

Supporting information

Title: Reproducible microbial community dynamics of two drinking water systems treating similar source waters.

Sarah Potgieter^a, Zihan Dai^b, Minette Havenga^a, Solize Vosloo^c, Makhosazana Sigudu^d, Ameet Pinto^c and Stefanus Venter^{a}*

Author Affiliations

^a Rand Water Chair in Water Microbiology, Department of Biochemistry, Genetics and Microbiology, University of Pretoria, South Africa.

^b School of Engineering, University of Glasgow, United Kingdom.

^c Department of Civil and Environmental Engineering, Northeastern University, Boston, USA.

^d Scientific Services, Rand Water, Vereeniging, South Africa.

***Corresponding author:**

*Prof. Stephanus N Venter,
Department of Biochemistry, Genetics and Microbiology,
University of Pretoria,
Pretoria,
South Africa, 0002
Email: fanus.venter@up.ac.za*

Supplementary tables

Table S1: Water quality parameters of the source water from both systems

Sample	Date	Source water quality			Treatment process	
		Alkalinity	Turbidity (NTU)	pH	Lime Silica CO2 Ferric	Polymeric Coag lime (low)
System R						
R_SW1	2016/02/22	61	64	8.09	46%	54%
R_SW2	2016/03/22	63	60	7.88	0%	100%
R_SW3	2016/04/19	63	61	8.04	0%	100%
R_SW4	2016/05/17	64	62	8.07	0%	100%
R_SW5	2016/06/20	61	55	8.11	0%	100%
R_SW6	2016/07/18	63	66	8.35	0%	100%
R_SW7	2016/08/16	60	77	8.23	18%	82%
R_SW8	2016/09/19	58	85	8.13	31%	69%
System S						
S_SW1	2016/02/01	58	58	8.2	0%	100%
S_SW2	2016/03/07	67	57	8.3	0%	100%
S_SW3	2016/04/04	59	62	8.3	0%	100%
S_SW4	2016/05/09	58	67	8.5	0%	100%
S_SW5	2016/06/06	59	58	8.7	0%	100%
S_SW6	2016/07/04	57	71	8.5	0%	100%
S_SW7	2016/08/01	57	75	8.8	0%	100%
S_SW8	2016/08/29	51	71	8.7	0%	100%

Table S2: Water quality parameters for DWDS sites (CHLA – DS2) from both systems for the dates of sample collection (February – September 2016). Blank cells in the table indicate parameter data was not available at specific locations on the dates of sampling

System R													
Sample name	Month	Conductivity (mS/m)	DOC (mg/l as C)	Free Cl ₂ (mg/l)	Total Cl ₂ (mg/l)	NH ₂ Cl (mg/l)	Alkalinity (mg/l CaCO ₃)	NH ₄ (mg/l as N)	NO ₂ (mg/l as N)	NO ₃ (mg/l as N)	pH	Temp (°C)	Turbidity (NTU)
R_CHLA1	FE	20.1	3.09	2.2			65.6	0.05		0.08	8.08	24.7	0.272
R_CHLA2	Mar	21.7	2.84	2.2			69.9	0.02		0.13	7.71	23.4	0.274
R_CHLA3	Apr	20.7	3.4	2.08			70.9	0.02		0.11	8.17	18.3	0.273
R_CHLA4	May	20.5	3.22	2.2			62.1	0.01	0	0.15	8.2	16.8	0.243
R_CHLA5	Jun	20.9	2.63	2.06			69.8	0.01		0.18	8.02	13.2	0.26
R_CHLA6	Jul	21.5		2.3			69	0.01	0	0.22	7.67	11.4	0.297
R_CHLA7	Aug	20.7		2.12			68.2		0	0.24	8.22	13.4	0.292
R_CHLA8	Sept	19		2.09			64.4			0.21	8.12	14.8	0.288
R_CHLB1	Feb	26.2		1.09	1.13	0.04	81.7				7.64	24.1	0.305
R_CHLB2	Mar	19.9		0.96	1.06	0.1	67.4				7.68	22.9	0.294
R_CHLB3	Apr	21.3		1.15	1	0.05	69.5				8.07	20.9	0.281
R_CHLB4	May	21.1		1.23	1.29	0.06	68.3				7.85	16.4	0.31
R_CHLB5	Jun	21.1		1.18	1.22	0.04	75.2				8.31	15.2	0.264
R_CHLB6	Jul	20.7		1.85	1.82	0.08	69.7	0.05	0	0.21	8.08	12.3	0.262
R_CHLB7	Aug	19.5		1.31	1.36	0.05	60.3		0	0.24	8.15	13.6	0.338
R_CHLB8	Sept	18.6		1.37	1.49	0.12	62.9	0.38		0.2	7.72	17.9	0.386
R_CHM1	Feb	21.4		0.07	2.16	2.09	71.4				7.83	24.6	0.299
R_CHM2	Mar	20.1		0.1	2.05	1.95	67				7.61	22.8	0.301
R_CHM3	Apr	20.4		0.1	1.95	1.85	65.9				8.03	22.2	0.265
R_CHM4	May	22.3		0.03	1.85	1.82	73.8				7.79	16.5	0.227
R_CHM5	Jun	20.5		0.04	1.8	1.76	71.6				8.25	15	0.26
R_CHM6	Jul	19.8		0.07	1.9	1.83	75.4	0.06			8.21	12.9	0.294
R_CHM7	Aug	18.7		0.11	1.79	1.68	56.7	0.12			7.85	14.1	0.347

R_CHM8	Sept	18.4		0.04	1.54	1.5	61.4	0.08			7.77	17.2	0.268
R_DS1A1	Feb	21.9	2.81	0.05	1.6	1.55	71.8	0.27	0.06	0.09	7.98	24.4	0.221
R_DS1A2	Mar	19.7	2.8	0.2	1.81	1.61	68.5	0.33	0.02	0.13	7.71	23.4	0.269
R_DS1A3	Apr	25	3.223	0.18	1.84	1.67	76.4	0.3772	0.0051	0.07	7.79	21.2	0.26
R_DS1A4	May	21.5	3.1912	0.05	1.92	1.87	66.6	0.4	0.0109	0.35	8.14	17.9	0.261
R_DS1A5	Jun	21.5	2.974	0.26	2.2	1.94	74.4	0.39	0.0089	0.17	8.03	14.3	0.282
R_DS1A6	Jul	17.7		0.06	1.91	1.85	66.2	0.36	0.01	0.3	8.17	13.5	0.254
R_DS1A7	Aug	20.7		0.04	1.54	1.5	69.5	0.22	0	0.45	8.15	13.4	0.364
R_DS1A8	Sept	18.8		0.2	1.84	1.64	63.7	0.35		0.24	8.4	16.1	0.306
R_DS1B1	Feb	21.2	2.85	0.08	1.97	1.89	73.5	0.29	0.01	0.16	7.99	24.5	0.308
R_DS1B2	Mar	20.3	2.71	0.58	1.32	0.74	101.6	0.37	0.01	0.2	7.72	23.8	0.359
R_DS1B3	Apr	22	3.22	0.56	1.9	1.34	73.3	0.44	0.01	0.14	8.11	21.5	0.239
R_DS1B4	May	21.4	3.27	0.08	1.95	1.87	66.4	0.4	0.01	0.08	8.02	17.8	0.19
R_DS1B5	Jun	21.3	3.43	0.16	2.05	1.89	73.4	0.39	0.01	0.17	8.02	14.5	0.318
R_DS1B6	Jul	17.5		0.07	1.75	1.68	67.4	0.35	0.01	0.29	8.1	14.5	0.347
R_DS1B7	Aug	20.8		0.02	1.67	1.65	68.9	0.26	0	0.31	8.13	13.4	0.269
R_DS1B8	Sept	18.8		0.17	1.84	1.67	66.8	0.32		0.25	8.19	16.1	0.32
R_DS2A1	Feb	21.6	2.97	0.05	1.33	1.28	70.9	0.24	0.2	0.19	8.12	25.8	0.21
R_DS2A2	Mar	20.6	3.62	0.72	1.44	0.72	68.8	0.24	0.15	0.18	7.86	23.6	0.328
R_DS2A3	Apr	21.1	2.68	0.63	1.66	1.03	67.9	0.39	0.09	0.31	7.74	22.3	0.265
R_DS2A4	May	21.7	3.29	0.05	1.69	1.64	72	0.67	0.02	0.7	8.18	19.4	0.264
R_DS2A5	Jun	21	3.12	0.13	2.01	1.88	76.1	0.42	0.02	0.51	8.19	16.9	0.237
R_DS2A6	Jul	19.5		0.41	1.85	1.44	69.9	0.35	0.01	0.26	8.24	14.3	0.349
R_DS2A7	Aug	21.4		0.05	1.53	1.48	65	0.23	0	0.44	8.19	14.5	0.267
R_DS2A8	Sept	19		0.11	1.48	1.37	60.7	0.31		0.17	7.97	19.1	0.313
R_DS2B1	Feb	21.4	3.31	0.07	1.27	1.2	70.3	0.28	0.17	0.2	8.05	25.8	0.211
R_DS2B2	Mar	20.5	2.71	0.65	1.21	0.56	68.1	0.21	0.16	0.18	7.72	23.5	0.291
R_DS2B3	Apr	20.3	2.72	0.26	1.65	1.39	74.3	0.42	0.07	0.1	7.88	22.3	0.338
R_DS2B4	May	21.7	3.3	0.02	1.62	1.6	70.6	0.76	0.02	0.19	8.04	19.7	0.227
R_DS2B5	Jun	21.1	3.08	0.04	1.96	1.92	76.4	0.41	0.02	0.19	8.11	16.8	0.247

R_DS2B6	Jul	19.4		0.14	1.67	1.53	68.9	0.36	0.01	0.29	8.13	14.4	0.373
R_DS2B7	Aug	20.8		0.05	1.57	1.52	63.1	0.27	0	0.25	8.11	14.4	0.251
R_DS2B8	Sept	18.8		0.1	1.57	1.47	69.6	0.31		0.19	7.79	18.7	0.29
R_DS2C1	Feb	21.5		0.04	1.18	1.14	71.2				8.12	25.9	0.209
R_DS2C2	Mar	21		0.26	1.3	1.04	67.6	0.26	0.17	0.35	7.85	23.9	0.344
R_DS2C3	Apr	20.3		0.23	1.63	1.4	66.4				8.06	21.6	0.289
R_DS2C4	May	21.5		0.12	1.75	1.63	72				8.16	18.6	0.316
R_DS2C5	Jun	20.1		0.09	1.9	1.81	71.9	0.39		0.16	8.06	17.9	0.249
R_DS2C6	Jul	18		0.02	1.83	1.81	66.3	0.37	0.17	0.21	8.12	13.8	0.266
R_DS2C7	Aug	20.9		0.06	1.62	1.56	64	0.1	0.01	0.3	8.14	14.1	0.364
R_DS2C8	Sept	19		0.12	1.51	1.39	59.9	0.31	0	0.2	7.93	18.1	0.257

