

Supplementary material to the article **From source to tap: tracking microbial diversity in a riverbank filtration based drinking water supply system under changing hydrological regimes**

Statistical tables

Table S1. Comparison of Danube water quality upstream and downstream from Budapest by Mann-Whitney U test with continuity correction. Marked tests in bold are significant at $p < 0.05000$.

Variable	Rank Sum NR	Rank SUM SR	U	Z	p-value	Z	p-value	Valid N	Valid N
Ammonium	7942,000	8348,000	3847,000	-0,57934	0,562360	-0,58444	0,558922	90	90
Nitrite	8080,500	8209,500	3985,500	-0,18310	0,854720	-0,20929	0,834222	90	90
Nitrate	7979,500	8310,500	3884,500	-0,47206	0,636888	-0,47245	0,636603	90	90
Chloride	7850,000	8440,000	3755,000	-0,84255	0,399482	-0,84588	0,397619	90	90
Sulphate	7403,500	8886,500	3308,500	-2,11996	0,034010	-2,12634	0,033476	90	90
Turbidity	7877,500	8412,500	3782,500	-0,76387	0,444945	-0,76410	0,444807	90	90
TOC	7645,500	8644,500	3550,500	-1,42761	0,153405	-1,43016	0,152671	90	90
DOC	7660,000	8630,000	3565,000	-1,38613	0,165709	-1,38851	0,164982	90	90
T	7620,000	7605,000	3777,000	0,02107	0,983190	0,02107	0,983187	87	87
pH	6558,500	8666,500	2730,500	-3,17093	0,001520	-3,17124	0,001518	87	87
Electric conductivity	7327,500	7897,500	3499,500	-0,85632	0,391823	-0,85803	0,390876	87	87
Redox potential	7433,000	7792,000	3605,000	-0,53877	0,590044	-0,53878	0,590040	87	87
Iron	7966,000	8324,000	3871,000	-0,51068	0,609577	-0,51087	0,609440	90	90
Manganese	7681,000	8609,000	3586,000	-1,32605	0,184825	-1,32695	0,184526	90	90

Table S2. Comparison of Northern and Southern wells by Mann-Whitney U test with continuity correction. Marked tests in bold are significant at $p < 0.05000$.

Variable	Rank Sum NW	Rank SUM SW	U	Z	p-value	Z	p-value	Valid N	Valid N
Ammonium	10690,50	15415,50	3669,500	-5,6661	0,000000	-7,2772	0,000000	118	110
Nitrite	12626,00	13480,00	5605,000	-1,7772	0,075538	-4,1356	0,000035	118	110
Nitrate	19517,00	6589,00	484,000	12,0666	0,000000	12,0699	0,000000	118	110
Chloride	15030,50	11075,50	4970,500	3,0521	0,002273	3,0616	0,002202	118	110
Sulphate	10949,50	15156,50	3928,500	-5,1457	0,000000	-5,1480	0,000000	118	110
Turbidity	8066,50	18039,50	1045,500	-10,9384	0,000000	-11,5337	0,000000	118	110
TOC	9598,00	16508,00	2577,000	-7,8612	0,000000	-7,8860	0,000000	118	110
DOC	9027,50	17078,50	2006,500	-9,0075	0,000000	-9,0406	0,000000	118	110
T	13422,00	12684,00	6401,000	-0,1778	0,858865	-0,1779	0,858827	118	110
pH	13297,50	12808,50	6276,500	-0,4280	0,668672	-0,4376	0,661677	118	110
Electric conductivity	12143,50	13962,50	5122,500	-2,7467	0,006021	-2,7468	0,006018	118	110
Redox potential	18721,50	7384,50	1279,500	10,4682	0,000000	10,4686	0,000000	118	110
Iron	7760,00	18346,00	739,000	-11,5542	0,000000	-12,1098	0,000000	118	110
Manganese	7043,50	18834,50	22,500	-12,9626	0,000000	-12,9854	0,000000	118	109

Table S3. Comparison of Danube water (SR) and well water (SW) quality by Mann-Whitney U test with continuity correction. Marked tests in bold are significant at $p < 0.05000$.

Variable	Rank Sum SR	Rank SUM SW	U	Z	p-value	Z	p-value	Valid N	Valid N
Ammonium	11164,50	8935,50	2830,500	5,2036	0,000000	5,3581	0,000000	90	110
Nitrite	10298,00	9802,00	3697,000	3,0758	0,002100	4,0754	0,000046	90	110
Nitrate	12570,00	7530,00	1425,000	8,6551	0,000000	8,6567	0,000000	90	110
Chloride	6829,50	13270,50	2734,500	-5,4394	0,000000	-5,4547	0,000000	90	110
Sulphate	4354,00	15746,00	259,000	-11,5185	0,000000	-11,5254	0,000000	90	110
Turbidity	13633,50	6466,50	361,500	11,2667	0,000000	11,2689	0,000000	90	110
TOC	13594,50	6505,50	400,500	11,1710	0,000000	11,1894	0,000000	90	110
DOC	13642,50	6457,50	352,500	11,2888	0,000000	11,3109	0,000000	90	110
T	8171,50	11331,50	4343,500	-1,1098	0,267091	-1,1099	0,267042	87	110
pH	10111,00	9392,00	3287,000	3,7685	0,000164	3,7843	0,000154	87	110
Electric conductivity	3828,00	15675,00	0,000	-12,0403	0,000000	-12,0426	0,000000	87	110
Redox potential	6083,50	13419,50	2255,500	-6,3643	0,000000	-6,3644	0,000000	87	110
Iron	9824,00	10276,00	4171,000	1,9118	0,055908	1,9123	0,055837	90	110
Manganese	4415,00	15485,00	320,000	-11,3379	0,000000	-11,3397	0,000000	90	109

Table S4. List of OTUs corresponding to the numbering on Figure 2a.

