SUPPLEMENTARY MATERIAL

for

How variations in DOM components affect the stability of microbial communities in drinking water supply system: from source to tap

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Table S1. Summary of the physiochemical characteristics of water samples.

Sample	pH	DO (mg/L)	Cond (μS/cm)	Turbidity (NTU)	COD_{Mn} (mg/L)	TOC (mg/L)	NH_4^+-N (mg/L)	NO_2^--N (mg/L)
SW-1	6.89	7.76	38.6	1.14	0.10	0.6	0.0180	0.002
SW-2	7.83	8.09	67.2	2.68	0.36	1.2	0.0530	0.024
SW-3	8.87	8.93	75.0	2.94	0.78	1.4	0.1490	0.036
SW-4	8.55	9.29	62.3	6.14	0.24	0.7	0.0710	0.019
RW-1	7.21	7.98	61.1	3.64	0.15	0.1	0.0540	0.032
RW-2	6.97	8.10	104.4	3.98	0.07	0.5	0.0110	0.001
RW-3	7.03	8.84	81.3	3.17	0.56	0.6	0.0530	0.028
RW-4	7.95	6.21	39.5	1.36	0.08	0.3	0.0130	0.002
RW-5	7.17	6.17	68.8	4.28	0.12	0.1	0.0170	0.004
RW-6	7.16	8.16	67.7	2.79	0.08	0.1	0.0100	0.003
RW-7	7.94	6.66	39.8	4.07	1.02	0.1	0.0190	0.003
TP1-1	7.01	7.60	46.4	1.37	1.05	0.1	0.0010	0.003
TP1-2	6.90	4.42	70.9	2.2	2.24	1.5	0.0130	0.008
TP1-3	7.33	9.23	56.4	1.25	1.25	0.5	0.0090	0.006

Sample	**pH**	**DO (mg/L)**	**Cond (μS/cm)**	**Turbidity (NTU)**	**COD_{Mn} (mg/L)**	**TOC (mg/L)**	**NH_4^+-N (mg/L)**	**NO_2^--N (mg/L)**
TP1-4	7.16	9.70	59.8	1.37	1.17	0.1	0.0360	0.002
TP1-5	7.27	10.30	58.8	1.24	1.16	0.1	0.0240	0.001
TP1-6	6.79	10.34	59.6	0.07	1.14	0.1	0.0060	0.002
TP1-7	6.76	9.42	59.1	0.07	0.63	0.1	0.0001	0.003
TP2-1	7.36	8.85	61.7	5.6	0.12	0.1	0.0270	0.026
TP2-2	7.12	8.19	69.3	10.1	0.05	0.1	0.0250	0.003
TP2-3	7.17	8.33	66.9	8.4	0.03	0.1	0.0380	0.004
TP2-4	7.13	8.23	66.4	1.65	0.03	0.1	0.0003	0.003
TP2-5	7.15	8.01	68.0	0.15	1.45	0.1	0.0340	0.004
TP2-6	7.16	8.38	70.7	0.11	1.06	0.1	0.0150	0.003
TP3-1	6.98	7.25	79.4	2.41	0.17	0.3	0.0020	0.005
TP3-2	7.06	7.69	83.2	5.64	0.19	0.4	0.0100	0.006
TP3-3	7.07	9.30	81.8	1.7	0.05	0.3	0.0320	0.003
TP3-4	7.11	10.19	81.4	0.26	0.59	0.1	0.0150	0.003
TP3-5	7.12	10.68	86.8	0.08	0.09	0.1	0.0190	0.002