System S

Sample name	Month	Conductivity (mS/m)	DOC (mg/l as C)	Free Cl ₂ (mg/l)	Total Cl ₂ (mg/l)	NH ₂ Cl (mg/l)	Alkalinity (mg/l CaCO ₃)	NH ₄ (mg/l as N)	NO ₂ (mg/l as N)	NO ₃ (mg/l as N)	pH	Temp (°C)	Turbidity (NTU)
S_CHLA1	Feb				2.1						8.25		0.22
S_CHLA2	Mar				2.1						8.25		0.18
S_CHLA3	Apr	17.7		2	2.3						8.6	21.09	0.12
S_CHLA4	May	19.3		1.85	1.94						8.3	18.83	0.13
S_CHLA5	Jun	19.9		2	1.85						8.4	16.06	0.14
S_CHLA6	Jul	19		2.25	1.99						7.99	14.58	0.26
S_CHLA7	Aug	19.3		2.1	2.13						8.35	14.57	0.15
S_CHLA8	Sept				1.9								
S_CHLB1	Feb			1.08	1.1	0.02						24.6	0.3
S_CHLB2	Mar			1.2	1.25	0.05						24.2	0.25
S_CHLB3	Apr	18.3		1.14	1.25	0.11					7.85	22	0.27
S_CHLB4	May			1.16	1.22	0.06						18.4	0.35
S_CHLB5	Jun			0.77	0.84	0.07						16	0.25
S_CHLB6	Jul	18		1.2	1.18	0.13		0.11	0.03	0.15	8.24	11.7	0.15
S_CHLB7	Aug	22		1.39	1.39	0.14	71	0.05	0.03	0.29	7.85	11.3	0.26

S_CHLB8	Sept	17		1.3	1.27	0.04		0.05	0.03	0.38	7.98	14.1	0.24
S_CHMA1	Feb	19	3.5	0.06	2.28	2.22	77	0.287	0.03	0.1	8.31	25.9	0.32
S_CHMA2	Mar	19	2.8	0.07	2.44	2.37	70	0.243	0.03	0.1	7.85	25	0.25
S_CHMA3	Apr	22	4	0.05	2.16	2.11	75	0.36	0.03	0.13	8.13	21.2	0.32
S_CHMA4	May	19	3.3	0.06	2.34	2.28	80	0.47	0.03	0.1	8.12	19.1	0.31
S_CHMA5	Jun	21	3.1	0.07	2.2	2.13	74	0.37	0.03	0.18	8.03	16.1	0.27
S_CHMA6	Jul	18		0.01	2.2	2.19			0.03	0.23	8.24	12.3	0.2
S_CHMA7	Aug	21		0.06	2.02	1.96	69		0.03	0.28	7.98	12.4	0.32
S_CHMA8	Sept	17		0.07	2.16	2.09			0.03	0.22	8	15.7	0.22
S_CHMB2	Mar	20	2.8	0.06	1.94	1.88	72	0.27	0.03	0.1	7.88	21.7	0.25
S_CHMB3	Apr	23	3.3	0.05	2.18	2.13	79	0.3	0.03	0.15	7.91	21.4	0.31
S_CHMB4	May	19	3	0.1	2.1	2	79	0.48	0.03	0.17	8.12	18.1	0.34
S_CHMB5	Jun	21	3.1	0.05	2.12	2.07	74	0.37	0.03	0.22	8.42	16	0.25
S_CHMB6	Jul	18	2.2	0.05	2.2	2.15	80		0.03	0.24	8.23	12	0.48
S_CHMB7	Aug	21	2.1	0.05	2.08	2.03	69		0.03	0.28	7.9	11.4	0.28
S_CHMB8	Sept			0.05	2.12	2.07						15.6	0.39
S_DS1A1	Feb	27	3.3	0.05	1.2	1.15	85	0.19	0.11	0.2	7.62	25.2	0.4
S_DS1A2	Mar	22	2.7	0.09	1.86	1.77	74	0.18	0.03	0.19	7.62	23.4	0.38
S_DS1A3	Apr	20	3.7	0.01	1.54	1.53	72	0.37	0.03	0.24	7.96	21.6	0.29
S_DS1A4	May	20	3.1	0.05	1.72	1.67	85	0.54	0.03	0.17	8.05	17	0.33
S_DS1A5	Jun	19	2.6	0.05	1.79	1.74	77	0.49	0.03	0.17	8.34	15.9	0.24
S_DS1A6	Jul	17		1.23	2.06	0.83		0.52	0.03	0.25	8	13.1	0.23
S_DS1A7	Aug	17		0.18	2.03	1.85		0.47	0.03	0.27	8.18	12.3	0.32
S_DS1A8	Sept	17		0.2	2.02	1.82		0.53	0.03	0.41	7.9	15	0.27
S_DS1B1	Feb	19	3.3	0.06	1.13	1.07	72	0.2	0.11	0.23	8.09	25.6	0.25
S_DS1B2	Mar	22	2.7	0.05	1.73	1.68	74	0.31	0.03	0.12	7.61	23.5	0.25
S_DS1B3	Apr	21	3.6	0.02	1.76	1.74	76	0.39	0.03	0.13	7.98	21.5	0.28
S_DS1B4	May	20	3.1	0.07	1.75	1.68	84	0.53	0.03	0.1	8.03	16.9	0.34
S_DS1B5	Jun	20	2.6	0.04	1.74	1.7	78	0.45	0.03	0.2	8.19	15.2	0.31
S_DS1B6	Jul	11		1.9	2	0.1		0.49	0.03	0.21	8.19	13.1	0.27

S_DS1B7	Aug	17		0.33	2.01	1.68		0.45	0.03	0.28	8.15	12.6	0.44
S_DS1B8	Sept	17		0.17	2.12	1.95		0.54	0.03	0.25	7.93	15	0.23
S_DS1C1	Feb	20	3.3	0.06	1.18	1.12	66	0.22	0.1	0.2	8.02	25.8	0.25
S_DS1C2	Mar	22	2.6	0.09	1.77	1.68	74	0.29	0.03	0.2	7.96	24.4	0.25
S_DS1C3	Apr	20	3.4	0.01	1.69	1.68	72	0.37	0.03	0.1	8.38	21.2	0.3
S_DS1C4	May	20	3	0.07	1.74	1.67	85	0.52	0.03	0.35	8.04	16.6	0.33
S_DS1C5	Jun	19	3.5	0.11	1.79	1.68	78	0.45	0.03	0.18	8.38	15.2	0.18
S_DS1C6	Jul	12		0.64	1.97	1.33		0.48	0.03	0.83	8.01	13.2	0.14
S_DS1C7	Aug	17		0.41	2.01	1.6		0.48	0.03	0.36	8.16	12.3	0.24
S_DS1C8	Sept	17		0.2	2.07	1.87		0.5	0.03	0.38	7.93	14.7	0.27
S_DS2A1	Feb	19	3.8	0.09	1.15	1.06	70	0.17	0.16	0.18	8.06	25.3	0.25
S_DS2A2	Mar	24	2.7	0.05	1.24	1.19	73	0.24	0.03	0.16	7.96	23.5	0.25
S_DS2A3	Apr	20	3.4	0.1	1.5	1.4	71	0.31	0.04	0.28	8.02	22.2	0.28
S_DS2A4	May	21	3.4	0.09	1.45	1.36	86	0.43	0.07	0.2	8.05	17.1	0.39
S_DS2A5	Jun	20	2.3	0.08	1.29	1.21	83	0.45	0.03	0.18	8.18	18	0.33
S_DS2A6	Jul	11		0.88	1.89	1.01		0.45	0.03	0.62	8.14	13.2	0.17
S_DS2A7	Aug	17		0.07	1.87	1.8		0.43	0.03	0.27	8.2	11.8	0.22
S_DS2A8	Sept	17		0.14	1.85	1.71		0.5	0.03	0.33	7.95	15.1	0.28
S_DS2B1	Feb	19	3.2	0.09	0.91	0.82	71	0.16	0.18	0.28	8.11	25	0.26
S_DS2B2	Mar	22	2.7	0.03	1.41	1.38	73	0.27	0.03	0.16	7.99	24.1	0.27
S_DS2B3	Apr	20	3.4	0.08	1.5	1.42	70	0.32	0.03	0.16	8.22	22.2	0.29
S_DS2B4	May	20	3.3	0.05	1.47	1.42	85	0.44	0.05	0.11	8.04	16.4	
S_DS2B5	Jun	20	2.3	0.06	1.67	1.61	84	0.42	0.03	0.2	8.27	16.7	0.3
S_DS2B6	Jul	12		0.5	1.92	1.42		0.47	0.03	0.26	8.18	13.1	0.25
S_DS2B7	Aug	17		0.08	1.98	1.9		0.45	0.03	0.27	8.24	11.7	0.23
S_DS2B8	Sept	17		0.14	1.79	1.65		0.5	0.03	0.42	7.95	14.8	0.21
S_DS2C1	Feb	18	3.3	0.03	0.93	0.9	66	0.11	0.16	0.23	7.92	24.4	0.28
S_DS2C2	Mar	22	2.7	0.05	1.53	1.48	74	0.25	0.03	0.22	8.01	24.6	0.29
S_DS2C3	Apr	20	3.2	0.06	1.49	1.43	69	0.32	0.03	0.1	7.83	22	0.31
S_DS2C4	May	21	3.2	0.04	1.64	1.6	81	0.5	0.03	0.35	8.37	16.3	0.36

S_DS2C5	Jun	19	2.5	0.04	1.53	1.49	77	0.43	0.03	0.18	8.36	16.4	0.39
S_DS2C6	Jul	12		0.37	1.99	1.62		0.45	0.03	0.21	8.28	13.2	0.26
S_DS2C7	Aug	17		0.42	2.05	1.63		0.52	0.03	0.27	8.23	11.8	0.22
S_DS2C8	Sept	17		0.1	1.92	1.82		0.52	0.03	0.25	7.95	15.1	0.23

Table S3: The number of samples collected and processed

Sample	Number of samples collected		Number of samples successfully sequenced	
	System R	System S	System R	System S
SW	8	8	7	6
FI	8	8	8	8
FB	8	8	8	8
FE	8	8	8	8
CHL	16	16	12	9
CHM	8	16	5	11
DS1	16	24	11	23
DS2	24	24	19	21

Table S4: Mean relative abundance of dominant bacterial phyla (> 0.1%) across all samples within the DWTPs and corresponding DWDS lines of both systems. Values depicted as *Mean* ± *SD* for each location within each system