OTU number	Domain	Phylum	Class	Order
1	Unassigned	—	—	—
2	Archaea	Aenigmarchaeota	Aenigmarchaeia	Aenigmarchaeales
3	Archaea	Aenigmarchaeota	Deep_Sea_Euryarchaeotic_Group (DSEG)	Deep_Sea_Euryarchaeotic_Group (DSEG)
4	Archaea	Crenarchaeota	Bathyarchaeia	Bathyarchaeia
5	Archaea	Crenarchaeota	Nitrososphaeria	—
6	Archaea	Crenarchaeota	Nitrososphaeria	Marine_Benthic_Group_A
7	Archaea	Crenarchaeota	Nitrososphaeria	Nitrosopumilales
8	Archaea	Crenarchaeota	Nitrososphaeria	Nitrosotaleales
9	Archaea	Halobacterota	Methanomicrobia	Methanomicrobiales
10	Archaea	Halobacterota	Methanosarcinia	Methanosarciniales
11	Bacteria			
12	Archaea	Micrarchaeota	Micrarchaeia	Micrarchaeales
13	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales
14	Archaea	Thermoplasmatota	Thermoplasmata	Methanomassiliicoccales
15	Bacteria	—	—	—
16	Bacteria	Acidobacteriota	—	—
17	Bacteria	Acidobacteriota	Acidobacteriae	
18	Bacteria	Acidobacteriota	Acidobacteriae	Acidobacteriae
19	Bacteria	Acidobacteriota	Acidobacteriae	Bryobacterales
20	Bacteria	Acidobacteriota	Blastocatellia	11-24
21	Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales
22	Bacteria	Acidobacteriota	Blastocatellia	Elev-16S-573
23	Bacteria	Acidobacteriota	Holophagae	Holophagales
24	Bacteria	Acidobacteriota	Subgroup_22	Subgroup_22
25	Bacteria	Acidobacteriota	Subgroup_5	Subgroup_5
26	Bacteria	Acidobacteriota	Vicinamibacteria	Subgroup_17

OTU number	Domain	Phylum	Class	Order
27	Bacteria	Acidobacteriota	Vicinamibacteria	Vicinamibacterales
28	Bacteria	Actinobacteriota	Acidimicrobiia	Microtrichales
29	Bacteria	Actinobacteriota	Actinobacteria	
30	Bacteria	Actinobacteriota	Actinobacteria	Corynebacterales
31	Bacteria	Actinobacteriota	Actinobacteria	Frankiales
32	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales
33	Bacteria	Actinobacteriota	Actinobacteria	PeM15
34	Bacteria	Actinobacteriota	Actinobacteria	Propionibacterales
35	Bacteria	Actinobacteriota	Actinobacteria	uncultured
36	Bacteria	Actinobacteriota	Thermoleophilia	Gaiellales
37	Bacteria	Armatimonadota	Fimbriimonadia	Fimbriimonadales
38	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales
39	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales
40	Bacteria	Bacteroidota	Bacteroidia	Cytophagales
41	Bacteria	Bacteroidota	Bacteroidia	Flavobacterales
42	Bacteria	Bacteroidota	Bacteroidia	Sphingobacterales
43	Bacteria	Bacteroidota	Ignavibacteria	Ignavibacterales
44	Bacteria	Bacteroidota	Kapabacteria	Kapabacterales
45	Bacteria	Bacteroidota	Kryptonia	Kryptoniales
46	Bacteria	Bacteroidota	SJA-28	SJA-28
47	Bacteria	Bdellovibrionota	Bdellovibrionia	Bacteriovoracales
48	Bacteria	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales
49	Bacteria	Bdellovibrionota	Oligoflexia	0319-6G20
50	Bacteria	Bdellovibrionota	Oligoflexia	Silvanigrellales
51	Bacteria	Campilobacterota	Campylobacteria	Campylobacterales
52	Bacteria	Chloroflexi	Anaerolineae	Anaerolineales
53	Bacteria	Chloroflexi	Anaerolineae	RBG-13-54-9
54	Bacteria	Chloroflexi	Chloroflexia	Chloroflexales
55	Bacteria	Chloroflexi	Dehalococcoidia	—
56	Bacteria	Chloroflexi	Dehalococcoidia	661239
57	Bacteria	Chloroflexi	Dehalococcoidia	S085
58	Bacteria	Chloroflexi	Dehalococcoidia	SAR202_clade
59	Bacteria	Chloroflexi	SL56_marine_group	SL56_marine_group
60	Bacteria	Cyanobacteria	Cyanobacteriia	Cyanobacterales
61	Bacteria	Cyanobacteria	Cyanobacteriia	Leptolyngbyales
62	Bacteria	Cyanobacteria	Cyanobacteriia	Oxyphotobacteria_Incertae_Sedis
63	Bacteria	Cyanobacteria	Cyanobacteriia	Phormidesmiales
64	Bacteria	Cyanobacteria	Cyanobacteriia	Pseudanabaenales
65	Bacteria	Cyanobacteria	Cyanobacteriia	SepB-3
66	Bacteria	Cyanobacteria	Cyanobacteriia	Synechococcales
67	Bacteria	Cyanobacteria	Sericytochromatia	Sericytochromatia
68	Bacteria	Cyanobacteria	Vampirivibrionia	Obscuribacterales
69	Bacteria	Cyanobacteria	Vampirivibrionia	Vampiropvibrionales
70	Bacteria	Deinococcota	Deinococci	Deinococcales
71	Bacteria	Desulfobacterota	Desulfuromonadia	—
72	Bacteria	Desulfobacterota	Desulfuromonadia	Desulfuromonadia
73	Bacteria	Desulfobacterota	Desulfuromonadia	Geobacterales
74	Bacteria	Desulfobacterota	Desulfuromonadia	PB19
75	Bacteria	Desulfobacterota	Syntrophia	Syntrophales

