

1 **Supplementary material**

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3 Comparative analysis of bacterial community diversity between soil and water of Dongzhai Harbor Mangrove reserve using 16S rRNA gene sequencing and shotgun
4 metagenomic sequencing

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19 **Table S1** Statistical results for 16S rDNA sequencing

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Sample\Info	Seq_num	Base_num	Mean_length	Min_length	Max_length
S01	50698	21238797	418.9277092	365	455
S02	55769	23398153	419.5548244	322	516
S03	50658	21217469	418.8374788	373	520
W01	53678	22421028	417.6949216	252	436
W02	53960	22461737	416.2664381	336	498
W03	56368	23505044	416.9926909	253	455

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27 **Table S2** Quality control statistics for the metagenomic sequences

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Samples	Clean reads	Clean bases (bp)	Percent of raw reads (%)	Percent of raw bases (%)
S01	96868527	14582404289	99.43369765	99.12953783
S02	103422475	15542200262	99.23220273	98.75822108
S03	95646725	14392757289	99.3108216	98.96771088
W01	93400965	14039938755	98.55320016	98.10872544
W02	98838591	14865410270	99.16789784	98.77442587
W03	101688183	15298581890	99.19616697	98.83223848

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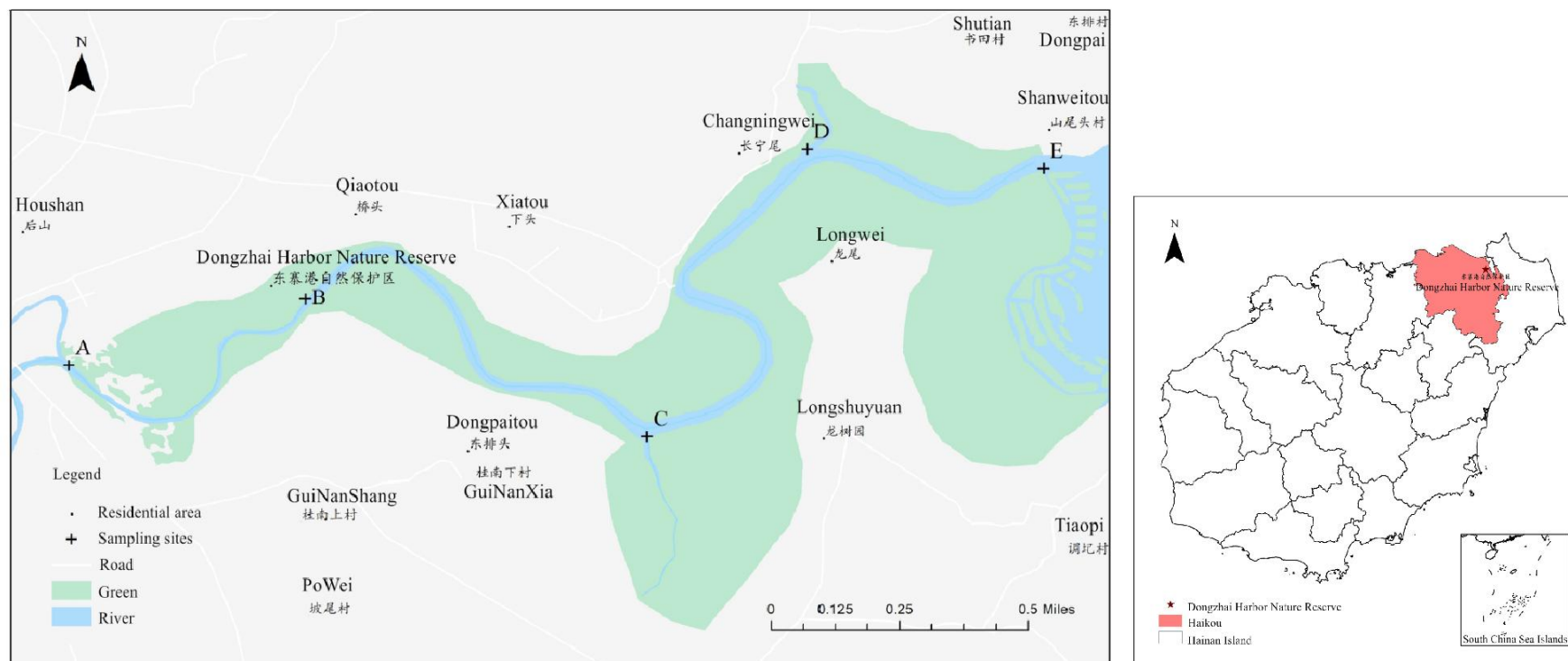


Fig. S1 Map Of study area, showing the location of the sampling stations.

A(110° 559836'E 19° 949968'N); B(110° 566490'E 19° 951913'N); C(110° 576107'E 19° 947881'N);

D(110° 580618'E 19° 956316'N); E(110° 587262'E 19° 955745'N)

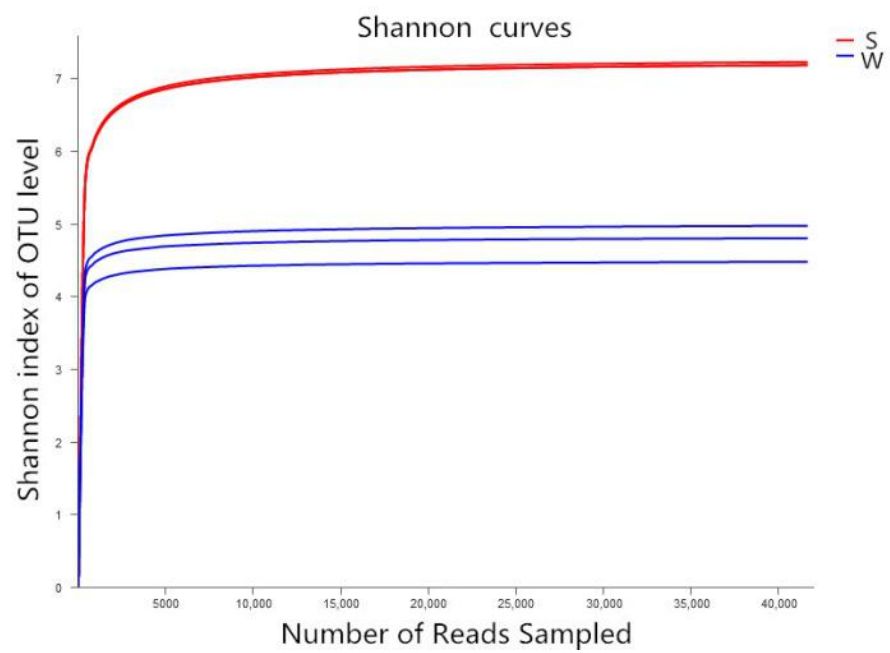


Fig. S2 Shannon rarefaction curves obtained from the Illumina sequence reads for soil and water. S: soil samples; W: water samples.