

Table 1 Environmental characteristic of the samples

Type	Redox (mv)	Ammonium ($\mu\text{mol/Kg}$ dry sed.)	Nitrite ($\mu\text{mol/Kg}$ dry sed.)	Nitrate ($\mu\text{mol/Kg}$ dry sed.)	$\text{NH}_4^+/\text{NO}_x^-$	Salinity (‰)	pH	Temp. ($^{\circ}\text{C}$)	% Water content (w/w)
Wall	213.7	30.91	0.74	23.6	1.30	23.0	6.11	20.25	57.08
Surface	228.5	112.7	2.60	23.26	3.67	22.5	6.47	20.1	57.61
Black	-108.6	39.04	1.08	1.82	11.79	29.5	6.44	19.9	58.04
Yellow	80.5	18.17	1.04	7.79	1.49	27.0	5.98	19.85	57.96

Table 2 Alpha diversity of AOA, AOB, anammox and n-damo bacteria in sediment samples

Sample	Related clones / Coverage (%)				OTU**				Shannon-Wiener				Chao1			
	1*	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4
Wall	47/90.4	31/77.5	44/88.0	42/93.3	8	17	12	3	1.7835	2.5921	2.0389	0.5010	9.0	24.5	17.0	3.0
Surface	45/86.5	44/84.6	46/92.0	35/77.8	6	20	17	4	1.4207	2.7535	2.2912	0.9790	6.0	29.0	50.0	4.5
Black	26/74.3	41/78.8	42/84.0	18/40.0	4	17	13	3	0.9693	2.3909	2.0078	0.5566	4.0	35.3	16.8	3.5
Yellow	33/94.3	48/92.3	50/66.7	15/33.3	5	5	5	3	1.2504	1.3410	0.6510	0.2449	5.0	5.0	5.0	2.0
Overall	151/86.8	164/83.7	182/80.9	110/61.1	11	43	28	10	1.7849	3.1528	2.3912	1.8043	14.0	53.9	39.0	10.3

*1-AOA; 2-AOB; 3-Anammox bacteria; 4-n-damo bacteria;

**Based on percentage sequence identity of 97% similarity for 16S rRNA gene and 95% for *pmoA* and *amoA* genes

Figure Captions

Fig. 1 The sampling map of this study at Mai Po Nature Reserve of Hong Kong (a) and a schematic of sample types (b). Sampling areas are cycled in red. This map was drawn based on Bing Map (Microsoft Co., www.bing.com/maps/).

Fig. 2 Consensus phylogenetic trees constructed after subjecting amplified translated archaeal (a) and bacterial (b) *amoA* amino acid, anammox bacterial 16S rRNA (c) and deduced n-damo *pmoA* amino acid (d) sequences to neighbor joining analyses. OTUs were defined with the variances of 3% (16S rRNA gene) or 5% (*amoA* and *pmoA* genes) difference by MOTHUR. Trees were reconstructed using alignments of 197 AOA amino acid positions, 167 AOB amino acid positions, 252 anammox nucleotide positions and 123 n-damo amino acid positions, respectively. The OTUs from the four sampling types in this study are highlighted using symbols according to the figure legend, and the representative clones of the relevant OTU are detailed in Fig. S6. The following numbers in parenthesis refer to how many detected sequences fell in the branch or subcluster. Numbers at the nodes represent the levels of bootstrap support based on 1000 re-sampled data sets (only >50% values are shown).

Fig. 3 Three dimensional discrete plots of PCoA based on the Fast UniFrac metric of n-damo bacteria diversity using *pmoA* gene sequences. The responses of different n-damo communities toward the first three principal components are shown in both unweighted qualitative measurement (a) and quantitative analysis (b) using normalized abundance weights.

Fig. 4 Abundance of archaeal and bacterial *amoA* gene copy numbers, anammox and n-damo

bacterial 16S rRNA gene copy numbers from the bioturbated areas in Mai Po mangrove sediments. Mean values and standard deviations were calculated according to the triplicate assay within a single qPCR setup.

Fig. 5 Redundancy analyses (RDA) for the physicochemical parameters (red solid arrow), targeting microbial groups (blue dot arrow) and the samples (black hollow circle) using archaeal (a) and bacterial (b) *amoA*, anammox 16S rRNA (c) and n-damo *pmoA* (d) gene sequences amplified in the present work.