Sample	**pH**	**DO (mg/L)**	**Cond (μS/cm)**	**Turbidity (NTU)**	**COD_{Mn} (mg/L)**	**TOC (mg/L)**	**NH_4^+-N (mg/L)**	**NO_2^--N (mg/L)**
TP3-6	7.17	9.90	84.8	0.09	0.04	0.1	0.0170	0.003
DN1-1	9.51	8.03	98.0	3.87	0.34	0.1	0.0180	0.001
DN1-2	7.15	8.66	87.2	0.056	0.02	0.1	0.0030	0.002
DN1-3	7.38	9.78	70.8	0.21	0.03	0.1	0.0070	0.003
DN1-4	7.12	9.83	69.2	0.36	0.02	0.1	0.0000	0.004
DN1-5	7.23	9.20	60.3	1.84	0.04	0.1	0.0230	0.001
DN1-6	7.22	10.04	66.5	0.114	0.04	0.1	0.0010	0.002
DN1-7	7.27	7.61	61.2	0.23	0.04	0.1	0.0120	0.005
DN1-8	7.11	9.63	72.2	0.61	0.04	0.1	0.0190	0.004
DN1-9	6.90	6.86	61.0	0.86	1.23	0.1	0.0190	0.007
DN1-10	7.48	10.26	84.0	0.29	0.02	0.1	0.0130	0.005
DN1-11	7.27	10.45	87.4	0.41	0.17	0.5	0.0190	0.004
DN2-1	7.34	10.96	82.1	0.25	0.05	0.1	0.0010	0.004
DN2-2	7.24	11.24	80.7	0.5	0.05	0.2	0.0000	0.004
DN2-3	7.39	10.35	68.1	0.93	0.03	0.1	0.0070	0.001

Sample	**pH**	**DO (mg/L)**	**Cond (μS/cm)**	**Turbidity (NTU)**	**COD_{Mn} (mg/L)**	**TOC (mg/L)**	**NH_4^+-N (mg/L)**	**NO_2^--N (mg/L)**
DN2-4	8.84	9.40	78.3	1.36	0.02	0.1	0.0150	0.004
DN2-5	7.31	9.53	66.5	0.58	0.07	0.1	0.0040	0.003
DN2-6	7.35	9.53	65.4	0.31	0.03	0.1	0.0002	0.002

Table S2. The detailed information of FI, BIX, and HIX indexes.

Index	Environmental significance	Reference
FI	A measure of the source and degradation status of DOM. An FI > 1.9 indicates the sample is primarily endogenous biological organic matter, while an FI < 1.4 suggests the sample is primarily terrestrial organic matter	(Mcknight et al., 2001)
BIX	A measure of the extent of localized contamination can be linked to recent biological processes. When BIX>1 indicates a source such as biological or bacterial; and a smaller BIX indicates a weaker autochthonous source signature.	(Huguet et al., 2009)
HIX	A measure of humification, with higher humification leading to increased stability of DOM. The HIX index is proportional to the degree of organic matter humification, with higher HIX values reflecting the presence of complex DOM components such as high molecular weight aromatic compounds, and HIX>0.8 indicating a significant increase in humic content caused by humic acid-like organic components.	(Zsolnay et al., 1999)

Table S3. Alpha diversity indices in the drinking water distribution system.

		Chao1	Shannon	Simpson	Pielou
RW	Mean	475	4.48	0.96	0.51
	Median	455	4.50	0.97	0.51
TP	Mean	277	3.29	0.89	0.41
	Median	219	3.34	0.91	0.41
DN	Mean	197	2.79	0.87	0.37
	Median	178	2.91	0.90	0.37

Table S4. Network properties in Network RW, TP, and DN.

Network indexes	RW	TP	DN
degree range	52 ~ 76	100 ~ 124	31 ~ 41
closeness centrality range	0.27 ~ 1.0	0.45 ~ 0.64	0.4 ~ 1.0
betweenness centrality range	0 ~ 3000	2.0 ~ 1239.6	0.0 ~ 100.0
nodes	561	264	76
edges	4549	6906	778
average degree	16.217	52.318	20.474
network diameter	13	4	5
modularity	0.558	0.336	0.237
average clustering coefficient	0.578	0.649	0.679
average path length	4.114	2.070	2.000

Table S5. The 8 observed variables (TOC, NO_2^--N, DO, C1, C2, total protein-like, Shannon, AVD) of structural equation model.

