

1 **Bacterial community assembly in a typical estuarine marsh with multiple**
2 **environmental gradients**

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11 **Running title:**

12 Bacterial community assembly in an estuarine marsh

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18 **Table S1** Comparison of relative abundances of dominant bacterial phyla (relative
 19 abundance >3 % at least in one sample) among sediment transects.

Taxonomy (%)	Sediment		
	S-N	S-M	S-F
Gammaproteobacteria	17.10(1.64)a	18.94(1.19)a	13.33(2.44)b
Deltaproteobacteria	16.34(0.95)a	15.93(1.35)a	14.22(4.11)b
Chloroflexi	14.68(1.54)b	15.32(1.29)b	18.90(2.39)a
Bacteroidetes	6.28(2.11)b	8.68(1.23)b	10.61(3.02)a
Alphaproteobacteria	6.93(1.29)a	6.25(0.42)b	6.74(1.25)a
Planctomycetes	4.97(1.32)b	7.43(1.59)a	4.79(1.53)b
Betaproteobacteria	8.45(2.69)a	4.91(1.10)b	8.89(2.40)a
Actinobacteria	3.25(0.54)a	1.81(0.37)b	2.47(1.33)a
Acidobacteria	3.30(0.77)c	5.90(1.22)b	6.94(0.71)a
Verrucomicrobia	1.83(0.84)b	2.66(0.85)a	2.91(0.56)a
Gemmatimonadetes	1.58(0.66)b	2.60(0.21)b	4.05(2.29)a
Others	15.29(5.61)a	9.56(0.52)c	6.15(3.08)b

20 Values are means(SD). Values at the same columns followed by different letters differed
 21 significantly at $P < 0.05$. See Table 1 for transect notation.

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23 **Table S2** ADONIS test of the sediment transects based on the bacterial Bray-Curtis
24 distance.

	16S rRNA gene	
	R ²	<i>P</i> -value
S-N vs S-M	0.5794	0.010
S-N vs S-F	0.3885	0.029
S-M vs S-F	0.4493	0.004

25 Data in bold are significantly correlated ($P < 0.05$). For abbreviations, see Table 1.

Table S3 Spearman's rank correlations between physico-chemical properties (Euclidean distance) and bacterial β -diversity (Bray-Curtis distance) for the sediment samples.

Variables	R ²	ρ
TN	0.3165	0.001
AP	0.3158	0.001
Silt	0.2942	0.003
pH	0.2833	0.001
Clay	0.2820	0.003
Fe _d	0.2702	0.003
Sand	0.2696	0.003
Ammonia	0.2558	0.003
OC	0.2258	0.004
EC	0.2237	0.008
AK	0.1759	0.023

ρ : correlation coefficients between physico-chemical properties and bacterial community distance derived from Mantel test with 9999 permutations. The abbreviations of physico-chemical properties are the same as shown in Table 1

Figure S1 Post-mean estimates and credible intervals (95%) of α -diversity indexes of the sediment bacterial communities. (A) Shannon's diversity and evenness. (B) PD index and observed species. See Table 1 for transect notation.

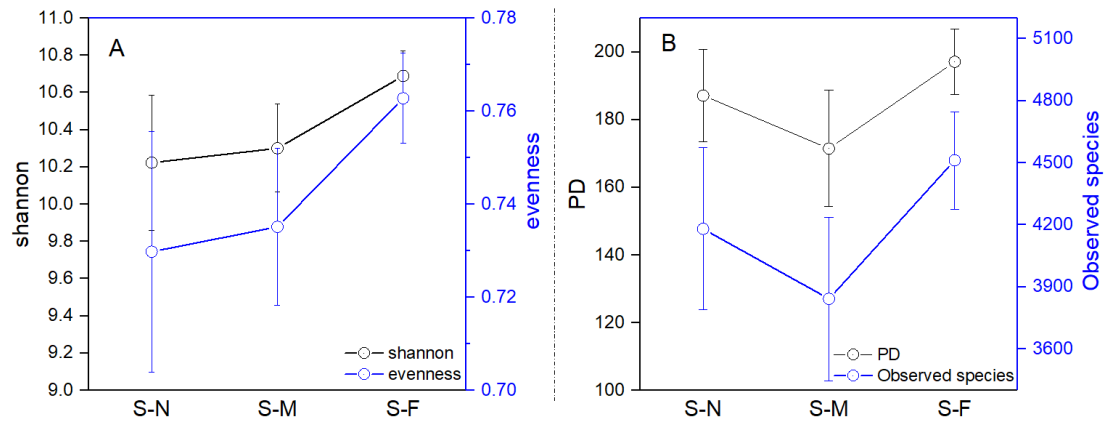


Figure S2 Relative abundances of the dominant bacterial phyla (relative abundance >3 % at least in one sample) in the sediment samples. The predominant phyla of *Proteobacteria*, is grouped at the class level. Five biological replicates are displayed in separate stacked bars. See Table 1 for transect notation. Average relative abundances of all phyla and significant effects across sampling groups are listed in Supplementary materials Table 1.

