**Supplementary information for**

Spatiotemporal variations dictate stable and resilient microbiome interactions in the Chesapeake Bay

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There are 5 tables and 3 figures in the supplementary information.

**Table S1.** Top 10 nodes based on abundance/degree/betweenness centrality in the network of all samples

**Table S2.** Top 10 nodes with highest abundance/degree/betweenness centrality in each season

**Table S3.** Top 10 nodes with the highest abundance/degree/betweenness centrality in upper Bay and Lower Bay

**Table S4.** Stepwise changes of network properties with removal of top ranked 10 nodes (betweenness centrality)

**Table S5.** Correspondence of microbial groups and environmental factors for structural equation model

**Fig. S1.** Map of the Chesapeake Bay showing sampling stations.

**Fig. S2.** Node connectedness (normalized degree) of microbial networks in each season, as well as the upper Bay and lower Bay.

**Fig. S3.** The multivariate regression tree (MRT) for Chesapeake Bay microbial samples with explanatory variables (environmental data). Red numbers represent the split times, and the variance explained by each split. The black numbers show the average frequency of all taxa in the samples: the total sample number before split.