System R									
Phyla	R_SW	R_FI	R_FB	F_FE	R_CHLA	R_CHLB	R_CHM	R_DS1	R_DS2
<i>Proteobacteria</i>	0.42 ± 0.07	0.23 ± 0.02	0.35 ± 0.1	0.3 ± 0.15	0.11 ± 0.09	0.16 ± 0.11	0.49 ± 0.28	0.56 ± 0.26	0.69 ± 0.18
<i>Alphaproteobacteria</i>	0.05 ± 0.02	0.05 ± 0.02	0.12 ± 0.07	0.12 ± 0.15	0.05 ± 0.03	0.05 ± 0.05	0.16 ± 0.15	0.13 ± 0.09	0.3 ± 0.18
<i>Gammaproteobacteria</i> <i>Betaproteobacteriales</i>	0.22 ± 0.04	0.12 ± 0.03	0.11 ± 0.05	0.12 ± 0.05	0.04 ± 0.07	0.07 ± 0.06	0.07 ± 0.04	0.22 ± 0.22	0.25 ± 0.16
<i>Gammaproteobacteria</i> Other	0.13 ± 0.08	0.05 ± 0.02	0.12 ± 0.06	0.05 ± 0.04	0.03 ± 0.02	0.04 ± 0.05	0.25 ± 0.29	0.21 ± 0.32	0.13 ± 0.15
<i>Deltaproteobacteria</i>	0.01 ± 0	0 ± 0	0 ± 0	0.01 ± 0.01	0 ± 0	0 ± 0	0.01 ± 0.02	0 ± 0	0.01 ± 0.01
<i>Epsilonproteobacteria</i>	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Unclassified <i>Proteobacteria</i>	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0.01	0 ± 0	0 ± 0
<i>Actinobacteria</i>	0.21 ± 0.07	0.31 ± 0.06	0.2 ± 0.07	0.28 ± 0.1	0.06 ± 0.13	0.09 ± 0.1	0.03 ± 0.02	0.04 ± 0.05	0.02 ± 0.04
<i>Bacteroidetes</i>	0.13 ± 0.09	0.17 ± 0.05	0.2 ± 0.03	0.14 ± 0.08	0.03 ± 0.06	0.12 ± 0.19	0.02 ± 0.03	0.04 ± 0.09	0.03 ± 0.03
<i>Planctomycetes</i>	0.06 ± 0.07	0.02 ± 0.02	0.03 ± 0.01	0.03 ± 0.03	0.18 ± 0.18	0.03 ± 0.06	0.25 ± 0.24	0.17 ± 0.15	0.14 ± 0.1
<i>Acidobacteria</i>	0.03 ± 0.02	0.12 ± 0.03	0.06 ± 0.03	0.13 ± 0.05	0.02 ± 0.04	0.01 ± 0.03	0.01 ± 0.02	0.02 ± 0.02	0.02 ± 0.02
<i>Cyanobacteria</i>	0.05 ± 0.03	0.02 ± 0.01	0.05 ± 0.03	0.01 ± 0	0.02 ± 0.02	0.1 ± 0.11	0.03 ± 0.02	0.02 ± 0.02	0.01 ± 0.01
<i>Verrucomicrobia</i>	0.03 ± 0.02	0.03 ± 0.01	0.03 ± 0.02	0.04 ± 0.02	0 ± 0.01	0.01 ± 0.02	0.02 ± 0.04	0.02 ± 0.02	0.01 ± 0.01
<i>Firmicutes</i>	0 ± 0	0 ± 0.01	0 ± 0	0 ± 0	0.01 ± 0.01	0.01 ± 0.02	0.01 ± 0.01	0.01 ± 0.02	0.01 ± 0.02
<i>Nitrospirae</i>	0 ± 0	0.01 ± 0	0 ± 0	0.01 ± 0.01	0 ± 0	0 ± 0	0 ± 0.01	0.01 ± 0.01	0.01 ± 0.01
<i>Chlorobi</i>	0.01 ± 0.01	0.01 ± 0.01	0.01 ± 0.01	0.01 ± 0	0 ± 0	0 ± 0.01	0 ± 0	0 ± 0	0 ± 0
<i>Chlamydiae</i>	0 ± 0	0.01 ± 0.01	0 ± 0	0.01 ± 0.01	0 ± 0	0 ± 0	0 ± 0	0 ± 0.01	0 ± 0
<i>Gemmatimonadetes</i>	0 ± 0	0.01 ± 0	0 ± 0	0.01 ± 0	0 ± 0	0 ± 0	0 ± 0	0.01 ± 0.01	0 ± 0
<i>Chloroflexi</i>	0 ± 0	0.01 ± 0.03	0 ± 0	0 ± 0	0 ± 0	0 ± 0.01	0 ± 0	0 ± 0	0 ± 0
<i>Elusimicrobia</i>	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.01 ± 0.02	0.01 ± 0.01
<i>Ignavibacteriae</i>	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.01 ± 0.01	0.01 ± 0.01
<i>Parcubacteria</i>	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
<i>Armatimonadetes</i>	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Unclassified	0 ± 0	0 ± 0	0.01 ± 0	0 ± 0	0.15 ± 0.07	0.07 ± 0.05	0.02 ± 0.02	0.01 ± 0.02	0.01 ± 0.01
Remaining 33 Phyla (<0.1%)	0.01 ± 0.01	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.01 ± 0.02	0 ± 0	0 ± 0	0 ± 0.01

System S									
Phyla	S_SW	S_FI	S_FB	S_FE	S_CHLA	S_CHLB	S_CHM	S_DS1	S_DS2
<i>Proteobacteria</i>	0.24 ± 0.09	0.27 ± 0.04	0.42 ± 0.12	0.26 ± 0.1	0.3 ± 0.19	0.26 ± 0.2	0.35 ± 0.24	0.76 ± 0.17	0.72 ± 0.18
<i>Alphaproteobacteria</i>	0.05 ± 0.01	0.04 ± 0.01	0.22 ± 0.18	0.05 ± 0.02	0.21 ± 0.14	0.17 ± 0.21	0.2 ± 0.18	0.49 ± 0.21	0.43 ± 0.19
<i>Gammaproteobacteria</i>									
<i>Betaproteobacteriales</i>	0.12 ± 0.04	0.18 ± 0.04	0.14 ± 0.07	0.18 ± 0.09	0.05 ± 0.06	0.02 ± 0.01	0.04 ± 0.03	0.18 ± 0.12	0.24 ± 0.15
Other	0.07 ± 0.05	0.04 ± 0.02	0.05 ± 0.03	0.03 ± 0.01	0.03 ± 0.03	0.06 ± 0.07	0.09 ± 0.15	0.06 ± 0.13	0.04 ± 0.1
<i>Deltaproteobacteria</i>	0.01 ± 0	0 ± 0	0.01 ± 0.01	0 ± 0	0.01 ± 0.01	0.01 ± 0.01	0.02 ± 0.02	0.02 ± 0.04	0.01 ± 0.01
<i>Epsilonproteobacteria</i>	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Unclassified <i>Proteobacteria</i>	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
<i>Actinobacteria</i>	0.31 ± 0.02	0.31 ± 0.08	0.18 ± 0.05	0.31 ± 0.07	0.06 ± 0.06	0.01 ± 0.01	0.03 ± 0.03	0.02 ± 0.01	0.03 ± 0.05
<i>Bacteroidetes</i>	0.09 ± 0.03	0.18 ± 0.09	0.18 ± 0.09	0.14 ± 0.04	0.01 ± 0.01	0.01 ± 0.01	0.06 ± 0.09	0.03 ± 0.03	0.03 ± 0.03
<i>Planctomycetes</i>	0.04 ± 0.02	0.01 ± 0	0.02 ± 0.01	0.01 ± 0.01	0.08 ± 0.08	0.04 ± 0.07	0.25 ± 0.16	0.08 ± 0.07	0.08 ± 0.08
<i>Acidobacteria</i>	0.06 ± 0.01	0.12 ± 0.03	0.05 ± 0.02	0.15 ± 0.03	0.01 ± 0.01	0 ± 0	0.01 ± 0.01	0.01 ± 0.01	0.02 ± 0.02
<i>Cyanobacteria</i>	0.04 ± 0.02	0.02 ± 0.01	0.04 ± 0.02	0.01 ± 0.01	0.08 ± 0.04	0.11 ± 0.1	0.08 ± 0.05	0.03 ± 0.03	0.03 ± 0.03
<i>Verrucomicrobia</i>	0.03 ± 0.01	0.02 ± 0	0.01 ± 0.01	0.02 ± 0.01	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
<i>Firmicutes</i>	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.02 ± 0.02	0.03 ± 0.05	0.03 ± 0.03	0.01 ± 0.01	0.01 ± 0.01
<i>Nitrospirae</i>	0.01 ± 0	0.01 ± 0.01	0.01 ± 0.01	0.02 ± 0.01	0 ± 0.01	0 ± 0	0 ± 0	0.01 ± 0	0.01 ± 0.01
<i>Chlorobi</i>	0.02 ± 0.01	0.01 ± 0.01	0.01 ± 0.01	0.01 ± 0.01	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
<i>Chlamydiae</i>	0.01 ± 0	0.01 ± 0.01	0.01 ± 0.01	0.01 ± 0.01	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
<i>Gemmatimonadetes</i>	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
<i>Chloroflexi</i>	0.01 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0.01	0 ± 0
<i>Elusimicrobia</i>	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.02 ± 0.03
<i>Ignavibacteriae</i>	0.01 ± 0.01	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.01 ± 0.04	0 ± 0
<i>Parcubacteria</i>	0.02 ± 0.02	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
<i>Armatimonadetes</i>	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Unclassified	0.02 ± 0.02	0 ± 0	0 ± 0	0 ± 0	0.11 ± 0.09	0.16 ± 0.05	0.02 ± 0.02	0.01 ± 0.01	0.01 ± 0.01
Remaining 33 Phyla (<0.1%)	0.02 ± 0.02	0 ± 0	0.01 ± 0.01	0 ± 0	0.01 ± 0.01	0 ± 0.01	0 ± 0	0 ± 0	0 ± 0.01

*Mean ± Standard deviation

Table S5: Mean and standard deviation of water quality parameters for the source water feeding each system, averaged over the 8-month study period

System	Temperature (°C)	pH	Turbidity (NTU)	TOC (mg/l-C)	DOC (mg/l-C)	Ammonium (mg/l-N)	Nitrate (mg/l-N)	Nitrite (mg/l-N)	Phosphate (mg/l-P)
System R	15.51 ± 4.6	7.98 ± 0.16	70.98 ± 13.23	3.94 ± 0.23	3.88 ± 0.39	0.12 ± 0.13	0.18 ± 0.12	0.001 ± 0.001	0.12 ± 0.2
System S	16.8 ± 4.6	8.37 ± 0.19	63.81 ± 10.04	3.765 ± 0.31	3.44 ± 0.12	0.19 ± 0.11	0.16 ± 0.07	0.03 ± 0.00	0.15 ± 0.03

Table S6: Mean and standard deviations of the number of sequences and alpha diversity indexes averaged over the duration of the study for each individual study site

