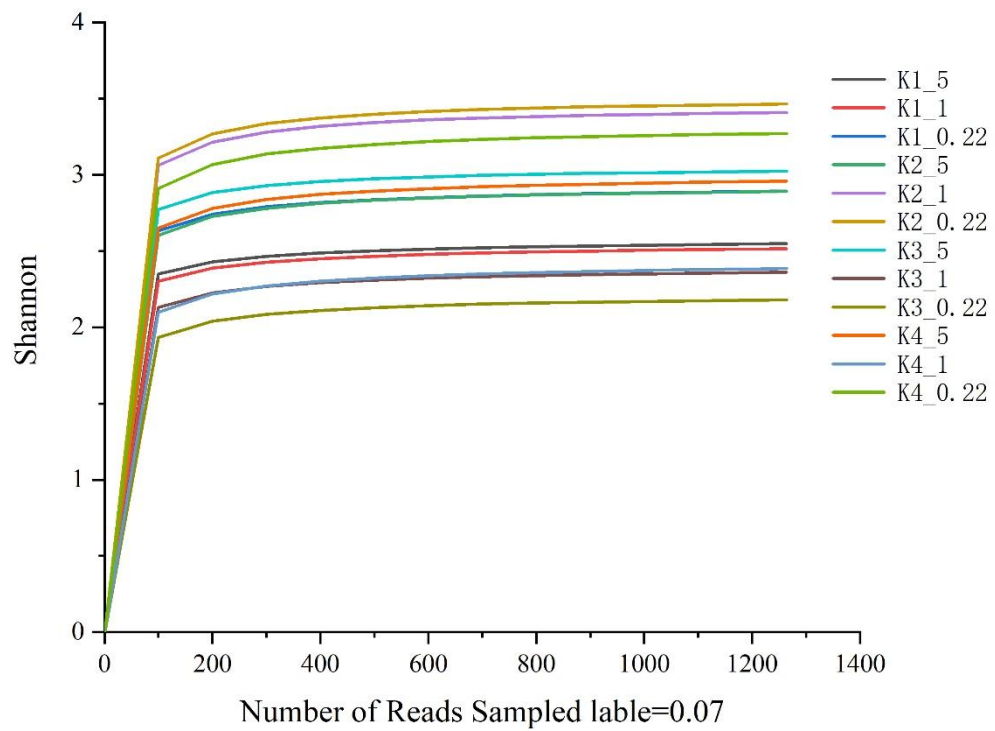
Site/Site	K1/K2	K1/K3	K1/K4	K2/K3	K2/K4	K3/K4
F	4.850	0.182	4.183	9.537	0.376	7.889
Sig.	0.040*	0.675	0.054	0.006**	0.546	0.011*

Note: * in the table indicates a significant difference, that is, $P < 0.05$; ** indicates that the difference is extremely significant, that is, $P < 0.01$.