TOC	NO_2^--N	DO	C1	C2	Total protein like	Shannon	AVD
0.6	0.002	7.76	3.310	3.671	0.650	4.961	0.061
1.2	0.024	8.09	11.450	8.711	0.623	4.422	0.045
1.4	0.036	8.93	9.174	6.581	0.647	4.681	0.047
0.7	0.019	9.29	9.662	7.780	0.646	4.497	0.046
0.1	0.003	8.16	10.783	5.618	0.779	4.094	0.041
0.1	0.003	6.66	9.517	5.552	0.760	3.865	0.045
0.1	0.032	7.98	13.040	6.149	0.783	4.846	0.045
0.5	0.001	8.10	16.774	10.006	0.725	4.398	0.044
0.6	0.028	8.84	15.060	8.093	0.727	4.487	0.047
0.1	0.003	7.60	5.493	4.972	0.697	4.656	0.062
1.5	0.008	4.42	10.940	9.511	0.602	3.891	0.072
0.5	0.006	9.23	5.540	5.038	0.698	4.718	0.054
0.1	0.002	9.70	4.919	3.846	0.688	2.257	0.059
0.1	0.001	10.30	3.470	2.698	0.709	2.722	0.059
0.1	0.002	10.34	2.601	1.838	0.772	2.527	0.035
0.1	0.026	8.85	7.052	6.097	0.649	4.027	0.045
0.1	0.003	8.19	1.714	2.225	0.688	3.911	0.076
0.1	0.003	8.23	5.056	3.229	0.721	3.891	0.065
0.1	0.004	8.01	4.198	2.608	0.737	4.435	0.072
0.1	0.003	8.38	2.440	0.791	0.830	3.271	0.037
0.3	0.005	7.25	13.685	9.433	0.691	4.398	0.050
0.4	0.006	7.69	11.397	8.318	0.675	4.487	0.066

TOC	NO_2^--N	DO	C1	C2	Total protein like	Shannon	AVD
0.3	0.003	9.3	10.478	6.355	0.703	4.594	0.065
0.1	0.003	10.19	9.957	6.481	0.697	3.390	0.061
0.1	0.002	10.68	9.425	5.495	0.710	3.398	0.065
0.1	0.003	9.9	7.956	4.493	0.715	3.338	0.030
0.1	0.001	9.2	4.087	1.627	0.790	2.873	0.026
0.1	0.002	10.04	3.555	1.502	0.790	2.873	0.029
0.1	0.005	7.61	4.191	2.149	0.786	3.117	0.029
0.1	0.004	9.63	3.396	1.021	0.812	3.321	0.024
0.1	0.007	6.86	5.350	3.938	0.726	2.955	0.026
0.1	0.005	10.26	6.924	3.524	0.746	2.301	0.025
0.5	0.004	10.45	8.060	4.281	0.741	2.867	0.025
0.1	0.002	8.66	7.323	4.409	0.720	3.011	0.029
0.1	0.003	9.78	2.039	1.170	0.800	2.993	0.030
0.1	0.004	9.83	3.134	0.994	0.841	2.157	0.027
0.1	0.004	10.96	6.371	3.894	0.732	2.955	0.033
0.2	0.004	11.24	6.859	3.839	0.729	2.374	0.030
0.1	0.001	10.35	2.209	1.209	0.798	2.464	0.026
0.1	0.004	9.4	2.351	1.213	0.833	3.070	0.029
0.1	0.003	9.53	5.019	1.084	0.854	2.775	0.027
0.1	0.002	9.53	2.454	1.330	0.820	3.028	0.032

Table S6. Standardized total effects of structural equation model.

	TOC	NO_2^--N	C2	DO	C1	Shannon	Total protein like
NO_2^--N	0.532	0.00	0.00	0.00	0.00	0.00	0.00
C2	0.609	0.183	0.00	0.00	0.00	0.00	0.00
DO	-0.397	0.00	0.00	0.00	0.00	0.00	0.00
C1	0.533	0.174	0.949	0.114	0.00	0.00	0.00
Shannon	0.391	0.560	0.305	-0.434	-0.613	-0.062	-0.423
Total protein like	-0.526	-0.124	-0.677	0.101	1.361	0.138	-0.062
AVD	0.296	0.056	0.308	-0.189	-0.619	0.306	-0.426

Supproting Figures

Figure captions

Figure S1. Changes in fluorescent substance components.