OTU number	Domain	Phylum	Class	Order
76	Bacteria	DTB120	DTB120	DTB120
77	Bacteria	Elusimicrobiota	Elusimicrobia	Lineage_IV
78	Bacteria	Elusimicrobiota	Lineage_IIC	Lineage_IIC
79	Bacteria	Firmicutes	Bacilli	Bacillales
80	Bacteria	Firmicutes	Bacilli	Exiguobacterales
81	Bacteria	Firmicutes	Bacilli	Lactobacillales
82	Bacteria	Firmicutes	Bacilli	Staphylococcales
83	Bacteria	Firmicutes	Clostridia	Clostridiales
84	Bacteria	Firmicutes	Clostridia	Peptostreptococcales-Tissierellales
85	Bacteria	Fusobacteriota	Fusobacteriia	Fusobacteriales
86	Bacteria	Gemmatimonadot a	Gemmatimonadetes	Gemmatimonadales
87	Bacteria	Latescibacterota	Latescibacterota	Latescibacterota
88	Bacteria	MBNT15	MBNT15	MBNT15
89	Bacteria	Methylomirabilota	Methylomirabilia	Methylomirabilales
90	Bacteria	Methylomirabilota	Methylomirabilia	Rokubacteriales
91	Bacteria	Myxococcota	bacteriap25	bacteriap25
92	Bacteria	Myxococcota	Myxococcia	Myxococcales
93	Bacteria	Myxococcota	Polyangia	Blfdi19
94	Bacteria	Myxococcota	Polyangia	Haliangiales
95	Bacteria	Myxococcota	Polyangia	Polyangiales
96	Bacteria	NB1-j	NB1-j	NB1-j
97	Bacteria	Nitrospirota	—	—
98	Bacteria	Nitrospirota	4-29-1	4-29-1
99	Bacteria	Nitrospirota	Leptospirillia	Leptospirillales
100	Bacteria	Nitrospirota	Nitrospira	Nitrospirales
101	Bacteria	Nitrospirota	Thermodesulfovibrionia	uncultured
102	Bacteria	Patescibacteria	Berkelbacteria	Berkelbacteria
103	Bacteria	Patescibacteria	Gracilibacteria	Absconditabacteriales_(SR1)
104	Bacteria	Patescibacteria	Gracilibacteria	Candidatus_Peribacteria
105	Bacteria	Patescibacteria	Gracilibacteria	Gracilibacteria
106	Bacteria	Patescibacteria	Kazania	Kazania
107	Bacteria	Patescibacteria	Parcubacteria	—
108	Bacteria	Patescibacteria	Parcubacteria	Candidatus_Adlerbacteria
109	Bacteria	Patescibacteria	Parcubacteria	Candidatus_Azambacteria
110	Bacteria	Patescibacteria	Parcubacteria	UBA9983
111	Bacteria	Planctomycetota	Phycisphaerae	CCM11a
112	Bacteria	Planctomycetota	Pla4_lineage	Pla4_lineage
113	Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales
114	Bacteria	Patescibacteria	Parcubacteria	
115	Bacteria	Patescibacteria	Parcubacteria	Parcubacteria
116	Bacteria	Patescibacteria	Saccharimonadia	Saccharimonadales
117	Bacteria	Proteobacteria	Alphaproteobacteria	
118	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales
119	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales
120	Bacteria	Proteobacteria	Alphaproteobacteria	Defluviicoccales
121	Bacteria	Proteobacteria	Alphaproteobacteria	Dongiales
122	Bacteria	Proteobacteria	Alphaproteobacteria	Holospirales
123	Bacteria	Proteobacteria	Alphaproteobacteria	Micropepsales

OTU number	Domain	Phylum	Class	Order
124	Bacteria	Proteobacteria	Alphaproteobacteria	Paracaedibacterales
125	Bacteria	Proteobacteria	Alphaproteobacteria	Reyranellales
126	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales
127	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales
128	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales
129	Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales
130	Bacteria	Proteobacteria	Alphaproteobacteria	SAR11_clade
131	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales
132	Bacteria	Proteobacteria	Alphaproteobacteria	Zavarziniales
133	Bacteria	Proteobacteria	Alphaproteobacteria	uncultured
134	Bacteria	Proteobacteria	Gammaproteobacteria	Acidiferrobacterales
135	Bacteria	Proteobacteria	Gammaproteobacteria	
136	Bacteria	Proteobacteria	Gammaproteobacteria	211ds20
137	Bacteria	Proteobacteria	Gammaproteobacteria	AT-s2-59
138	Bacteria	Proteobacteria	Gammaproteobacteria	Aeromonadales
139	Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales
140	Bacteria	Proteobacteria	Gammaproteobacteria	B2M28
141	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales
142	Bacteria	Proteobacteria	Gammaproteobacteria	CCD24
143	Bacteria	Proteobacteria	Gammaproteobacteria	CCM19a
144	Bacteria	Proteobacteria	Gammaproteobacteria	Cellvibrionales
145	Bacteria	Proteobacteria	Gammaproteobacteria	Diplorickettsiales
146	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales
147	Bacteria	Proteobacteria	Gammaproteobacteria	Ga0077536
148	Bacteria	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_Incertae_Sedis
149	Bacteria	Proteobacteria	Gammaproteobacteria	KF-JG30-C25
150	Bacteria	Proteobacteria	Gammaproteobacteria	KI89A_clade
151	Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales
152	Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales
153	Bacteria	Proteobacteria	Gammaproteobacteria	Oceanospirillales
154	Bacteria	Proteobacteria	Gammaproteobacteria	PLTA13
155	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales
156	Bacteria	Proteobacteria	Gammaproteobacteria	R7C24
157	Bacteria	Proteobacteria	Gammaproteobacteria	Steroidobacterales
158	Bacteria	Proteobacteria	Gammaproteobacteria	Tenderiales
159	Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales
160	Bacteria	Proteobacteria	Gammaproteobacteria	uncultured
161	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales
162	Bacteria	RCP2-54	RCP2-54	RCP2-54
163	Bacteria	Verrucomicrobiota	Omnitrophia	Omnitrophales
164	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales
165	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Methylacidiphilales
166	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitutales
167	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales

OTU number	Domain	Phylum	Class	Order
168	Bacteria	Verrucomicrobiot a	Verrucomicrobiae	Verrucomicrobiales
169	Bacteria	Verrucomicrobiot a	Verrucomicrobiae	uncultured
170	Bacteria	WOR-1	WOR-1	WOR-1

Table S5. List of OTUs corresponding to the numbering on Figures 3a, 4a and 5b.

OTU number	Domain	Phylum	Class	Order	Family	Genus
1	Unassigned	—	—	—	—	—
2	Archaea	Aenigmarchaeota	Aenigmarchaeia	Aenigmarchaeales	Aenigmarchaeales	Aenigmarchaeales
3	Archaea	Aenigmarchaeota	Deep_Sea_Euryarchaeotic_Group (DSEG)	Deep_Sea_Euryarchaeotic_Group (DSEG)	Deep_Sea_Euryarchaeotic_Group (DSEG)	Deep_Sea_Euryarchaeotic_Group (DSEG)
4	Archaea	Crenarchaeota	Bathyarchaeia	Bathyarchaeia	Bathyarchaeia	Bathyarchaeia
5	Archaea	Crenarchaeota	Nitrososphaeria	—	—	—
6	Archaea	Crenarchaeota	Nitrososphaeria	Marine_Benthic_Group_A	Marine_Benthic_Group_A	Marine_Benthic_Group_A
7	Archaea	Crenarchaeota	Nitrososphaeria	Nitrosopumilales	Nitrosopumilaceae	Nitrosarchaeum
8	Archaea	Crenarchaeota	Nitrososphaeria	Nitrosopumilales	Nitrosopumilaceae	Nitrosopumilaceae
9	Archaea	Crenarchaeota	Nitrososphaeria	Nitrosotaleales	Nitrosotaleaceae	Nitrosotaleaceae
10	Archaea	Micrarchaeota	Micrarchaeia	Micrarchaeales	CG1-02-32-21	CG1-02-32-21
11	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	—	—
12	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	GW2011_GWC1_47_15	GW2011_GWC1_47_15
13	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	SCGC_AAA011-D5	SCGC_AAA011-D5
14	Archaea	Nanoarchaeota	Nanoarchaeia	Woesearchaeales	Woesearchaeales	Woesearchaeales
15	Archaea	Thermoplasmatota	Thermoplasmata	Methanomassiliicoccales	uncultured	uncultured
16	Bacteria	—	—	—	—	—
17	Bacteria	Acidobacteriota	—	—	—	—
18	Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae	Aridibacter
19	Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae	JGI_0001001-H03
20	Bacteria	Acidobacteriota	Blastocatellia	Blastocatellales	Blastocatellaceae	uncultured
21	Bacteria	Acidobacteriota	Subgroup_22	Subgroup_22	Subgroup_22	Subgroup_22
22	Bacteria	Acidobacteriota	Subgroup_5	Subgroup_5	Subgroup_5	Subgroup_5
23	Bacteria	Acidobacteriota	Vicinamibacteria	Vicinamibacterales	Vicinamibacteraceae	Vicinamibacteraceae
24	Bacteria	Acidobacteriota	Vicinamibacteria	Vicinamibacterales	uncultured	uncultured
25	Bacteria	Actinobacteriota	Actinobacteria	Corynebacteriales	Corynebacteriaceae	Corynebacterium
26	Bacteria	Actinobacteriota	Actinobacteria	Corynebacteriales	Corynebacteriaceae	Lawsonella
27	Bacteria	Actinobacteriota	Actinobacteria	Micrococcales	Micrococcaceae	Rothia
28	Bacteria	Actinobacteriota	Actinobacteria	Propionibacteriales	Propionibacteriaceae	Cutibacterium
29	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	Crocinitomicaceae	Fluviicola