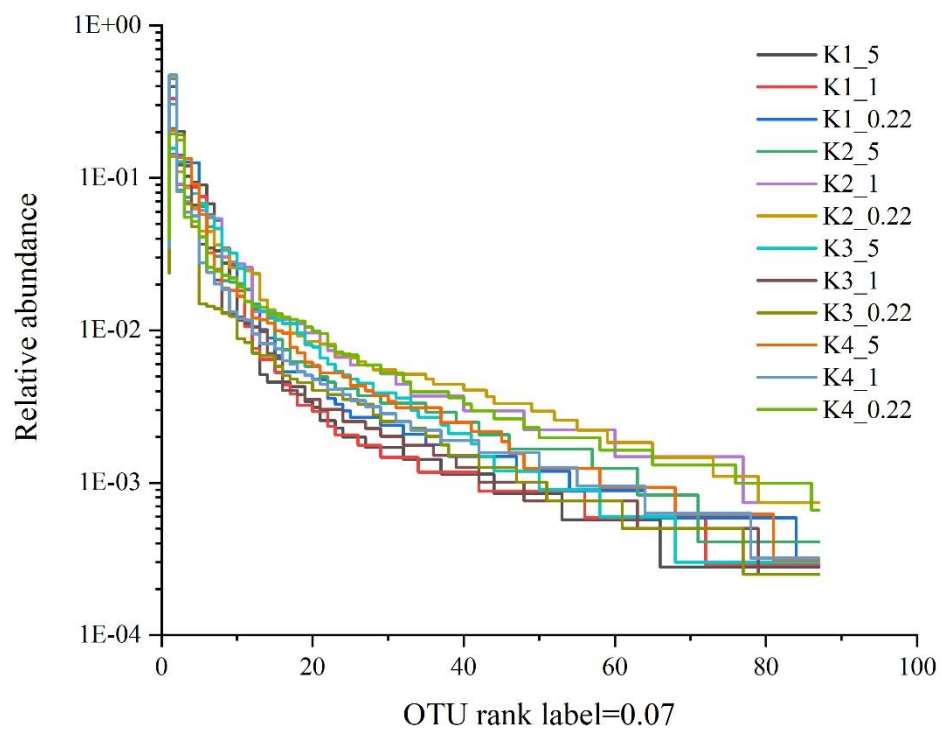
Supplementary Fig. S1. The dilution curve diagram.

Note: The flattening indicates that the sequencing depth basically covers all species in all samples, and the species diversity in the samples has been basically detected.



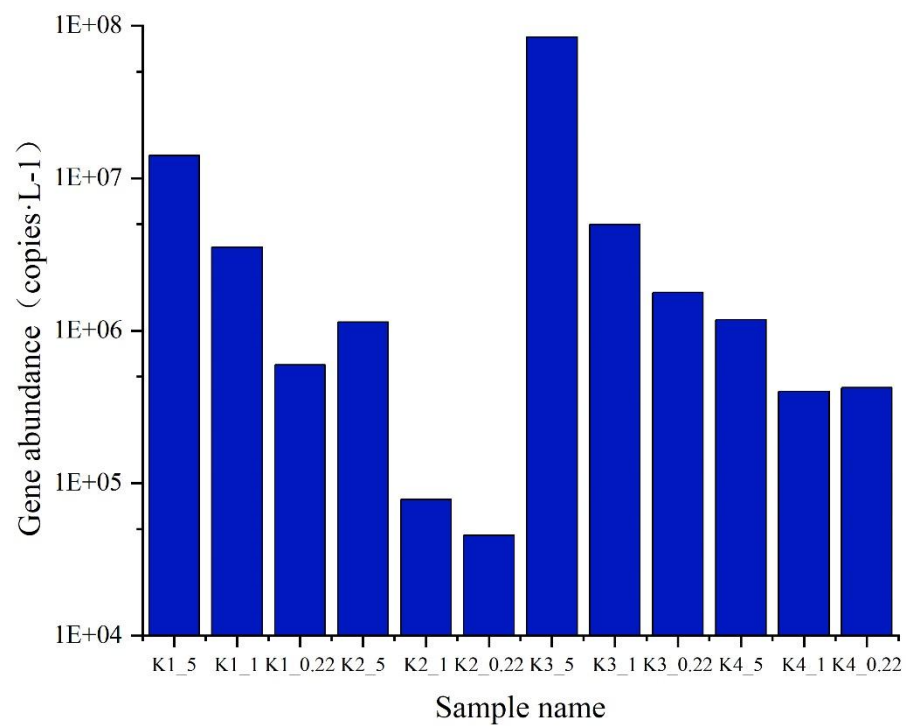
Supplementary Fig. S2. The Shannon index diagram.

Note: The gentle trend indicated that the amount of data sequenced in this study was large enough to reflect the vast majority of microbial information in all samples.



[Supplementary Fig. S3](#). The Rank-Abundance curve diagram.

Note: The Rank-Abundance graph. The rapid decline indicated that the proportion of dominant bacteria in all samples was high and the diversity was low.



Supplementary Fig. S4. The abundance distributions of the *nirS* gene in the high place pond.