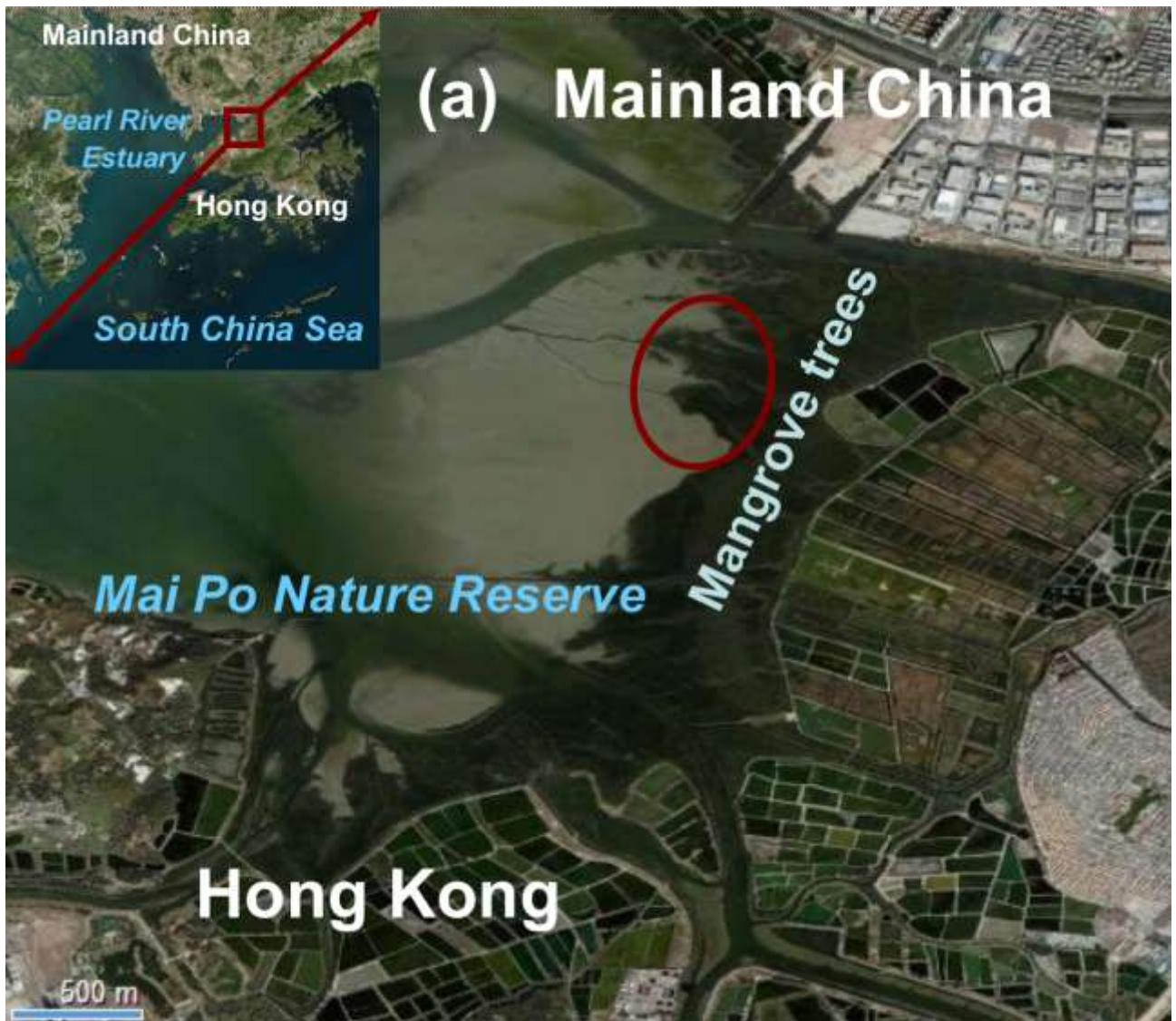


Fig.1-a