	Number of sequences		Number of observed taxa (Sobs)		Inverse Simpson Diversity Index		Shannon Diversity Index		Pielou's evenness		Good's coverage	
	<i>Mean</i>	<i>SD</i>	<i>Mean</i>	<i>SD</i>	<i>Mean</i>	<i>SD</i>	<i>Mean</i>	<i>SD</i>	<i>Mean</i>	<i>SD</i>	<i>Mean</i>	<i>SD</i>
R_SW	34465.71	19422.11	208.52	70.03	39.58	16.05	4.30	0.55	0.82	0.03	0.94	0.03
S_SW	60236.00	17308.25	304.32	17.09	40.69	5.40	4.66	0.10	0.82	0.01	0.88	0.01
R_FI	35137.71	15165.55	196.28	52.47	36.04	11.11	4.27	0.30	0.81	0.02	0.94	0.02
S_FI	49732.13	13430.06	185.92	28.20	27.60	8.75	4.04	0.31	0.77	0.04	0.94	0.01
R_FB	39244.88	21034.37	229.43	70.23	43.79	19.38	4.39	0.62	0.81	0.06	0.92	0.03
S_FB	46060.38	28383.14	232.39	56.01	42.36	13.16	4.41	0.33	0.81	0.03	0.92	0.03
R_FE	35808.13	13983.04	159.10	32.14	28.98	9.96	4.01	0.41	0.79	0.05	0.96	0.01
S_FE	51383.50	24773.13	160.79	20.54	21.84	6.60	3.86	0.20	0.76	0.04	0.95	0.01
R_CHLA	18781.29	16926.91	58.35	42.94	9.94	9.42	2.64	0.67	0.68	0.07	0.99	0.01
S_CHLA	15748.00	11454.43	82.79	36.36	13.08	7.56	3.14	0.55	0.72	0.06	0.99	0.01
R_CHLB	18146.60	28495.57	80.63	76.63	15.65	10.93	3.02	0.97	0.75	0.09	0.98	0.03
S_CHLB	15234.00	25980.55	48.23	25.33	8.86	2.17	2.70	0.17	0.72	0.07	0.99	0.01
R_CHM	10565.40	6432.02	78.96	31.22	12.81	9.36	2.98	0.83	0.69	0.15	0.99	0.01
S_CHM	18030.45	14458.32	86.94	33.26	12.77	6.01	3.14	0.44	0.71	0.07	0.98	0.01
R_DS1	29708.09	25598.37	106.48	41.71	18.13	10.94	3.26	1.04	0.70	0.19	0.98	0.01
S_DS1	23499.52	14113.34	99.37	47.07	10.37	7.19	2.87	0.75	0.63	0.12	0.97	0.02
R_DS2	25236.84	17138.83	129.81	37.40	16.04	7.88	3.50	0.52	0.72	0.08	0.97	0.02
S_DS2	26578.38	16234.82	115.24	45.57	12.99	8.37	3.14	0.80	0.66	0.12	0.97	0.02

Table S7: Mean percentage relative abundance of the top 33 abundant sequence variants (MRA > 0.5%) across all samples from both systems

System R										
ASV	ASV Taxonomy	R_RW	R_FI	R_FB	R_FE	R_CHLA	R_CHLB	R_CHM	R_DS1	R_DS2
ASV_1	<i>Proteobacteria Alphaproteobacteria Rhizobiales Beijerinckiaceae Methylobacterium</i>	0.00	0.00	0.00	0.00	0.00	0.63	2.36	2.82	9.14
ASV_2	<i>Actinobacteria Actinobacteria Frankiales Sporichthyaceae</i>	4.82	9.48	6.11	8.43	2.29	2.82	0.38	0.65	0.33
ASV_3	<i>Planctomycetes Planctomycetacia Gemmatales Gemmataceae</i>	0.45	0.38	0.22	0.94	14.20	1.17	10.63	8.64	6.72
ASV_4	<i>Acidobacteria Holophagae Holophagales Holophagaceae</i>	2.01	5.62	3.30	7.14	0.89	0.64	0.79	0.62	0.56
ASV_5	<i>Actinobacteria Actinobacteria Frankiales Sporichthyaceae</i>	5.37	5.15	4.38	4.67	1.00	0.90	0.42	0.43	0.14
ASV_6	<i>Proteobacteria Gammaproteobacteria Betaproteobacteriales Nitrosomonadaceae Nitrosomonas</i>	0.01	0.00	0.01	0.00	0.00	0.00	0.49	1.45	10.92
ASV_7	<i>Actinobacteria Actinobacteria Frankiales Sporichthyaceae</i>	2.95	5.22	2.23	4.75	0.93	1.77	0.24	0.60	0.23
ASV_8	<i>Proteobacteria Gammaproteobacteria Betaproteobacteriales Burkholderiaceae Limnohabitans</i>	2.18	1.76	1.02	2.74	0.45	1.45	0.77	0.07	0.00
ASV_10	<i>Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae Pseudomonas</i>	0.52	2.69	4.45	2.69	0.48	0.87	3.61	0.94	1.69
ASV_11	<i>Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae Sphingomonas</i>	0.00	0.06	3.91	3.89	0.48	0.11	2.50	1.59	4.92
ASV_12	<i>Acidobacteria</i>	0.62	3.25	1.50	3.79	0.94	0.59	0.02	0.18	0.08
ASV_13	<i>Proteobacteria Alphaproteobacteria Rhizobiales Phreatobacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.60	1.68
ASV_15	<i>Thaumarchaeota Nitrososphaeria Nitrosopumilales Nitrosopumilaceae Candidatus Nitrosoarchaeum</i>	2.76	0.98	1.47	0.99	0.07	0.00	0.18	0.09	0.02
ASV_16	<i>Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae Pseudomonas</i>	0.68	0.07	0.10	0.00	0.00	0.00	0.00	6.67	0.00
ASV_17	<i>Actinobacteria Acidimicrobiia Acidimicrobiales Acidimicrobiaceae</i>	0.65	2.65	0.75	2.77	0.43	1.17	0.08	0.30	0.15
ASV_18	<i>Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae</i>	0.00	0.35	0.92	0.15	0.02	0.54	0.00	0.02	0.06
ASV_19	<i>Proteobacteria Gammaproteobacteria Pseudomonadales Moraxellaceae Acinetobacter</i>	0.00	0.00	0.01	0.00	0.56	0.14	6.66	5.00	0.16
ASV_22	<i>Proteobacteria Gammaproteobacteria Betaproteobacteriales Burkholderiaceae</i>	1.87	1.00	1.32	0.81	0.25	0.00	0.00	0.04	0.66
ASV_23	<i>Proteobacteria Gammaproteobacteria Beggiatoales Beggiatoaceae</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.40	4.94
ASV_25	<i>Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Cereibacter</i>	0.00	0.01	0.29	0.08	0.00	0.00	0.39	0.72	0.30
ASV_26	<i>Cyanobacteria Melainabacteria Obscuribacterales</i>	0.00	0.00	0.00	0.01	0.15	0.26	0.82	0.66	0.30
ASV_29	<i>Proteobacteria Alphaproteobacteria Caulobacteriales Hyphomonadaceae</i>	0.00	0.00	0.00	0.00	0.00	0.00	2.94	0.41	0.19
ASV_30	<i>Planctomycetes Planctomycetacia Planctomycetales</i>	0.00	0.00	0.11	0.10	0.63	0.00	4.59	3.18	2.61
ASV_31	<i>Proteobacteria Gammaproteobacteria Pseudomonadales Moraxellaceae Acinetobacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	5.15	3.86	0.06

ASV_32	<i>Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobium</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.68	1.07
ASV_33	<i>Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae Sphingomonas</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.37	1.45
ASV_34	<i>Proteobacteria Gammaproteobacteria Betaproteobacteriales Gallionellaceae</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.78	2.56
ASV_36	<i>Planctomycetes Phycisphaerae Phycisphaerales Phycisphaeraceae</i>	0.00	0.00	0.00	0.01	0.65	0.08	2.85	0.56	0.58
ASV_37	<i>Proteobacteria Gammaproteobacteria Betaproteobacteriales Sulfuricellaceae Sulfuricella</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.99	1.30
ASV_40	<i>Proteobacteria Alphaproteobacteria Rickettsiales</i>	0.00	0.03	0.05	0.01	5.20	2.27	0.57	0.19	0.10
ASV_41	<i>Proteobacteria Alphaproteobacteria Rickettsiales</i>	0.01	0.00	0.00	0.01	6.71	3.36	0.81	0.80	0.26
ASV_44	<i>Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Flavobacterium</i>	4.13	1.64	3.64	0.35	0.07	0.39	0.01	0.00	0.02
ASV_80	<i>Proteobacteria Alphaproteobacteria Rhizobiales Beijerinckiaceae Methylobacterium</i>	0.00	0.00	0.00	0.00	0.46	0.05	0.00	0.00	0.01
System S										
ASV	ASV Taxonomy	S_SW	S_FI	S_FB	S_FE	S_CHLA	S_CHLB	S_CHM	S_DS1	S_DS2
ASV_1	<i>Proteobacteria Alphaproteobacteria Rhizobiales Beijerinckiaceae Methylobacterium</i>	0.01	0.01	0.00	0.00	0.91	0.06	0.74	19.31	15.19
ASV_2	<i>Actinobacteria Actinobacteria Frankiales Sporichthyaceae</i>	8.42	9.75	5.74	9.55	1.47	0.56	0.48	0.36	0.86
ASV_3	<i>Planctomycetes Planctomycetacia Gemmatales Gemmataceae</i>	0.41	0.19	0.11	0.25	4.20	1.24	14.92	4.68	4.83
ASV_4	<i>Acidobacteria Holophagae Holophagales Holophagaceae</i>	1.69	7.14	2.32	9.44	0.87	0.01	0.39	0.55	0.94
ASV_5	<i>Actinobacteria Actinobacteria Frankiales Sporichthyaceae</i>	7.63	6.34	4.45	5.91	1.43	0.05	0.27	0.16	0.45
ASV_6	<i>Proteobacteria Gammaproteobacteria Betaproteobacteriales Nitrosomonadaceae Nitrosomonas</i>	0.01	0.04	0.02	0.03	1.10	0.41	0.36	10.32	12.96
ASV_7	<i>Actinobacteria Actinobacteria Frankiales Sporichthyaceae</i>	4.28	6.25	2.25	5.72	1.20	0.04	0.22	0.23	0.40
ASV_8	<i>Proteobacteria Gammaproteobacteria Betaproteobacteriales Burkholderiaceae Limnohabitans</i>	0.41	7.26	2.49	10.47	0.64	0.03	0.12	0.03	0.30
ASV_10	<i>Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae Pseudomonas</i>	0.32	0.85	1.04	0.46	0.09	0.00	0.14	1.36	1.63
ASV_11	<i>Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae Sphingomonas</i>	0.05	0.03	2.32	0.28	0.92	0.06	1.43	3.61	4.70
ASV_12	<i>Acidobacteria</i>	1.60	3.40	1.29	4.13	0.13	0.02	0.05	0.22	0.30
ASV_13	<i>Proteobacteria Alphaproteobacteria Rhizobiales Phreatobacter</i>	0.00	0.00	0.00	0.00	2.48	0.19	0.14	7.05	7.92
ASV_15	<i>Thaumarchaeota Nitrososphaeria Nitrosopumilales Nitrosopumilaceae Candidatus Nitrosoarchaeum</i>	6.40	1.00	2.08	0.79	0.11	0.01	0.02	0.04	0.07
ASV_16	<i>Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae Pseudomonas</i>	0.01	0.00	0.00	0.00	0.00	3.18	0.00	0.00	0.00
ASV_17	<i>Actinobacteria Acidimicrobiia Acidimicrobiales Acidimicrobiaceae</i>	0.93	1.56	0.70	2.86	0.14	0.00	0.03	0.09	0.19
ASV_18	<i>Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae</i>	0.13	2.23	5.54	1.25	0.09	0.00	0.03	0.06	0.06