OTU number	Domain	Phylum	Class	Order	Family	Genus
30	Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	AKYH767	AKYH767
31	Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	KD3-93	KD3-93
32	Bacteria	Bacteroidota	Bacteroidia	Sphingobacteriales	env.OPS_17	env.OPS_17
33	Bacteria	Bacteroidota	Kryptonia	Kryptoniales	BSV26	BSV26
34	Bacteria	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio
35	Bacteria	Bdellovibrionota	Oligoflexia	0319-6G20	0319-6G20	0319-6G20
36	Bacteria	Campilobacterota	Campylobacteria	Campylobacterales	Sulfurimonadaceae	Sulfuricurvum
37	Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured
38	Bacteria	Chloroflexi	Anaerolineae	RBG-13-54-9	RBG-13-54-9	RBG-13-54-9
39	Bacteria	Chloroflexi	Dehalococcoidia	—	—	—
40	Bacteria	Chloroflexi	Dehalococcoidia	661239	661239	661239
41	Bacteria	Chloroflexi	Dehalococcoidia	S085	S085	S085
42	Bacteria	Chloroflexi	Dehalococcoidia	SAR202_clade	SAR202_clade	SAR202_clade
43	Bacteria	Cyanobacteria	Vampirivibrionia	Obscuribacterales	Obscuribacteraceae	Candidatus_Obscuribacter
44	Bacteria	DTB120	DTB120	DTB120	DTB120	DTB120
45	Bacteria	Desulfobacterota	Desulfuromonadia	—	—	—
46	Bacteria	Elusimicrobiota	Elusimicrobia	Lineage_IV	Lineage_IV	Lineage_IV
47	Bacteria	Elusimicrobiota	Lineage_IIC	Lineage_IIC	Lineage_IIC	Lineage_IIC
48	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
49	Bacteria	Firmicutes	Bacilli	Staphylococcales	Staphylococcaceae	Staphylococcus
50	Bacteria	Latescibacterota	Latescibacterota	Latescibacterota	Latescibacterota	Latescibacterota
51	Bacteria	MBNT15	MBNT15	MBNT15	MBNT15	MBNT15
52	Bacteria	Methyloirabilota	Methyloirabilia	Methyloirabiales	Methyloirabilaceae	Candidatus_Methyloirabilis
53	Bacteria	Methyloirabilota	Methyloirabilia	Methyloirabiales	Methyloirabilaceae	MIZ17
54	Bacteria	Methyloirabilota	Methyloirabilia	Methyloirabiales	Methyloirabilaceae	Sh765B-TzT-35
55	Bacteria	Methyloirabilota	Methyloirabilia	Rokubacteriales	Rokubacteriales	Rokubacteriales
56	Bacteria	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	P3OB-42
57	Bacteria	Myxococcota	bacteriap25	bacteriap25	bacteriap25	bacteriap25
58	Bacteria	Nitrospirota	—	—	—	—
59	Bacteria	Nitrospirota	4-29-1	4-29-1	4-29-1	4-29-1
60	Bacteria	Nitrospirota	Leptospirillia	Leptospirillales	Leptospirillaceae	Leptospirillum
61	Bacteria	Nitrospirota	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira
62	Bacteria	Nitrospirota	Thermodesulfovibrionia	uncultured	uncultured	uncultured

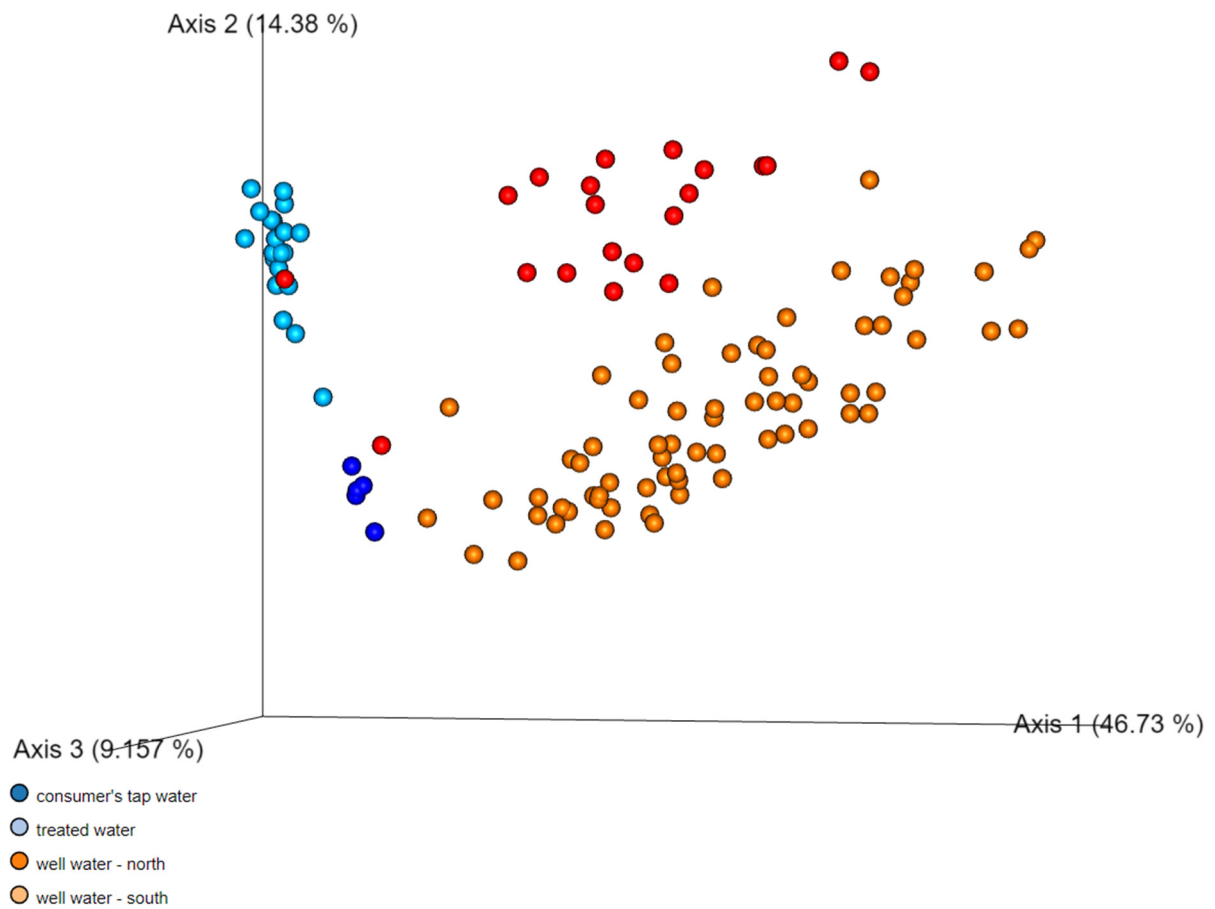
OTU number	Domain	Phylum	Class	Order	Family	Genus
63	Bacteria	Patescibacteria	Berkelbacteria	Berkelbacteria	Berkelbacteria	Berkelbacteria
64	Bacteria	Patescibacteria	Gracilibacteria	Candidatus_Peribacteria	Candidatus_Peribacteria	Candidatus_Peribacteria
65	Bacteria	Patescibacteria	Gracilibacteria	Gracilibacteria	Gracilibacteria	Gracilibacteria
66	Bacteria	Patescibacteria	Kazania	Kazania	Kazania	Kazania
67	Bacteria	Patescibacteria	Parcubacteria	—	—	—
68	Bacteria	Patescibacteria	Parcubacteria	Candidatus_Adlerbacteria	Candidatus_Adlerbacteria	Candidatus_Adlerbacteria
69	Bacteria	Patescibacteria	Parcubacteria	Candidatus_Azambacteria	Candidatus_Azambacteria	Candidatus_Azambacteria
70	Bacteria	Patescibacteria	Parcubacteria	Parcubacteria	Parcubacteria	Parcubacteria
71	Bacteria	Patescibacteria	Parcubacteria	UBA9983	UBA9983	UBA9983
72	Bacteria	Patescibacteria	Saccharimonadia	Saccharimonadales	—	—
73	Bacteria	Planctomycetota	Phycisphaerae	CCM11a	CCM11a	CCM11a
74	Bacteria	Planctomycetota	Pla4_lineage	Pla4_lineage	Pla4_lineage	Pla4_lineage
75	Bacteria	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella
76	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas
77	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	—
78	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Parvularculaceae	Amphiplicatus
79	Bacteria	Proteobacteria	Alphaproteobacteria	Dongiales	Dongiaceae	Dongia
80	Bacteria	Proteobacteria	Alphaproteobacteria	Paracaedibacterales	Paracaedibacteraceae	Candidatus_Paracaedibacter
81	Bacteria	Proteobacteria	Alphaproteobacteria	Reyranellales	Reyranellaceae	Reyranella
82	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Bosea
83	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium- Methylorubrum
84	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Microvirga
85	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	alphaI_cluster
86	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium
87	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium
88	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	uncultured
89	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales_Incertae_Sedis	Phreatobacter
90	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	uncultured
91	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	—
92	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	—
93	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium
94	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Rhizorhapis