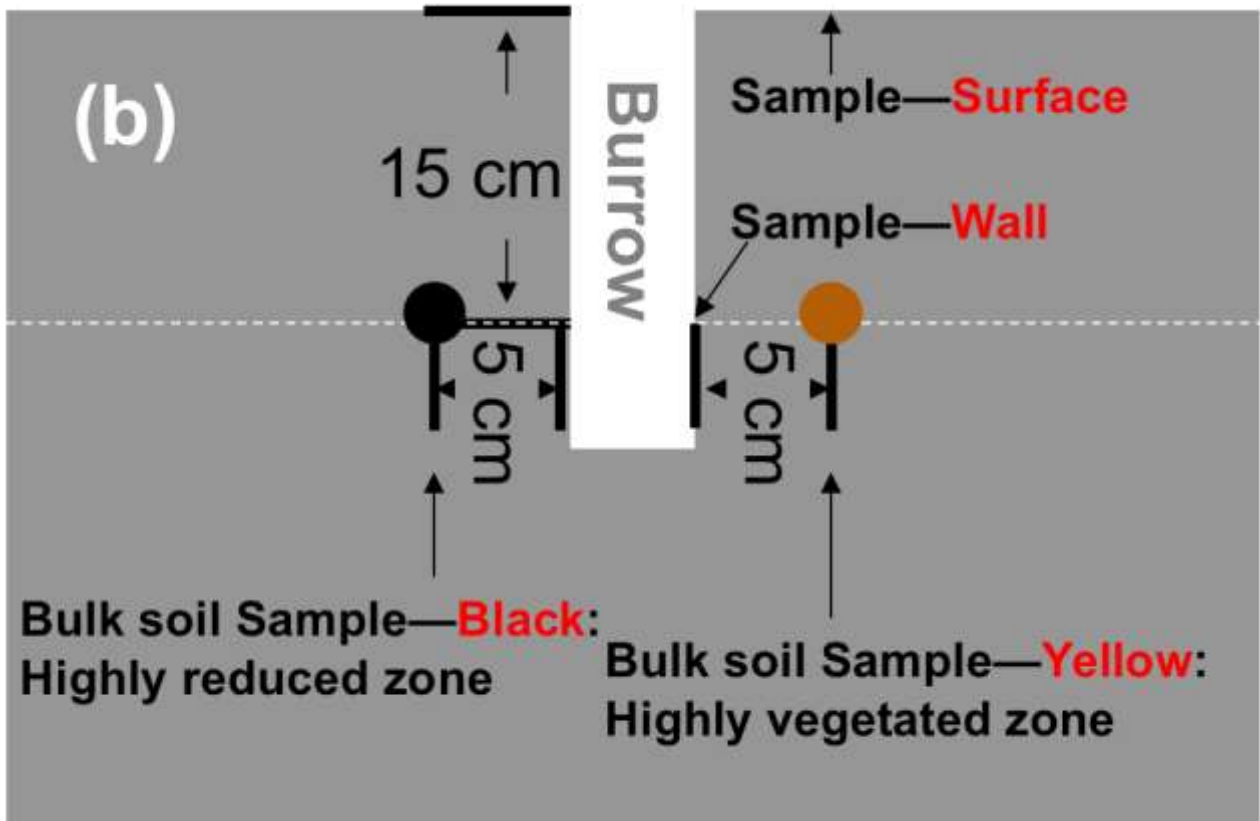


Fig. 1-b

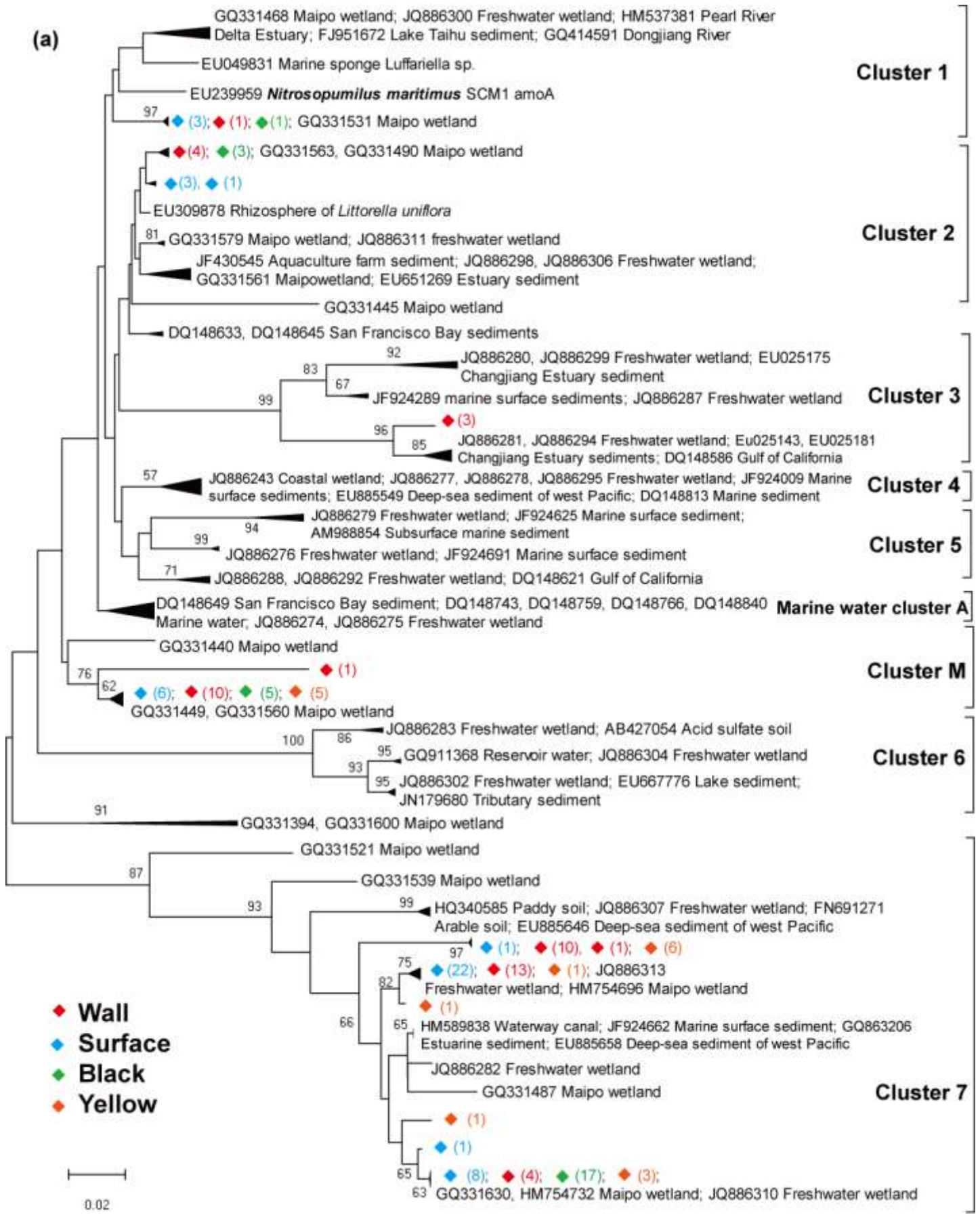