ASV_19	<i>Proteobacteria Gammaproteobacteria Pseudomonadales Moraxellaceae Acinetobacter</i>	0.02	0.00	0.00	0.00	0.03	0.40	0.31	0.24	0.12
ASV_22	<i>Proteobacteria Gammaproteobacteria Betaproteobacteriales Burkholderiaceae</i>	0.06	1.91	1.17	0.63	0.00	0.00	0.10	0.05	0.45
ASV_23	<i>Proteobacteria Gammaproteobacteria Beggiatoales Beggiatoaceae</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.19	0.01
ASV_25	<i>Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Cereibacter</i>	0.01	0.00	3.33	0.10	0.18	0.00	0.73	1.40	0.80
ASV_26	<i>Cyanobacteria Melainabacteria Obscuribacterales</i>	0.00	0.01	0.01	0.01	0.99	0.17	3.56	1.44	1.34
ASV_29	<i>Proteobacteria Alphaproteobacteria Caulobacterales Hyphomonadaceae</i>	0.00	0.00	0.06	0.01	6.21	0.92	3.12	0.72	0.70
ASV_30	<i>Planctomycetes Planctomycetacia Planctomycetales</i>	0.00	0.00	0.23	0.00	0.22	0.01	2.00	0.40	0.28
ASV_31	<i>Proteobacteria Gammaproteobacteria Pseudomonadales Moraxellaceae Acinetobacter</i>	0.00	0.00	0.00	0.00	0.13	0.02	0.22	0.17	0.01
ASV_32	<i>Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobium</i>	0.00	0.00	0.00	0.00	0.07	0.09	0.01	2.62	1.86
ASV_33	<i>Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae Sphingomonas</i>	0.00	0.00	0.00	0.00	0.46	0.00	0.00	2.28	1.43
ASV_34	<i>Proteobacteria Gammaproteobacteria Betaproteobacteriales Gallionellaceae</i>	0.28	0.00	0.00	0.00	0.00	0.00	0.01	0.28	0.29
ASV_36	<i>Planctomycetes Phycisphaerae Phycisphaerales Phycisphaeraceae</i>	0.00	0.00	0.18	0.00	1.23	1.29	2.52	0.73	0.64
ASV_37	<i>Proteobacteria Gammaproteobacteria Betaproteobacteriales Sulfuricellaceae Sulfuricella</i>	0.05	0.00	0.00	0.00	0.10	0.00	0.00	1.70	1.54
ASV_40	<i>Proteobacteria Alphaproteobacteria Rickettsiales</i>	0.00	0.02	0.02	0.01	5.00	6.43	1.03	0.19	0.30
ASV_41	<i>Proteobacteria Alphaproteobacteria Rickettsiales</i>	0.00	0.00	0.00	0.00	4.23	8.53	1.02	0.48	0.44
ASV_44	<i>Bacteroidetes Flavobacteriia Flavobacteriales Flavobacteriaceae Flavobacterium</i>	0.22	0.87	0.26	0.75	0.02	0.00	0.81	0.01	0.00
ASV_80	<i>Proteobacteria Alphaproteobacteria Rhizobiales Beijerinckiaceae Methylobacterium</i>	0.00	0.00	0.00	0.01	0.04	1.70	4.66	0.87	0.53

Table S8: Pair-wise beta diversity comparisons between corresponding locations from each system

Sample comparison	Structure based metrics				Membership based metrics			
	Bray-Curtis		Weighted UniFrac		Jaccard		Unweighted UniFrac	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD
R_SW vs S_SW	0.71	0.10	0.47	0.13	0.84	0.06	0.71	0.06
R_FI vs S_FI	0.49	0.11	0.31	0.09	0.66	0.10	0.56	0.10
R_FB vs S_FB	0.66	0.08	0.42	0.13	0.75	0.05	0.63	0.03
R_FE vs S_FE	0.48	0.13	0.34	0.16	0.58	0.08	0.50	0.04
R_CHLA vs S_CHLA	0.72	0.20	0.60	0.24	0.92	0.04	0.82	0.07
R_CHLB vs S_CHLB	0.72	0.24	0.51	0.32	0.93	0.06	0.82	0.10
R_CHM vs S_CHM	0.74	0.21	0.67	0.16	0.82	0.06	0.69	0.05
R_DS1 vs S_DS1	0.72	0.23	0.67	0.11	0.83	0.08	0.72	0.04
R_DS2 vs S_DS2	0.67	0.17	0.56	0.10	0.83	0.06	0.72	0.04

Table S9. Permutation test for distance-based redundancy analysis (dbRDA) under reduced model

	SumOfSqs	F	Pr(>F)
Conductivity	0.382	1.1569	0.2335
DOC	0.58	1.7565	0.0233*
Free Cl2	0.762	2.3074	0.0021**
Total Cl2	0.241	0.73	0.8524
Monochloramine	0.645	1.954	0.0095**
Alkalinity	0.515	1.559	0.0461*
Ammonium	0.972	2.9447	0.0001***
Nitrite	0.391	1.1849	0.2105
Nitrate	0.379	1.1487	0.2421
pH	0.37	1.121	0.2779
Temperature	0.697	2.1121	0.0062**
Turbidity	0.207	0.6271	0.9505

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table S10. Variance Partition analyses using water chemistry/environmental parameters identified as significant being significantly associated with Bray-Curtis distances by dbRDA analyses.

Explanatory tables:

X1 = Ammonium, X2 = Free_Cl2, X3 = Temp, X4 = Monochloramine

No. of explanatory tables: 4

Total variation (SS): 40.502

No. of observations: 111

Variables and their combinations	Degrees of Freedom	R square	Adjusted R square	Testable
[aeghklno] = X1	1	0.04908	0.04036	TRUE
[befiklmo] = X2	1	0.05648	0.04782	TRUE
[cfgjlmno] = X3	1	0.02175	0.01277	TRUE
[dhijklmno] = X4	1	0.04074	0.03194	TRUE
[abefghijklmno] = X1+X2	2	0.07773	0.06065	TRUE
[acefghijklmno] = X1+X3	2	0.07754	0.06046	TRUE
[adehijklmno] = X1+X4	2	0.07341	0.05625	TRUE
[bcefgijklmno] = X2+X3	2	0.07574	0.05862	TRUE
[bdefhijklmno] = X2+X4	2	0.07748	0.0604	TRUE
[cdfghijklmno] = X3+X4	2	0.06379	0.04646	TRUE
[abcefgijklmno] = X1+X2+X3	3	0.10414	0.07902	TRUE
[abdefghijklmno] = X1+X2+X4	3	0.10786	0.08284	TRUE
[acdefghijklmno] = X1+X3+X4	3	0.10194	0.07676	TRUE
[bcdefghijklmno] = X2+X3+X4	3	0.09554	0.07018	TRUE
[abcdefghijklmno] = All	4	0.12838	0.09549	TRUE
Individual fractions				
[a] = X1 X2+X3+X4	1		0.02531	TRUE
[b] = X2 X1+X3+X4	1		0.01873	TRUE
[c] = X3 X1+X2+X4	1		0.01265	TRUE
[d] = X4 X1+X2+X3	1		0.01647	TRUE
[e]	0		0.00499	FALSE
[f]	0		0.00786	FALSE
[g]	0		-0.00287	FALSE
[h]	0		-0.00491	FALSE
[i]	0		-0.00017	FALSE
[j]	0		0.00572	FALSE
[k]	0		0.0223	FALSE
[l]	0		-0.00312	FALSE

[m]	0		-0.00613	FALSE
[n]	0		-0.0047	FALSE
[o]	0		0.00336	FALSE
[p] = Residuals	0		0.90451	FALSE
Controlling 2 tables X				
[ae] = X1 X3+X4	1		0.0303	TRUE
[ag] = X1 X2+X4	1		0.02244	TRUE
[ah] = X1 X2+X3	1		0.0204	TRUE
[be] = X2 X3+X4	1		0.02372	TRUE
[bf] = X2 X1+X4	1		0.02659	TRUE
[bi] = X2 X1+X3	1		0.01856	TRUE
[cf] = X3 X1+X4	1		0.02051	TRUE
[cg] = X3 X2+X4	1		0.00978	TRUE
[cj] = X3 X1+X2	1		0.01837	TRUE
[dh] = X4 X2+X3	1		0.01156	TRUE
[di] = X4 X1+X3	1		0.0163	TRUE
[dj] = X4 X1+X2	1		0.02219	TRUE
Controlling 1 table X				
[aghn] = X1 X2	1		0.01283	TRUE
[aehk] = X1 X3	1		0.04768	TRUE
[aegl] = X1 X4	1		0.02431	TRUE
[bfim] = X2 X1	1		0.02029	TRUE
[beik] = X2 X3	1		0.04585	TRUE
[befl] = X2 X4	1		0.02846	TRUE
[cfjm] = X3 X1	1		0.02009	TRUE
[cgjn] = X3 X2	1		0.0108	TRUE
[cagl] = X3 X4	1		0.01452	TRUE
[dijm] = X4 X1	1		0.01589	TRUE
[dhjn] = X4 X2	1		0.01258	TRUE
[dhik] = X4 X3	1		0.03368	TRUE

