2	stronger niche segregation in summer than in winter subtropical bay
3	
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Bacterioplankton metacommunity processes across thermal gradients: weaker species sorting but

SUPPLEMENTARY MATERIALS

21 Table S1 Significance tests of bacterioplankton community compositions (BCCs) across the

thermal gradients in winter and in summer seawater, respectively. Permutational multivariate

23 analysis of variance (PERMANOVA) based on Bray-Curtis dissimilarity matrices was used. Bold

24	values	indicate	the	test	results	s with a	<i>p</i> <	0.05.
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~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	winte	er	summer		
group –	F	р	F	р	
Whole	5.919	0.001	9.284	0.001	
S1 vs S2	4.319	0.001	1.445	0.098	
S1 vs S3	5.192	0.001	6.183	0.024	
S1 vs S4	4.494	0.001	8.123	0.008	
S1 vs S5	18.608	0.007	12.942	0.032	
S2 vs S3	3.462	0.056	6.621	0.012	
S2 vs S4	3.499	0.038	8.840	0.001	
S2 vs S5	3.210	0.036	12.533	0.001	
S3 vs S4	1.321	0.409	3.035	0.001	
S3 vs S5	9.660	0.001	11.662	0.001	
S4 vs S5	3.148	0.001	6.306	0.021	

- **Table S2** Co-presence and exclusion links of the bacterioplankton co-occurrence subnetworks in
- 26 winter and in summer seawater under thermal impacts.

Parameters	Winter subnetwork	Summer subnetwork
Co-presence links between temperature related and unrelated nodes	719	593
Exclusion links between temperature related and unrelated nodes	188	323
Exclusion links /total links between temperature related and unrelated nodes	0.21	0.35
Co-presence links between temperature unrelated nodes	507	207
Exclusion links between temperature unrelated nodes	173	323
Exclusion links /total links between temperature unrelated nodes	0.26	0.61



29 Fig. S1 Environmental characteristics across the thermal gradient in winter seawater.



31 Fig. S2 Environmental characteristics across the thermal gradient in summer seawater.





Fig. S3 Heatmap depicts the thermal impacts on the distributions of top 50 keystone OTUs in

- 34 winter (a) and in summer (b) co-occurrence networks. A refers Actinobacteria, B refers
- 35 Bacteroidetes, C refers Cyanobacteria, Al refers Alphaproteobacteria, G refers
- 36 Gammaproteobacteria, P refers Planctomycetes, V refers Verrucomicrobia and O refers other rare
- 37 phyla with the relative abundance of the total sequences < 1%.



- 39 Fig. S4 Heatmap depicts the distributions of OTUs (nodes) that have significant correlations with
- 40 temperature in winter (a) and in summer (b) seawater. A refers Actinobacteria, B refers
- 41 Bacteroidetes, C refers Cyanobacteria, Al refers Alphaproteobacteria, G refers
- 42 Gammaproteobacteria, P refers Planctomycetes, V refers Verrucomicrobia and O refers other rare
- 43 phyla with the relative abundance of the total sequences < 1%.



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Fig. S5 The subnetworks of OTUs that have non-significantly correlations with temperature in both winter (a) and summer seawater (b) under thermal impacts. The networks are visualized with group attribute layouts based on phylum or subphylum. Colors of the nodes indicate different phylum or subphylum OTUs. The orange line indicates a positive interaction between two OTUs (nodes), while the black line indicates a negative interaction.