Fig. 2-a

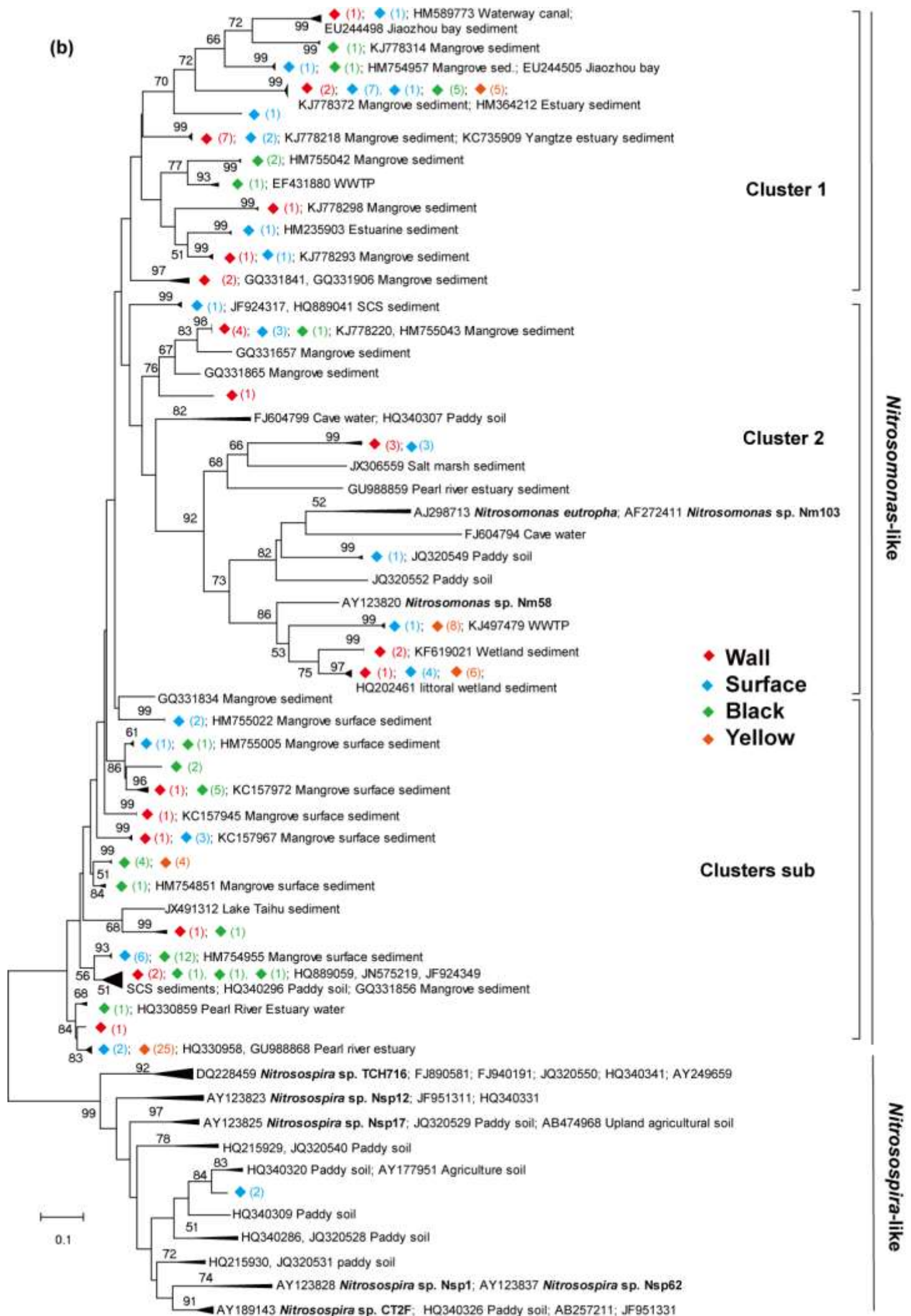