Figure S2. Fluorescence index (FI), humus index (HIX), and biological index (BIX) of DOM in the whole process of water supply system.

Figure S3. Alpha Diversity (Chao1, Simpson, Shannon, and Pielou) in the water source (RW), water plant (TP), and water supply network (DN) in the water supply system.

Figure S4. Microbial community assembly mechanisms in WSS based on (a) null model and (b) neutral community model (NCM) analysis.

Figure S5. Heatmap of the taxonomic differences of microbial communities in different treatments based on Bray-Curtis distance.

Figure S6. The Average Variation Degree (AVD) for each group in the whole process of the water supply system.

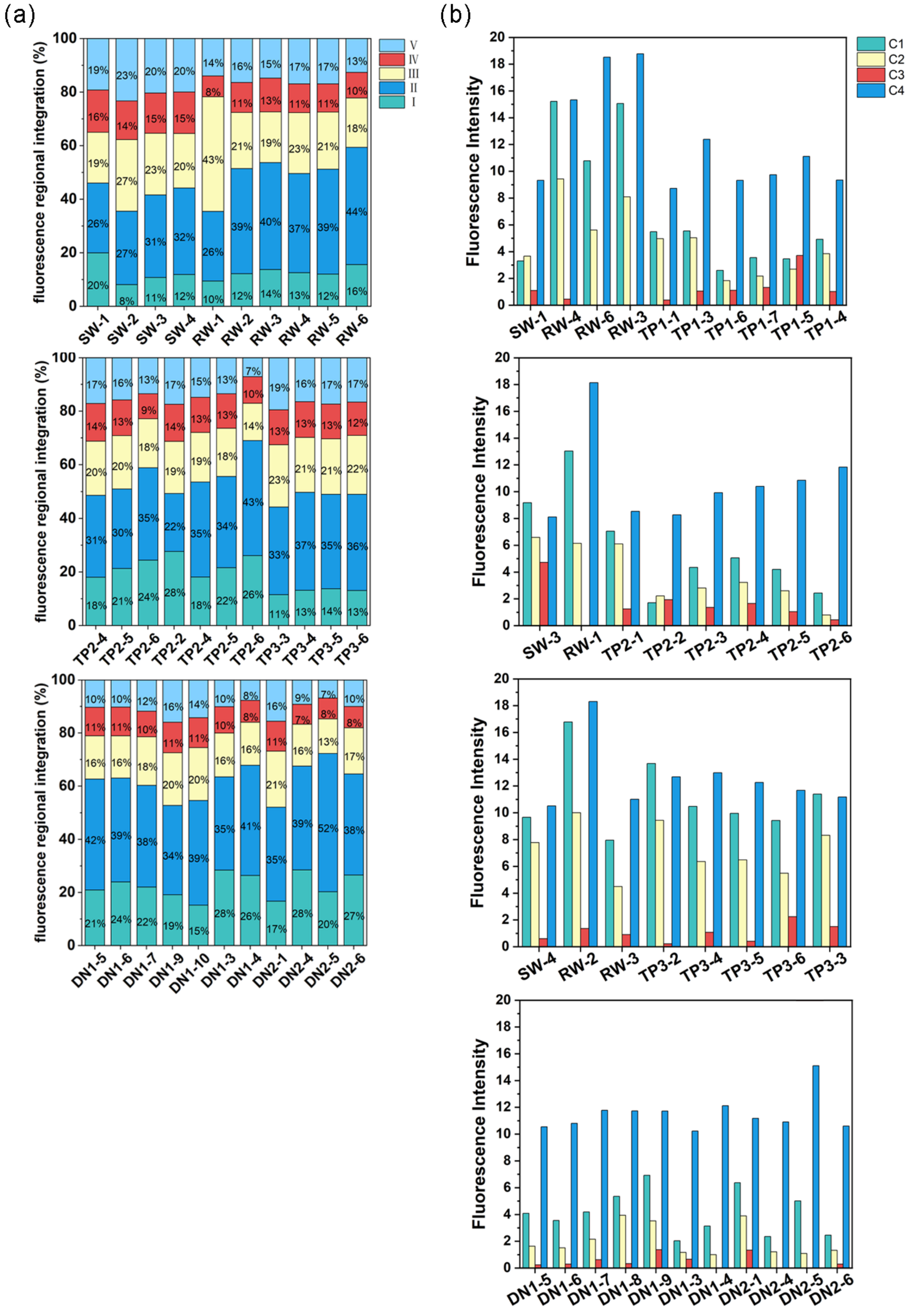

Figure S1. Changes in fluorescent substance components. Fluorescence regional integration (FRI) (a) and change of fluorescent substances during water treatment in each water plant (b).

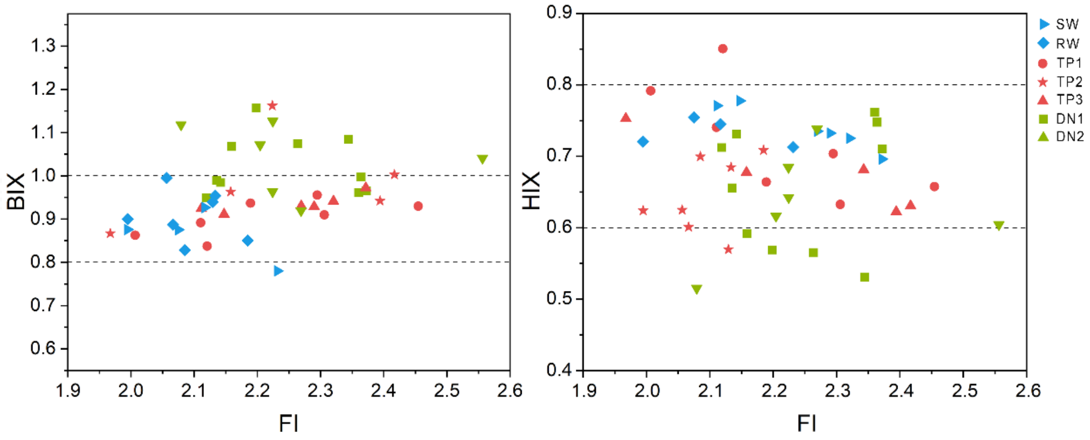

Figure S2. Fluorescence index (FI), biological index (BIX), and humus index (HIX) of DOM in the whole process of water supply system.

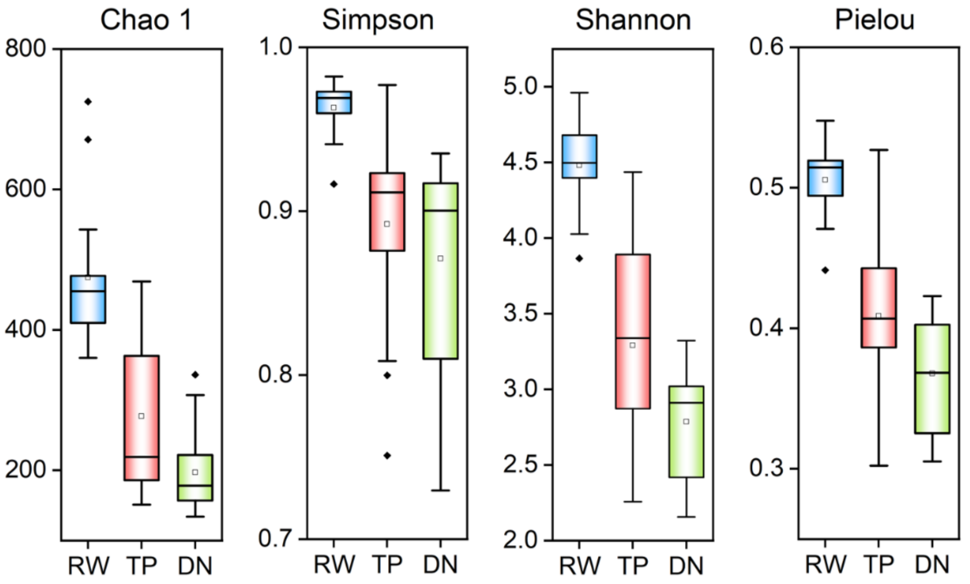

Figure S3. Alpha Diversity (Chao1, Simpson, Shannon and Pielou) in the water source (RW), water plant (TP), and water supply network (DN) in the water supply system.