OTU number	Domain	Phylum	Class	Order	Family	Genus
95	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium
96	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
97	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingopyxis
98	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingorhabdus
99	Bacteria	Proteobacteria	Alphaproteobacteria	Zavarziniales	uncultured	uncultured
100	Bacteria	Proteobacteria	Alphaproteobacteria	uncultured	uncultured	uncultured
101	Bacteria	Proteobacteria	Gammaproteobacteria	Acidiferrobacterales	Acidiferrobacteraceae	—
102	Bacteria	Proteobacteria	Gammaproteobacteria	Acidiferrobacterales	Acidiferrobacteraceae	Sulfurifustis
103	Bacteria	Proteobacteria	Gammaproteobacteria	B2M28	B2M28	B2M28
104	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	—
105	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Aquabacterium
106	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Rhizobacter
107	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Rhodoferax
108	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Gallionellaceae	—
109	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Gallionellaceae	Candidatus_Nitrotoga
110	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Gallionellaceae	Ferriphaselus
111	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Gallionellaceae	Gallionella
112	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Gallionellaceae	Sideroxydans
113	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Gallionellaceae	uncultured
114	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Leeiaceae	Leeia
115	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	GOUTA6
116	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	IS-44
117	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	Nitrosomonas
118	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	Nitrosospira
119	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Herminiimonas
120	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
121	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	Undibacterium
122	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	Dechloromonas
123	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Rhodocyclaceae	Ferribacterium
124	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Sulfuricellaceae	Sulfuricella
125	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	TRA3-20	TRA3-20
126	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia-Shigella
127	Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methyломonadaceae	Crenothrix

OTU number	Domain	Phylum	Class	Order	Family	Genus
128	Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylomonadaceae	Methylobacter
129	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter
130	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Enhydrobacter
131	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Perlucidibaca
132	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
133	Bacteria	Proteobacteria	Gammaproteobacteria	Tenderiales	Tenderiaceae	Candidatus_Tenderia
134	Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Thiotrichaceae	Thiothrix
135	Bacteria	Proteobacteria	Gammaproteobacteria	uncultured	uncultured	uncultured
136	Bacteria	RCP2-54	RCP2-54	RCP2-54	RCP2-54	RCP2-54
137	Bacteria	Verrucomicrobiota	Omnitrophia	Omnitrophales	Omnitrophaceae	Candidatus_Omnitrophus
138	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Chthoniobacter
139	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Opitutales	Opitutaceae	Opitutus
140	Bacteria	Verrucomicrobiota	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	uncultured
141	Bacteria	WOR-1	WOR-1	WOR-1	WOR-1	WOR-1

Figure S1. Diversity indexes. a) PCoA biplot of the weighted unifracs distances of the samples (beta diversity) b) Rarefaction curves in terms of the observed features as function of the sequencing depth (alpha diversity)

a)



b)