Fig. 2-b

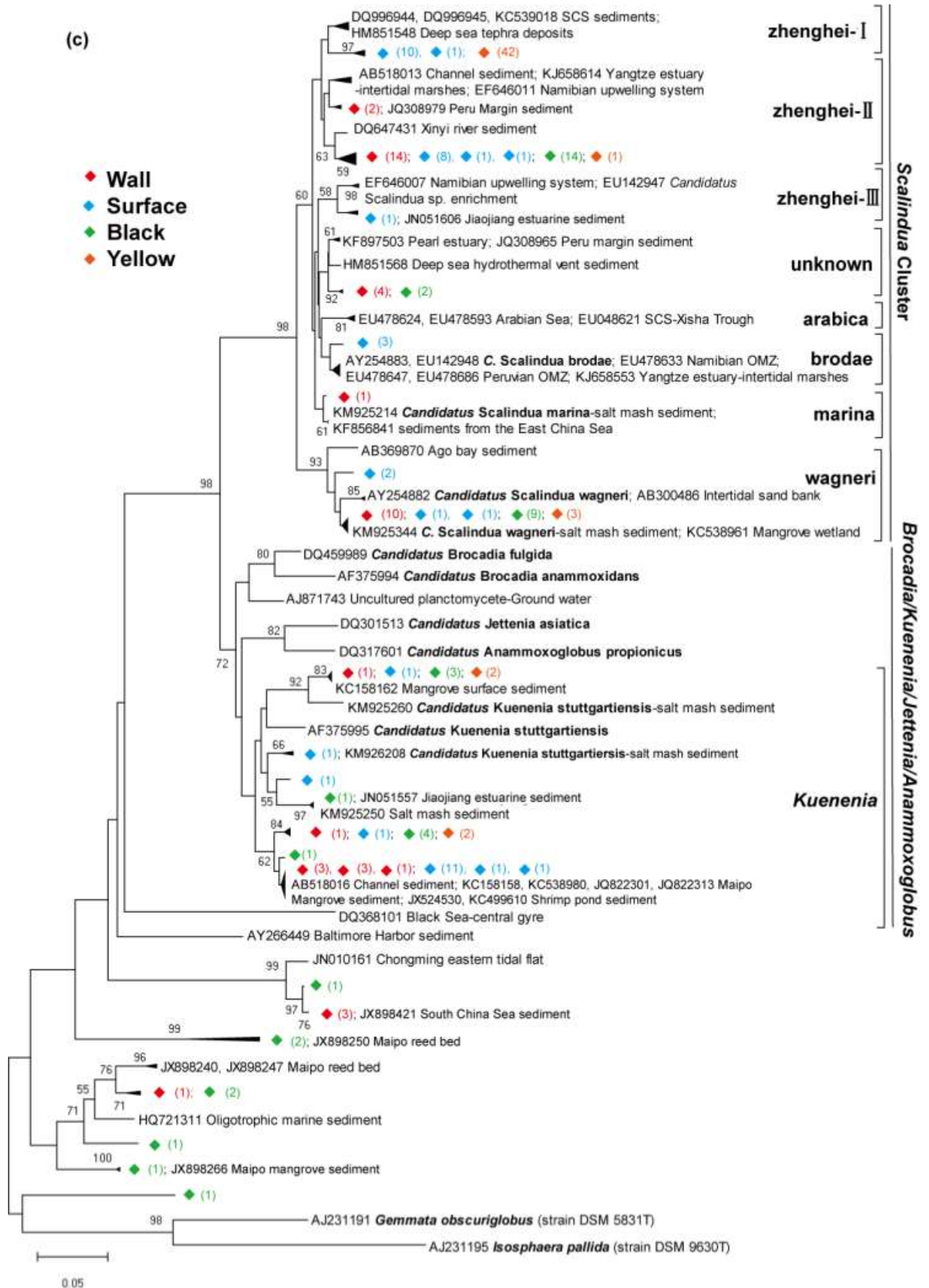


Fig. 2-c

(d)