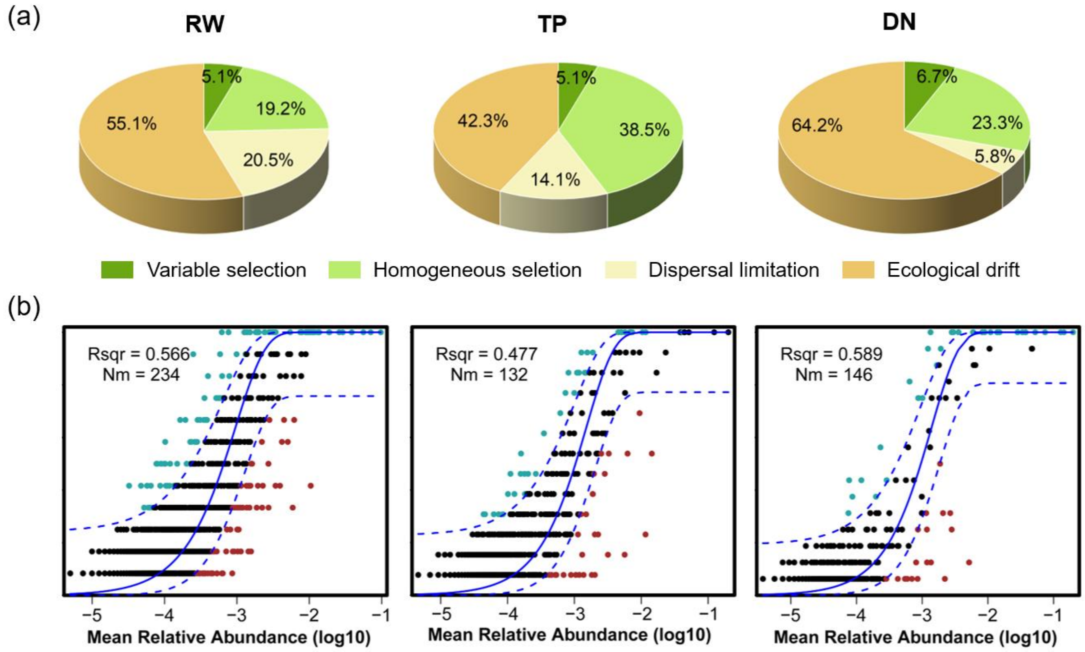

Figure S4. Microbial community assembly mechanisms based on (a) null model and (b) neutral community model (NCM) analysis. (a) homogeneous selection and variable selection are deterministic processes. Dispersal limitation and ecological drift are stochastic processes. (b) Rsqr determines the overall fit to this model, Nm reflects the diffusivity of species. The neutral-model predictions were represented as solid lines, and the dashed lines indicate the 95% confidence intervals.