Supplementary figures

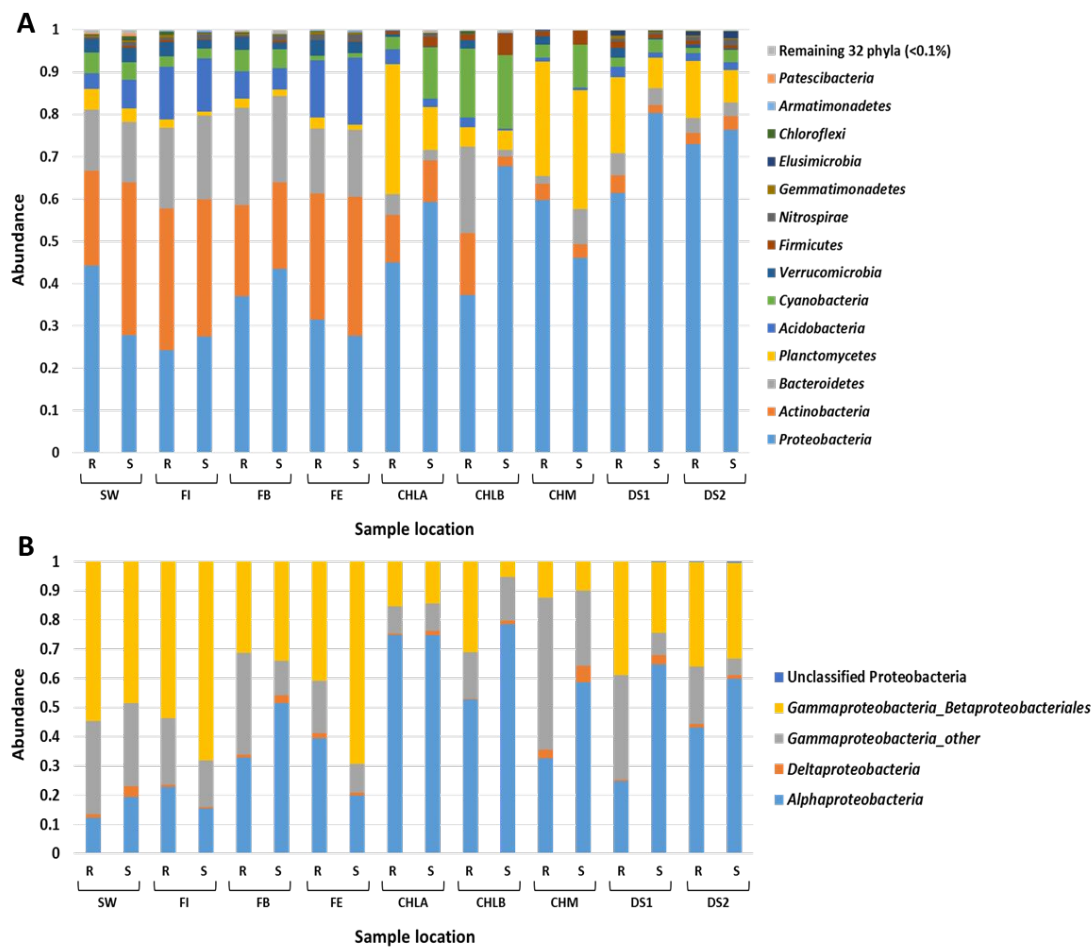


Fig. S1: (A) Phylum-level mean relative abundance of bacterial sequences detected over the duration of the study at each sample location within the two DWTPs and corresponding DWDS (R and S DWDS sections). The 14 most abundant and unclassified phyla ($> 0.1\%$) are shown here, with the remaining 32 phyla ($< 0.1\%$) grouped together as a single group. Phyla are shown in the legend on the right of the figure. See Table S3 for mean relative abundances. (B) Mean relative abundance of proteobacterial classes detected over the duration of the study at each sample location for each system.

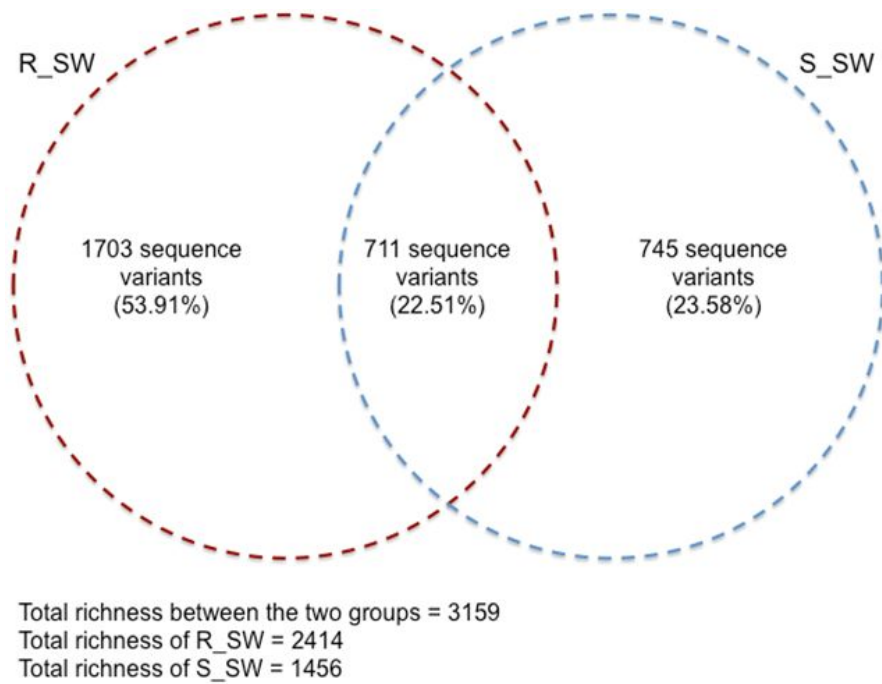
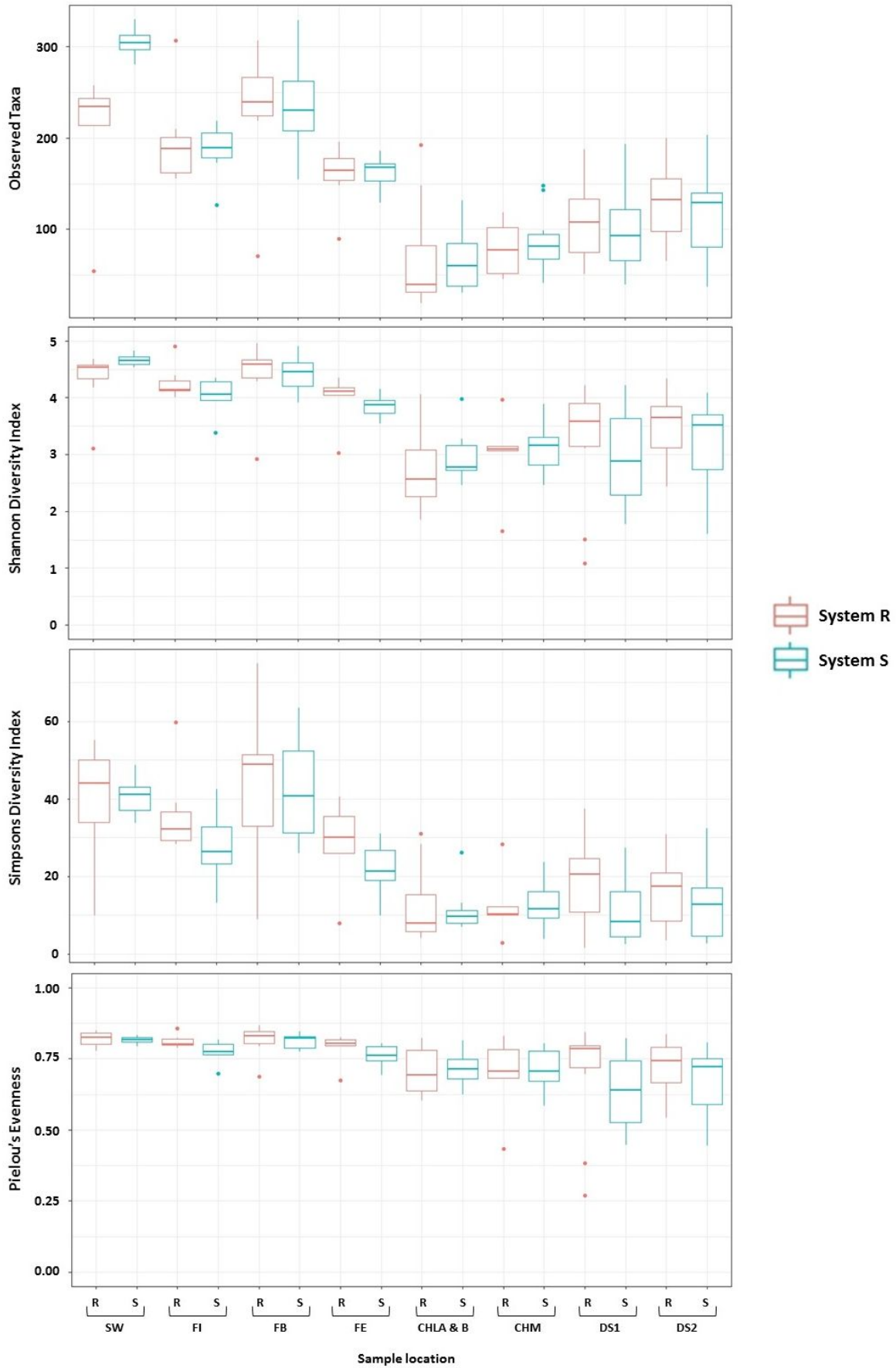


Fig. S2: Venn diagram showing the shared amplicon sequence variants (ASVs) between the two source waters.



1
2 **Fig. S3:** Spatial changes in richness (observed taxa), diversity (Shannon Diversity Index and

3 Inverse Simpson Diversity Index) and evenness (Pielou's evenness) averaged across all
4 sampling locations for each month. Points represent all sample sites collected for each
5 month. Samples colored based on DWTP and corresponding DWDS (Lines R and S)
6 (subsamped at 1263 iterations=1000).