- ◆ Wall
- ◆ Surface
- ◆ Black
- ◆ Yellow

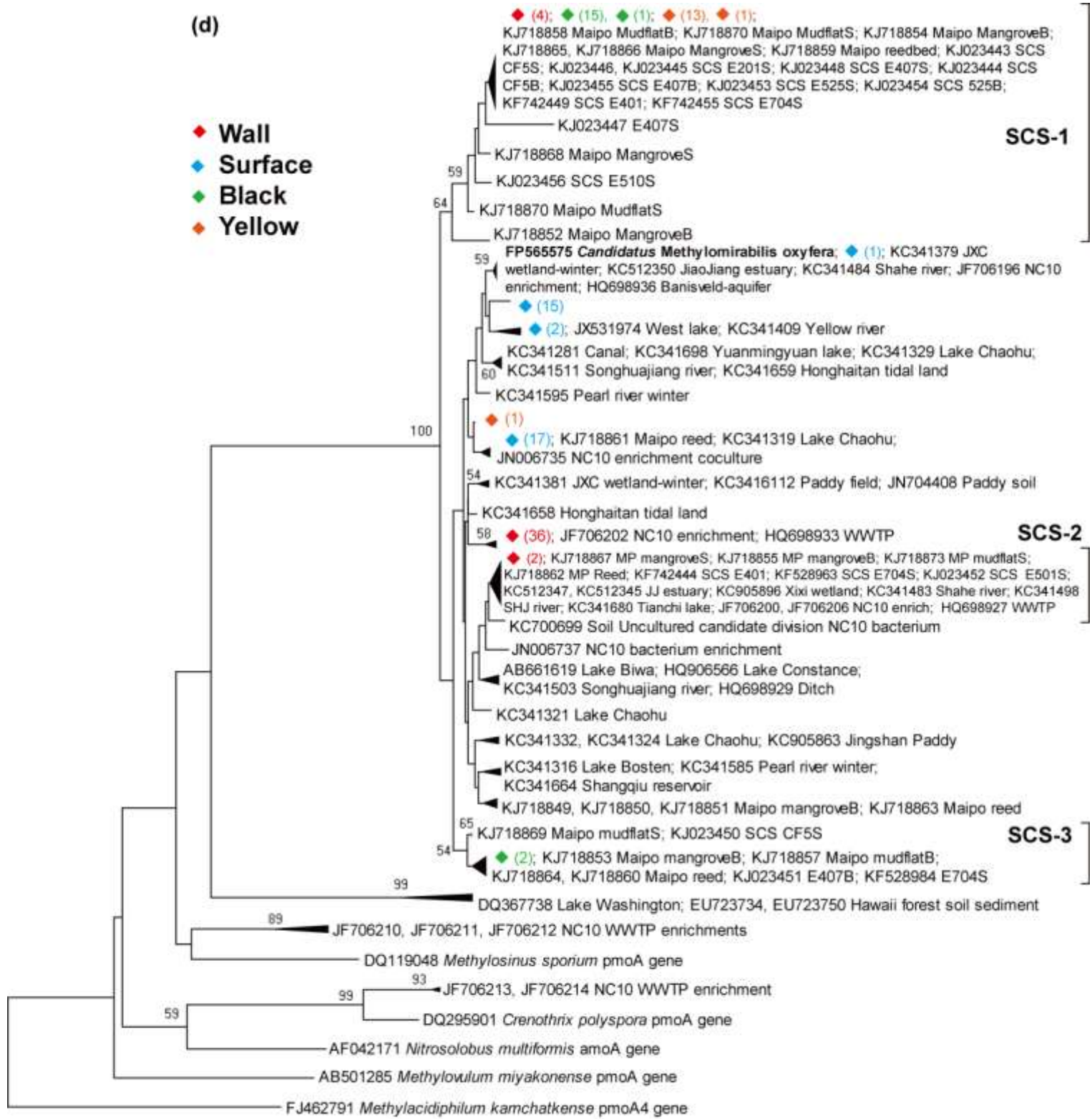