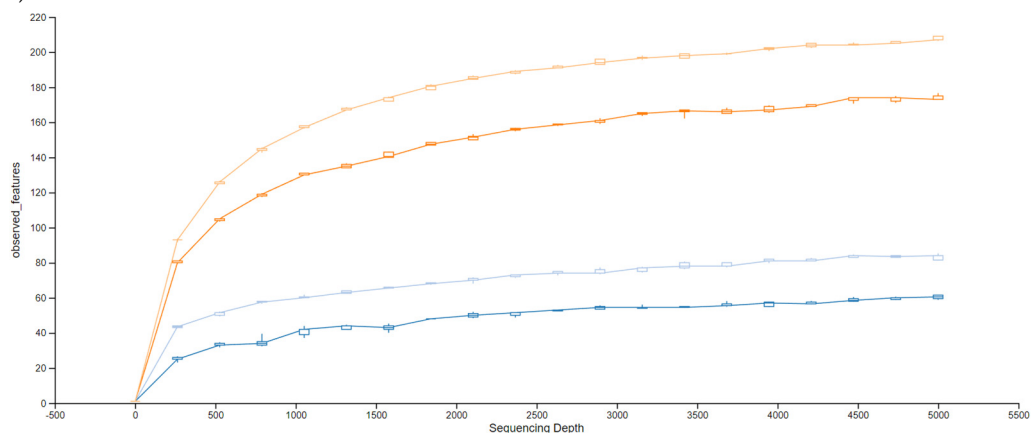
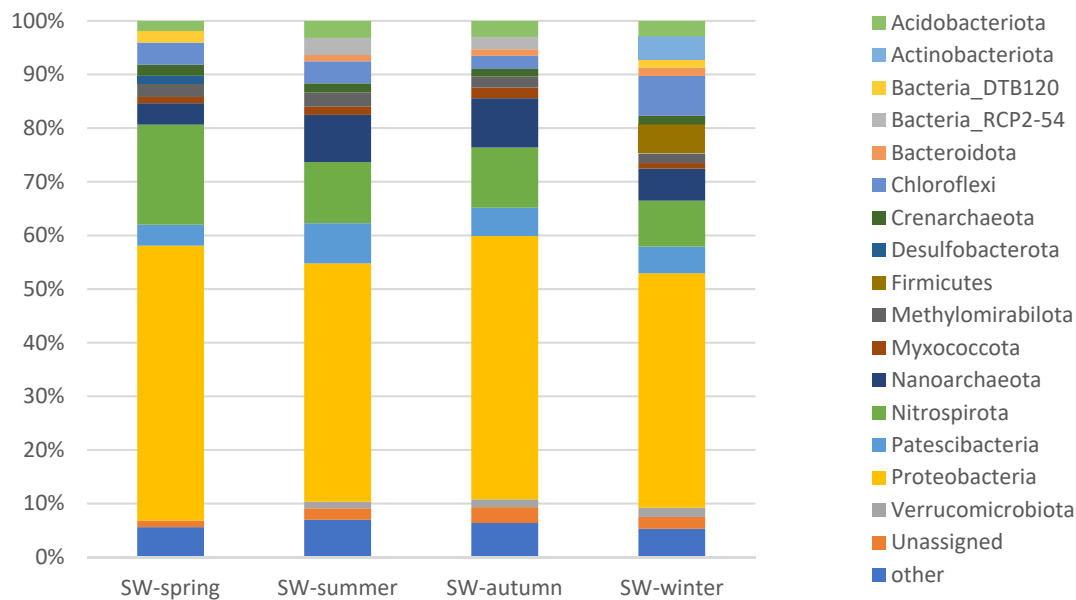


Figure S2. Seasonal variation of microbial community in the Southern wells. a) Visualization of relative abundance of sequences at phylum level. Phyla with abundance below 1% are indicated as “other”. b) Visualization of relative abundance of sequences at order level. Orders with abundance below 1% are indicated as “other”.

a)



b)

