

Table S3 Library coverage estimations and sequence diversity of *amoA* and *nosZ*

Sample	No. of clones sequenced	No. of filtered sequences	No. of OTU (>98% identity)	% Coverage	Chao 1 value	Shannon index
Caohai( <i>amoA</i> )	50	49	12	85.7%	19(13, 49)	1.53
Caohai( <i>nosZ</i> )	50	38	28	42.1%	85(47, 207)	3.21
Waohai( <i>amoA</i> )	50	50	3	98.0%	3(3, 0)	0.32
Waohai( <i>nosZ</i> )	50	30	15	70.0%	24(17, 55)	2.45

Library coverage was calculated as  $C=1-n/N$ , where  $n$  is the number of OTUs without a replicate, and  $N$  is the total number of sequences. The Shannon index =  $-\sum p_i \ln p_i$ , where  $p_i = n_i/N$ ,  $n_i$  is the number of OTUs with  $i$  individuals, and  $N$  is the total number of individuals. The numbers in parentheses are lower and upper 95% confidence intervals for the Chao 1 estimators.