7

8

9

10

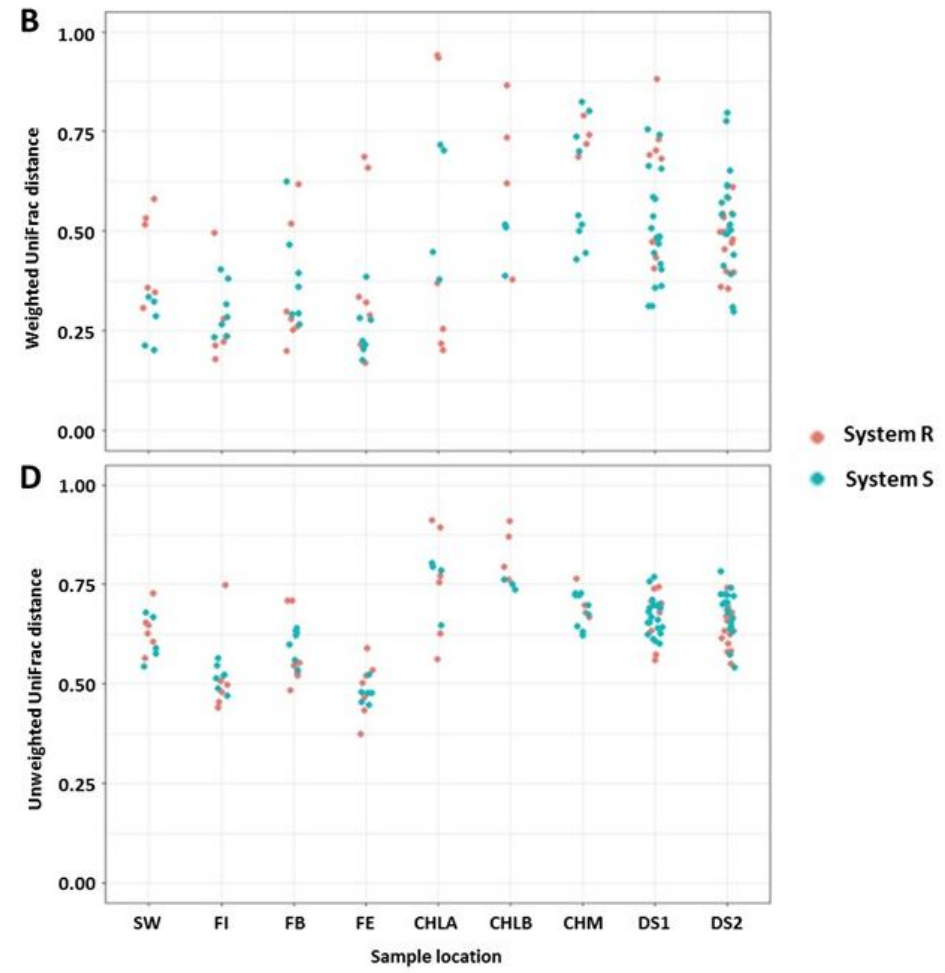
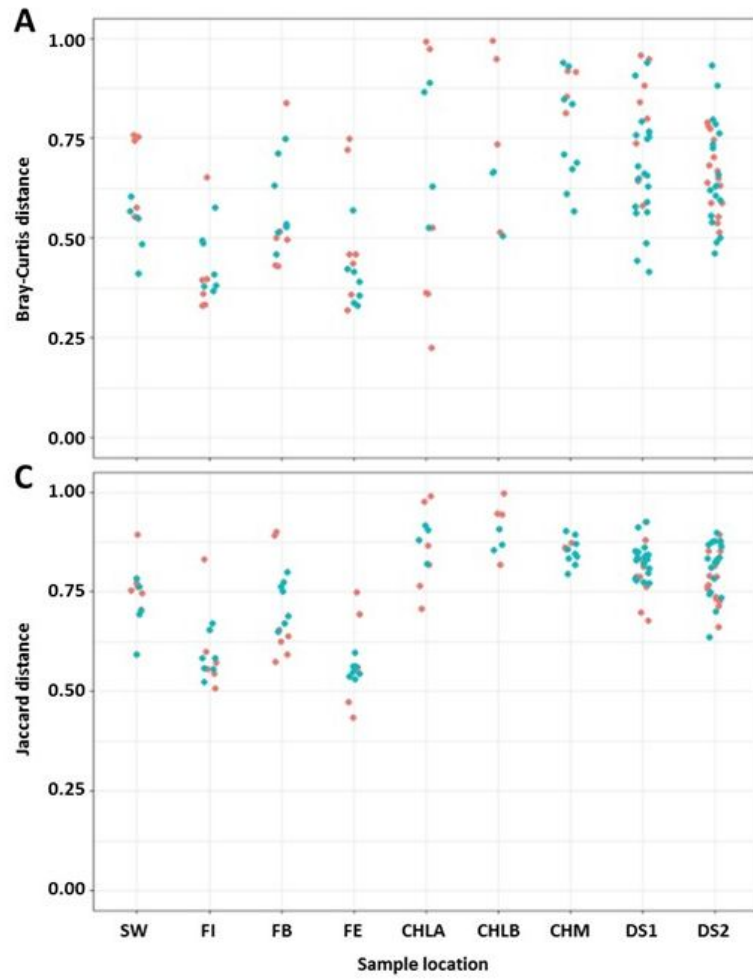
11

12

13

14

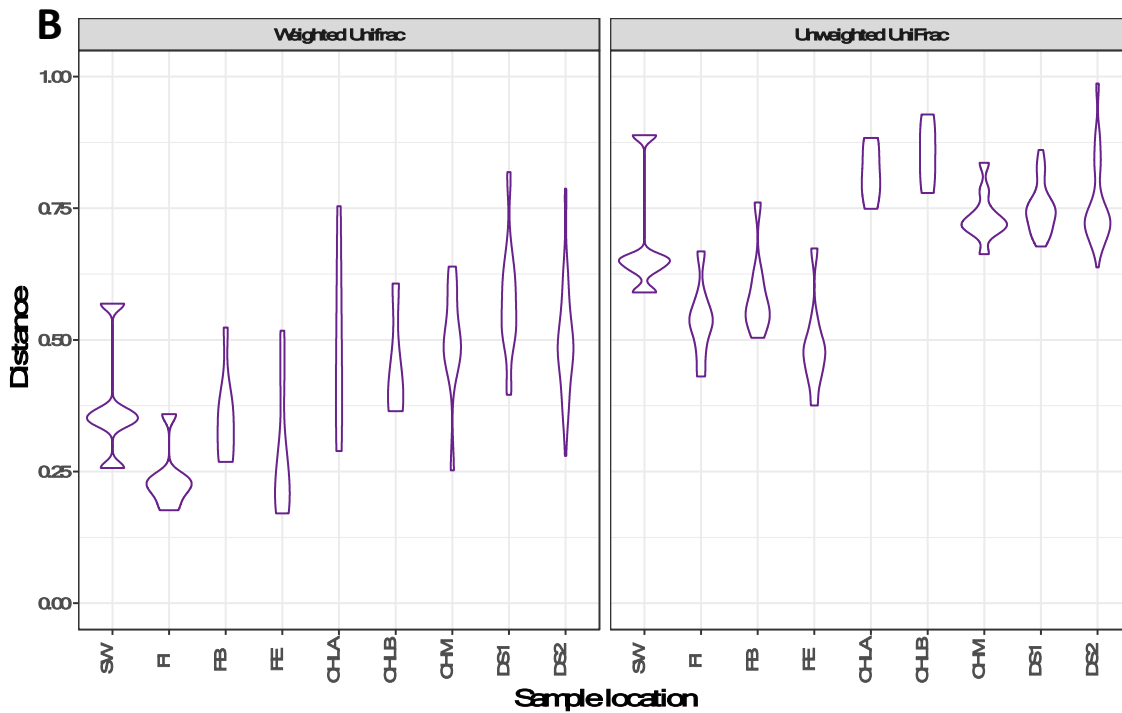
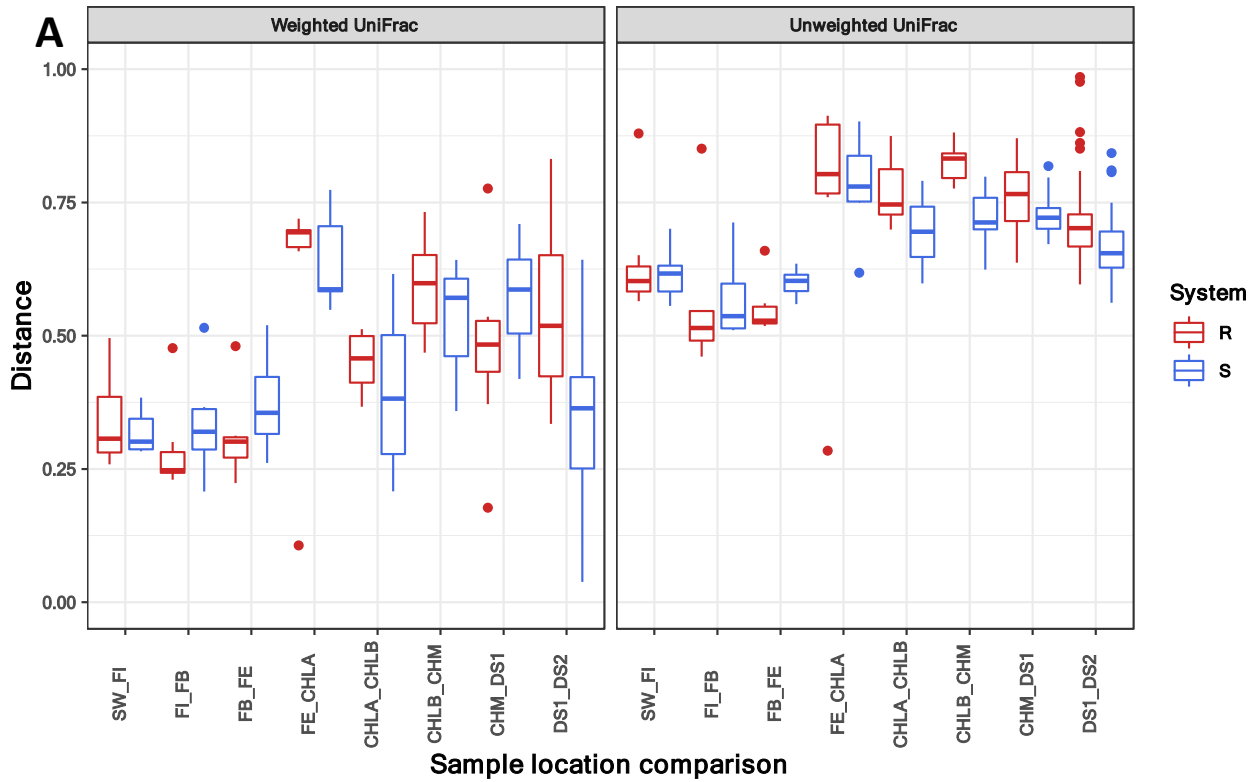
15



18 **Fig. S4** Temporal variation within each sample location from each system. Beta diversity
19 pair-wise comparisons include samples from consecutive months within each location over
20 the eight month study period for both structure-based metrics: (A) Bray-Curtis, (B)
21 Weighted UniFrac and membership-based metrics: (C) Jaccard, (D) Unweighted UniFrac.
22 Samples from System R are indicated in red and samples from System S are indicated in
23 blue.

24

25



26
 27 **Fig S5:** (A) Average pairwise beta diversity comparisons of both weighted
 28 UniFrac analyses. Comparisons are between consecutive locations within each of the two
 29 systems for corresponding months. Sample abbreviations on the x-axis refer to comparisons
 30 of samples following the flow of bulk water through both systems, i.e. source water and filter

31 inflow (SW_FI), filter inflow and filter bed media (FI_FB), filter bed media and filter
32 effluent (FB_FE), filter effluent and chlorinated water leaving the DWTP (FE_CHLA),
33 chlorinated water leaving the DWTP and chlorinated water entering the secondary
34 disinfection boosting station (CHLA_CHLB), chlorinated water entering the secondary
35 disinfection boosting station and chloraminated water (CHLB_CHM), chloraminated water
36 and distribution system site 1 (CHM_DS1) and finally distribution system site 1 and
37 distribution system site 2 (DS1_DS2). Sample comparisons from System R indicated in red
38 and System S in blue. (B) Direct pairwise beta diversity comparisons (weighted and
39 unweighted UniFrac) between corresponding sampling locations from the two systems.
40 Pairwise beta diversity comparisons include samples from the same month. Sample
41 abbreviations on the x-axis refer to comparisons between the source waters (SW), filter
42 inflows (FI), filter bed medias (FB), filter effluents (FE), chlorinated waters leaving the
43 DWTP (CHLA), chlorinated waters entering the secondary disinfection boosting station
44 (CHLB), chloraminated waters (CHM), distribution system sites 1 (DS1) and distribution
45 system sites 2 (DS2). Mean and standard deviations of each comparison is shown in Table
46 S7.