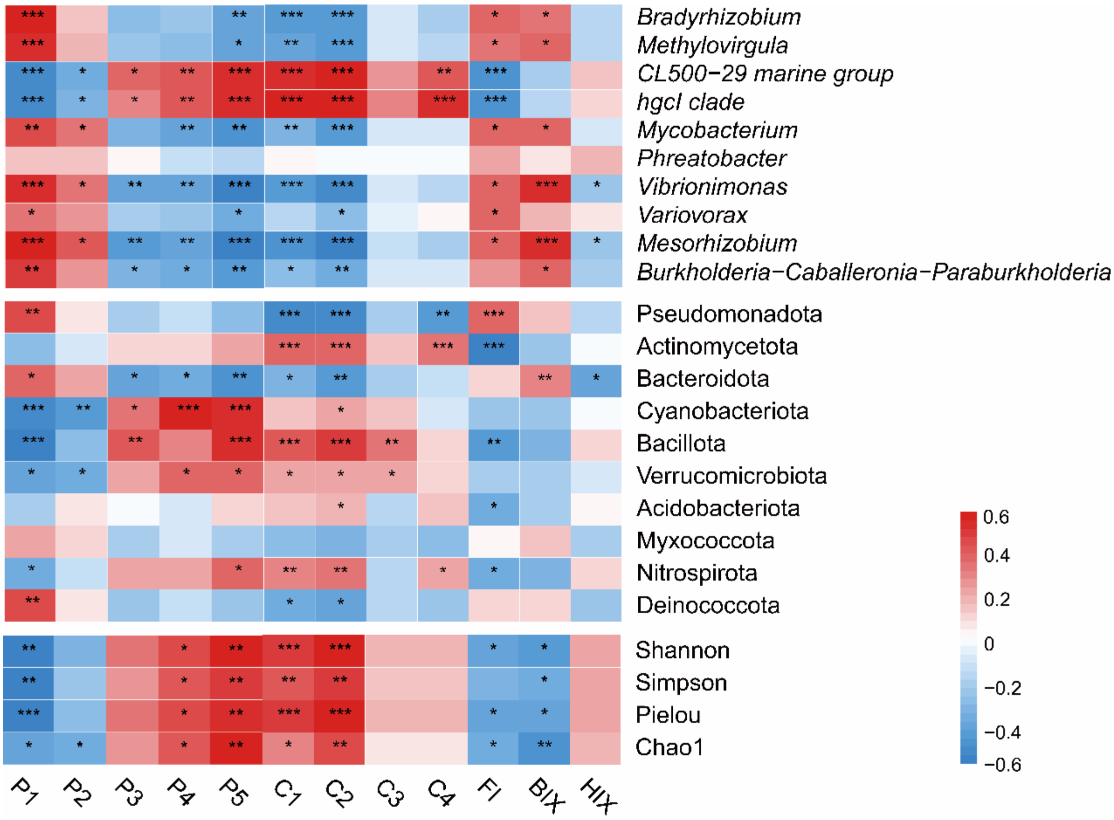

Figure S5. Heatmap of the taxonomic differences of microbial communities in different treatments based on Bray-Curtis distance. Bray-Curtis distances were calculated using relative abundances of ASVs. Negative and positive correlation coefficients are shown in blue and red, respectively. **p <0.05, ***p < 0.01. In the context of fluorescence region integrals, P1 to P5 represent the proportions of fluorescence responses in regions I to V, respectively. These proportions are calculated as the ratio of the EEM (excitation-emission matrix) volume in a specific region to the total EEM volume.

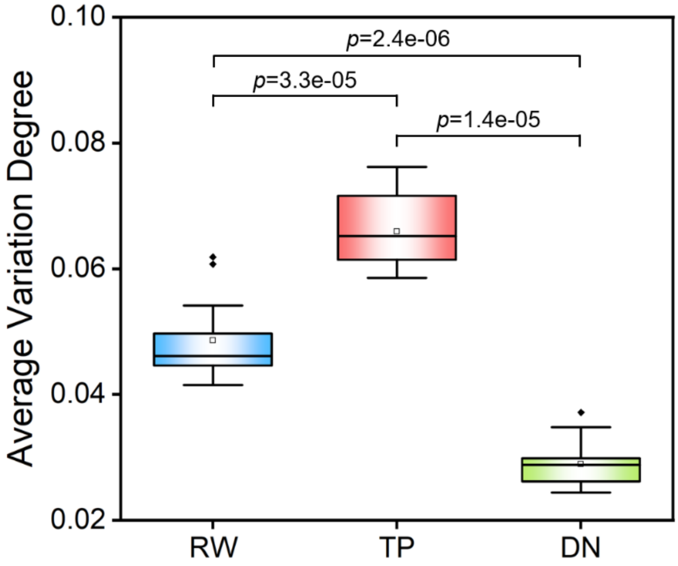

Figure S3. The Average Variation Degree (AVD) for each group in the whole process of the water supply system. A lower AVD value suggests higher microbiome stability, indicating that a microbial community with higher biodiversity is more resistant to disturbances. The *p*-value was calculated by Wilcox test.