Fig. 2-d

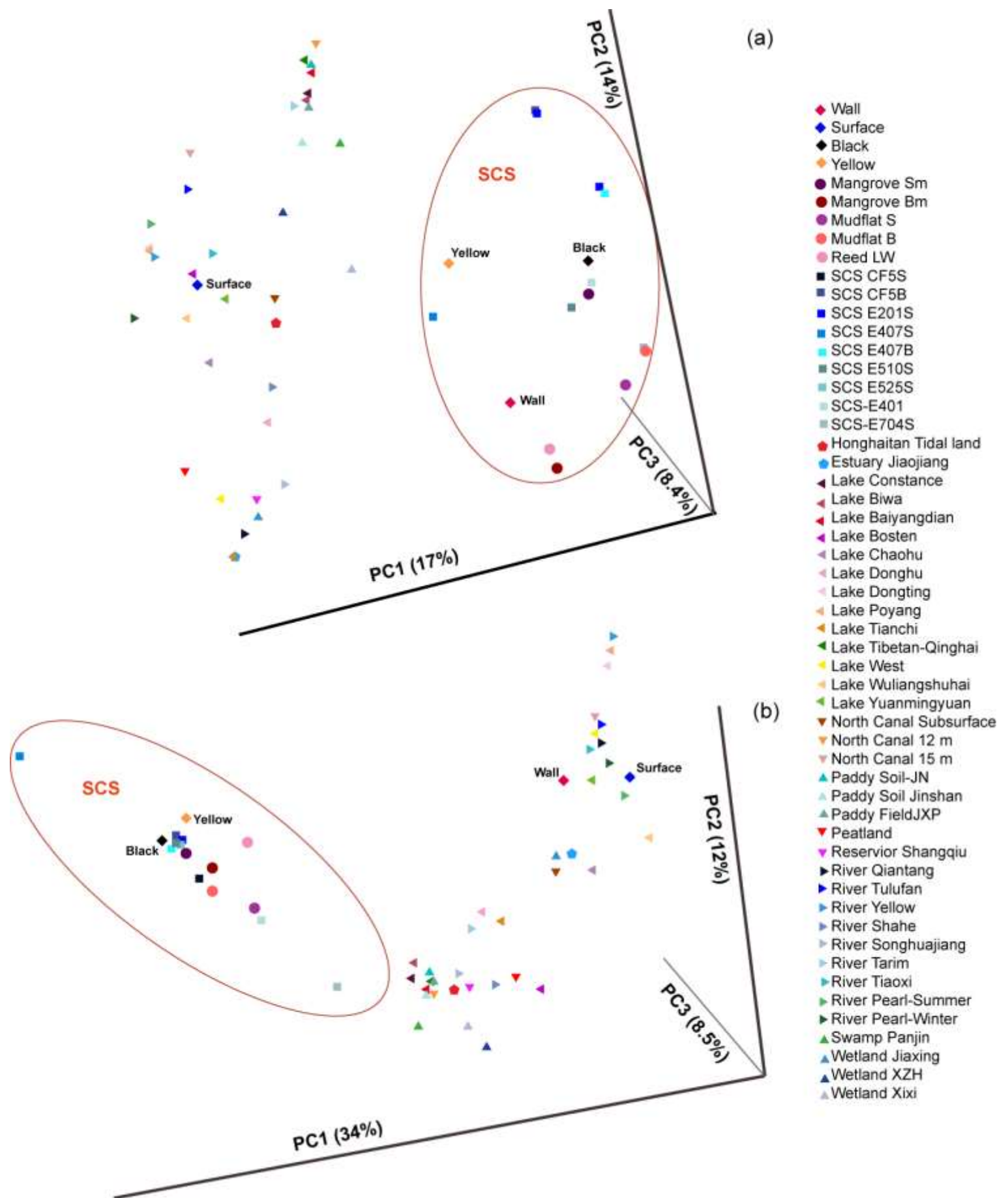


Fig. 3