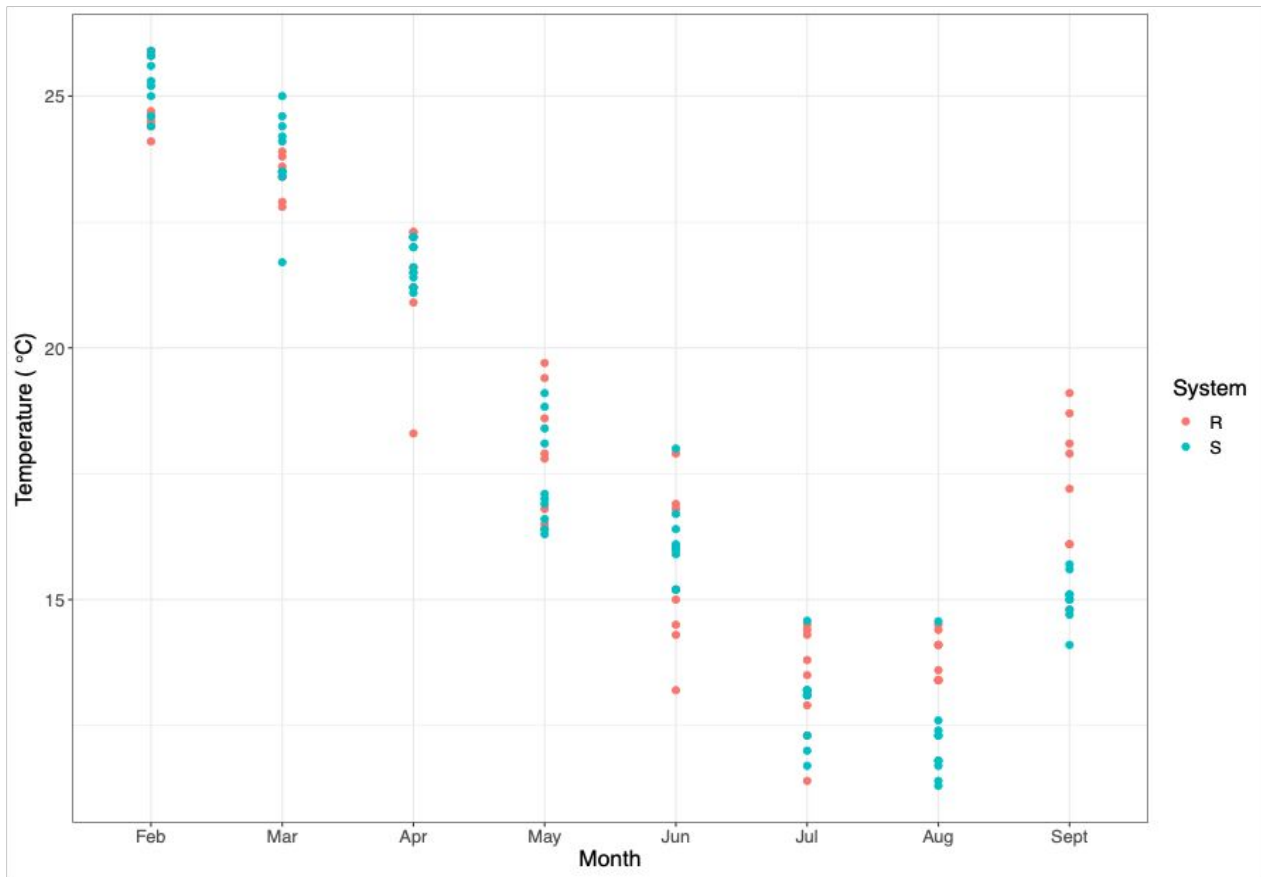


Fig. S6. Variation in temperature over the course of the study (8 months).

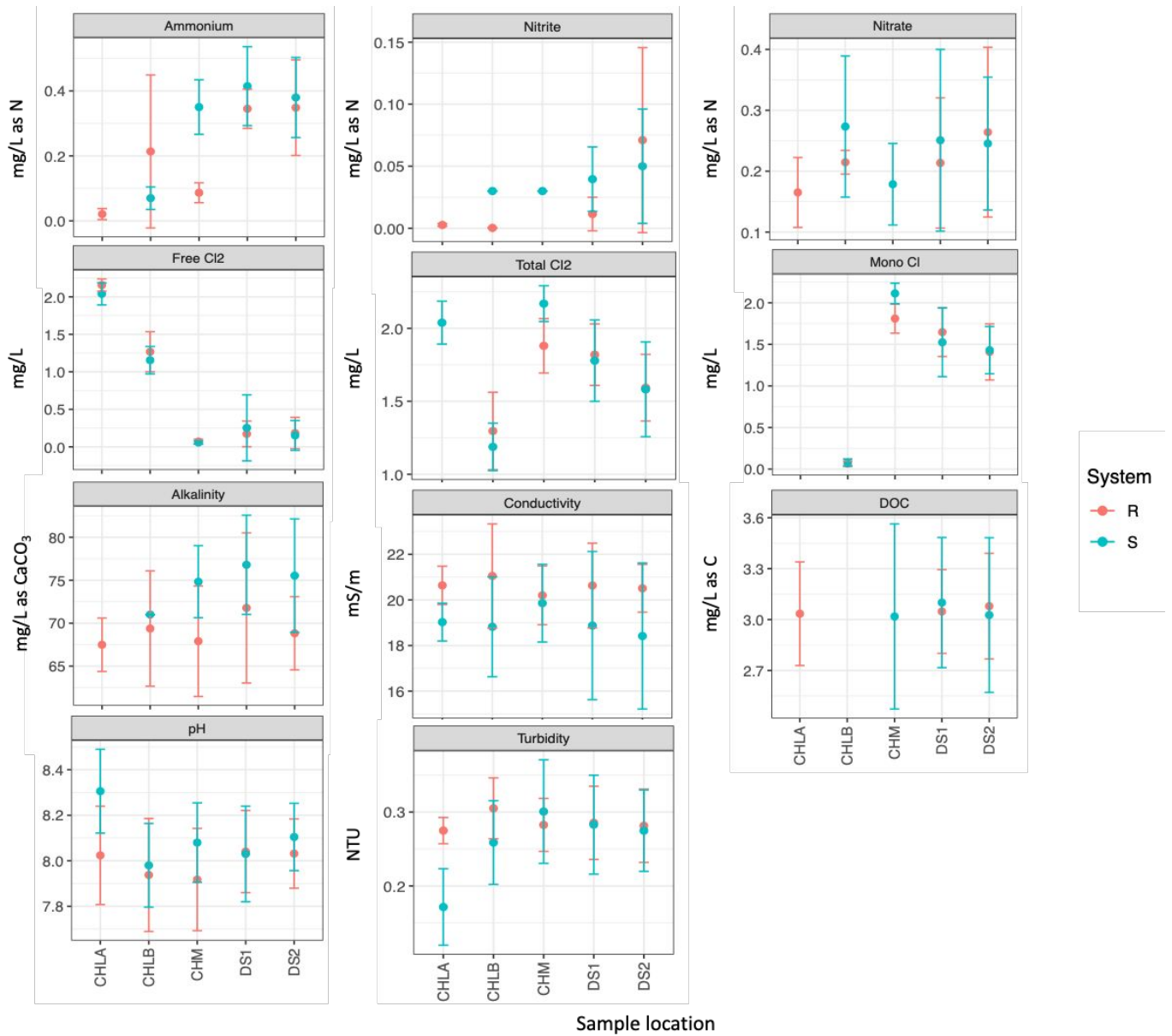


Fig S7. Variation in water quality parameters measured throughout the duration of the study for each location for both systems.

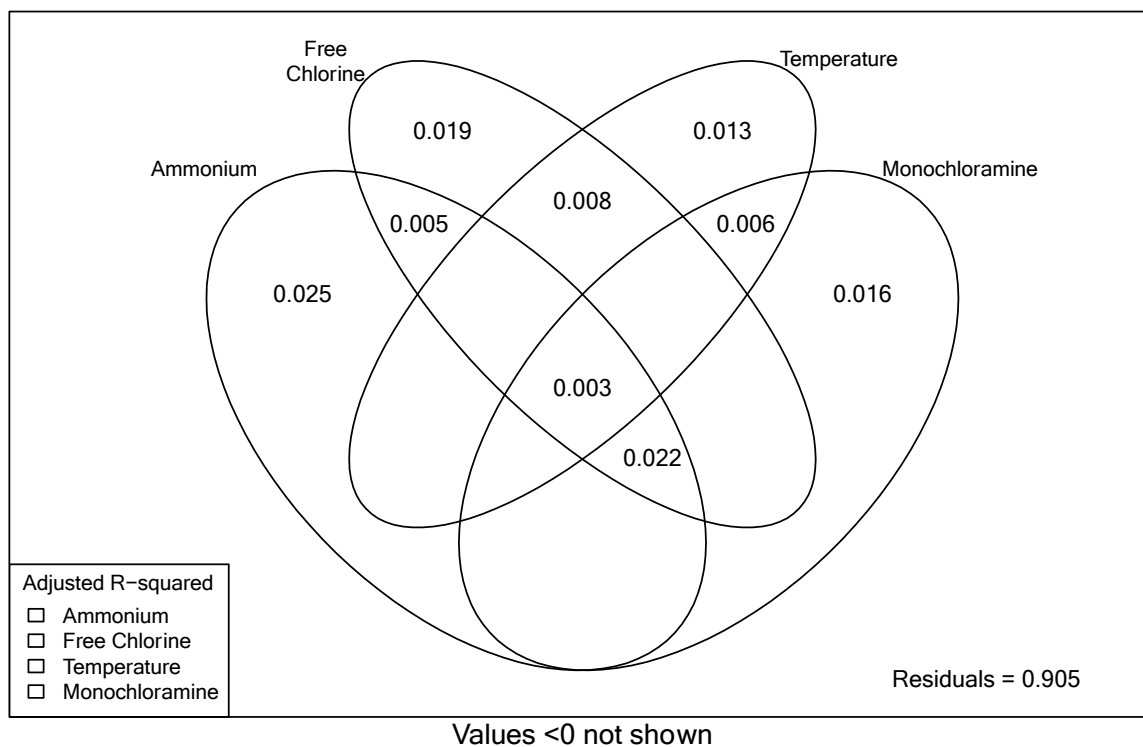


Fig. S8. Venn diagram indicates the fraction of variation explained by the environmental parameters identified as significantly associated with ASV count-based Bray-Curtis distance matrices (Varpart analysis).