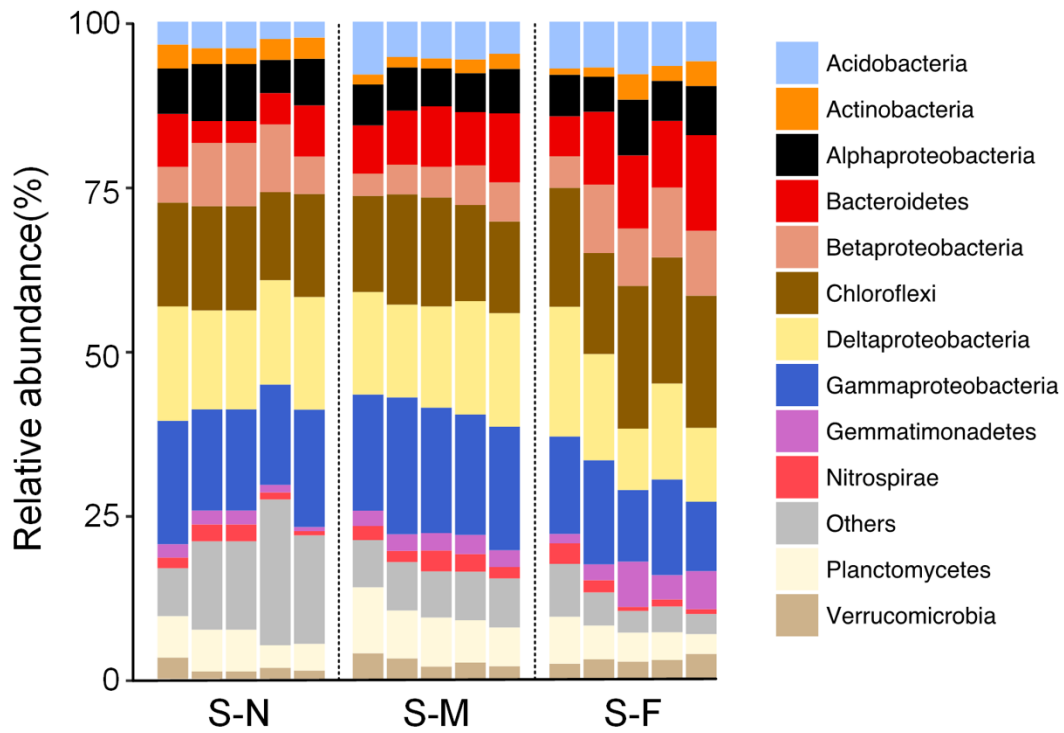


Figure S4 Degree distribution for S-N, S-M and S-F networks.

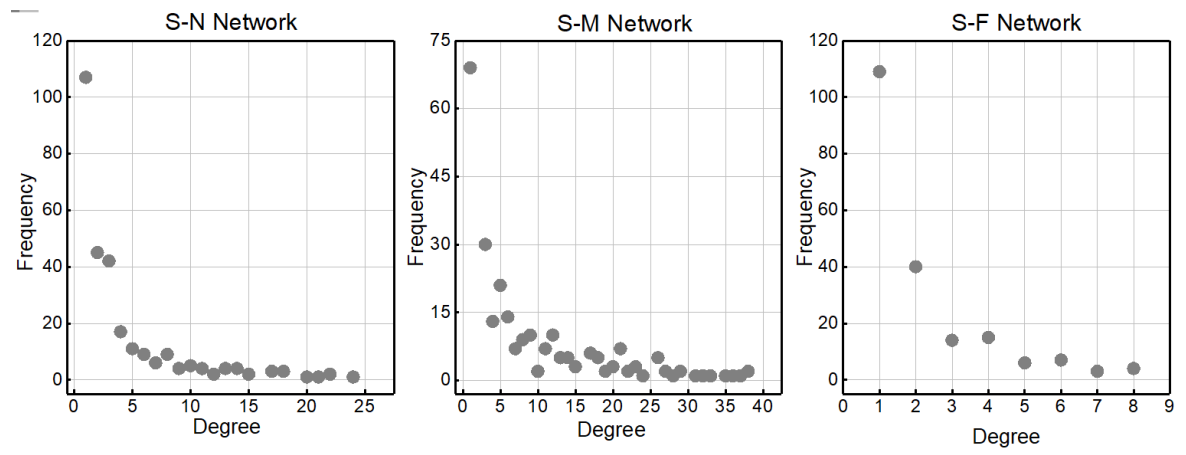


Figure S5 Modularity of co-occurrence network in each sediment transect. Each dot represents a bacterial phylotype (an OTU clustered at 97%). Nodes are colored according to modularity class. The modules have different colors, and nodes in modules with less than 20 nodes are colored gray. Node size is proportional to the number of connections (that is, degree). Edges represent the correlation between two nodes. A connection represents a strong ($r > 0.8$) and significant ($P < 0.01$) correlation. See Table 1 for transect notation.