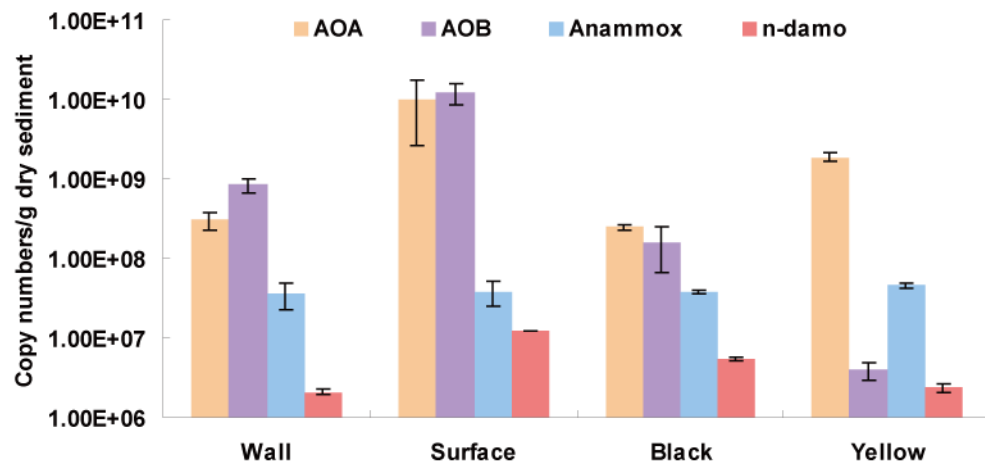


Fig. 4

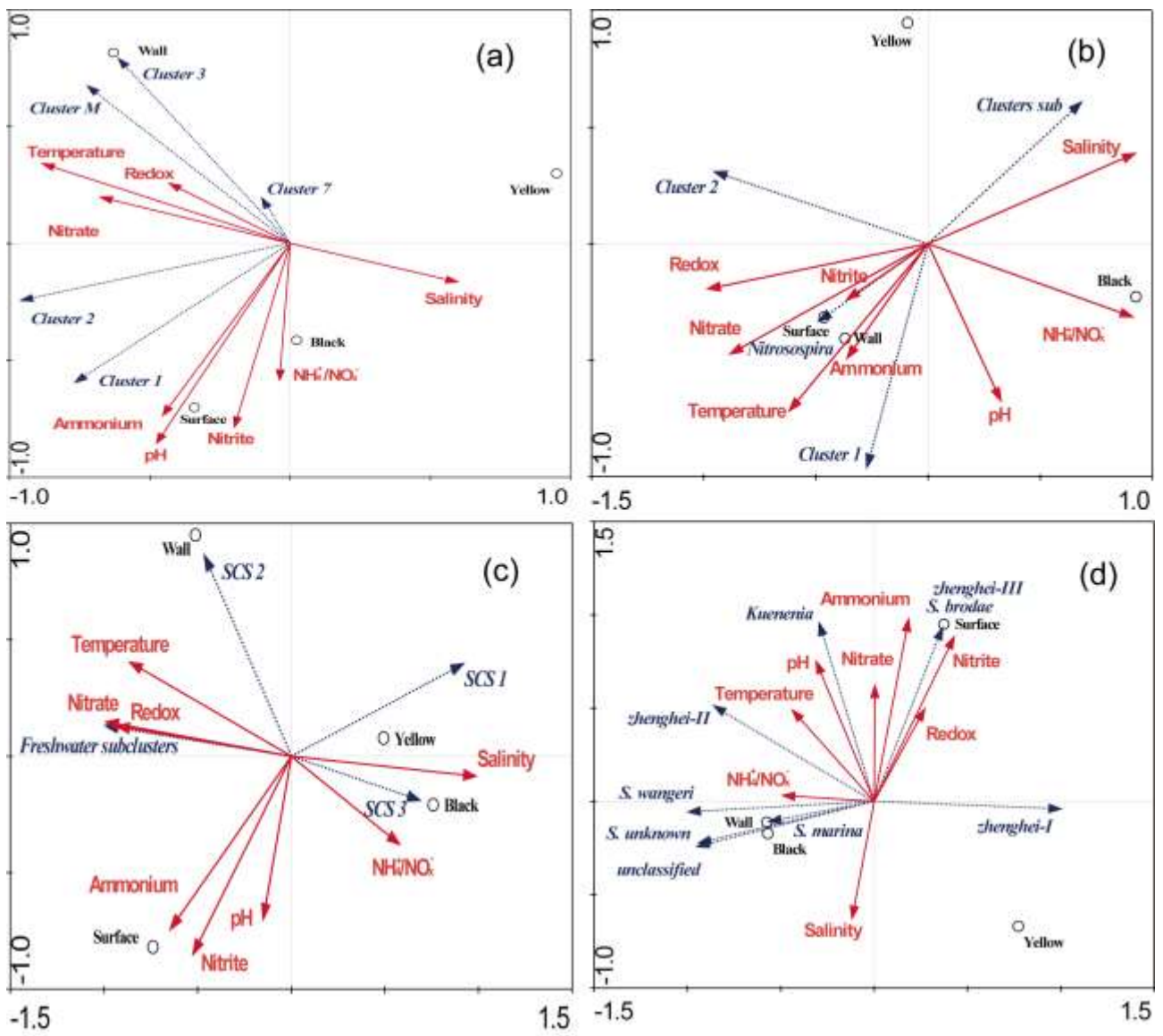


Fig. 5