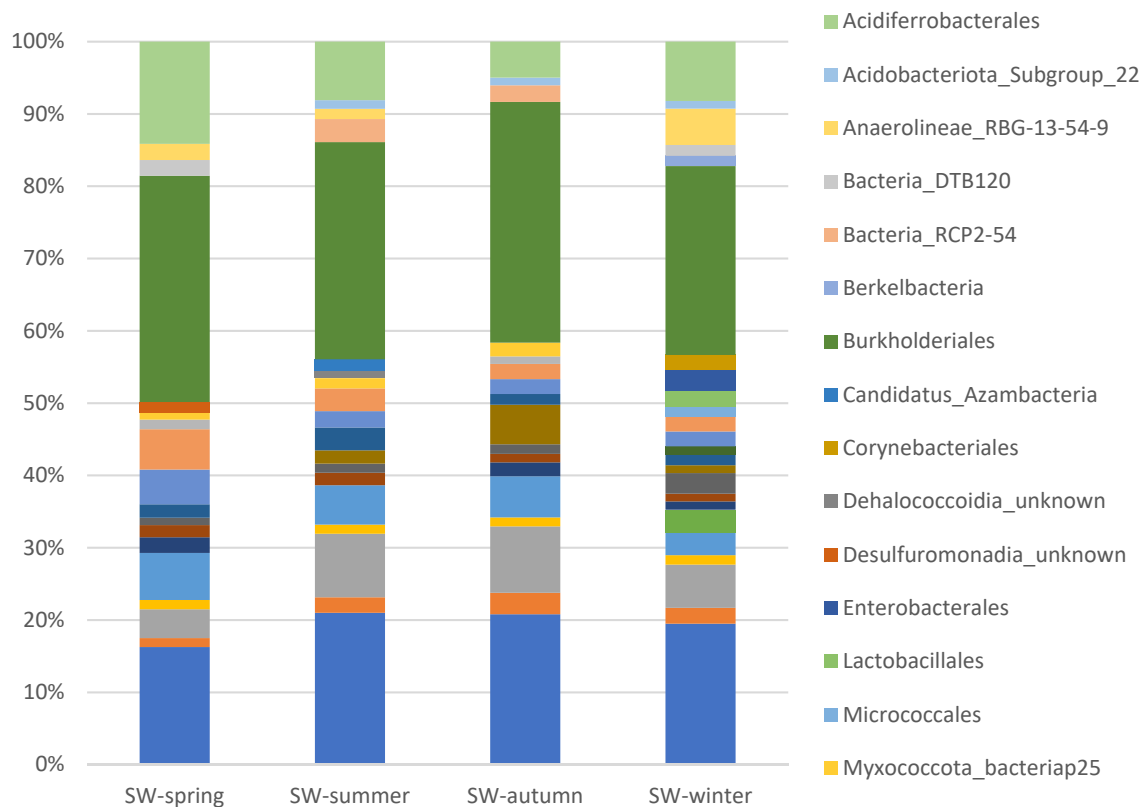


Table S6. Microbial community structure comparison of river water (NR1-3 and SR1-3) well waters and treated water samples. Relative abundances of sequences at phylum level. Phyla with abundance below 1% are indicated as “other”.

Phylum	Danube river	well water	treated water
Acidobacteriota		3,77	6,80
Actinobacteriota	19,27	1,43	2,07
Bacteria_DTB120		1,09	
Bacteria_RCP2-54		1,86	
Bacteroidota	21,73	1,68	
Bdellovibrionota			5,10
Chloroflexi		3,84	
Crenarchaeota		1,94	
Cyanobacteria			1,45
Firmicutes		1,69	3,93
Methyloirabiolota		3,27	
Myxococcota		2,76	
Nanoarchaeota		6,75	
Nitrospirota		10,79	4,15
Patescibacteria		4,62	
Proteobacteria	50,03	45,96	75,64
Verrucomicrobiota	7,33	1,25	
Unassigned		2,07	
other	1,65	5,23	0,87

Table S7. Microbial community structure comparison of river water (NR1-3 and SR1-3) well waters and treated water samples. Relative abundances of sequences at order level. Orders with abundance below 1% are indicated as “other”.

Order	Danube river	well water	treated water
Acidiferrobacterales		6,78	
Alphaproteobacteria_SAR11_clade	1,82		
Alphaproteobacteria_uncultured			5,47
Anaerolineae_RBG-13-54-9		1,82	
Bacteria_DTB120		1,09	
Bacteria_RCP2-54		1,86	
Bdellovibrionales			5,10
Berkelbacteria		1,05	
Blastocatellales			6,75
Burkholderiales	37,85	27,12	32,24
Caulobacterales			3,87
Chitinophagales	4,82		
Cytophagales	6,02		
Enterobacterales		1,04	1,72
Flavobacteriales	6,71		
Frankiales	15,50		
Methylococcales			1,03
Methylospirales		1,48	
Micrococcales	1,45		
Microtrichales	2,25		
Myxococcota_bacteriap25		2,50	
Nitrospirales		2,20	4,07
Nitrospirota_4-29-1		2,29	
Nitrospirota_unknown		2,09	
Obscuribacterales			1,45
Parcubacteria_unknown		1,48	
Pseudomonadales	3,67	2,57	4,01
Reyranellales			2,79
Rhizobiales		3,68	10,71
Rhodobacterales			1,13
Rokubacterales		1,79	
Sphingobacteriales	3,99	1,13	
Sphingomonadales	2,86	2,30	10,67
Staphylococcales		1,08	3,07
Thermodesulfovibrionia_uncultured		3,88	
Verrucomicrobiae_uncultured	4,53		
Verrucomicrobiales	1,22		
Vicinamibacterales		2,06	
Woesearchaeales		6,75	
Unassigned		2,07	
other	7,31	19,88	5,94

Table S8. Microbial community structure comparison of Northern wells (NW2, NW3, NWM) and Southern wells (SW1, SW2, SW3, SWM). Relative abundance of sequences at phylum level. Phyla with abundance below 1% are indicated as “other”.

Phylum	North well	South well
Acidobacteriota	6,92	2,77
Actinobacteriota		1,62
Bacteria_DTB120		1,36
Bacteria_RCP2-54	3,06	1,48
Bacteria_WOR-1	1,58	
Bacteroidota	3,30	1,17
Bdellovibrionota	1,54	
Chloroflexi	2,04	4,57
Crenarchaeota	2,71	1,65
Firmicutes	1,35	1,79
Methyloirabilota	7,55	2,13
Myxococcota	6,88	1,46
Nanoarchaeota	5,49	7,01
Nitrospirota	6,28	11,95
Patescibacteria	2,84	5,11
Proteobacteria	42,52	47,35
Unassigned	1,39	2,27
Verrucomicrobiota		1,37
other	4,55	4,95

Table S9. Microbial community structure comparison of Northern wells (NW2, NW3, NWM) and Southern wells (SW1, SW2, SW3, SWM). Relative abundance of sequences at order level. Orders with abundance below 1% are indicated as “other”.

Order	North well	South well
Acidiferrobacterales		8,27
Acidobacteriota_Subgroup_5	1,12	
Anaerolineae_RBG-13-54-9		2,46
Azospirillales	1,31	
Bacteria_DTB120		1,36
Bacteria_RCP2-54	3,06	1,48
Bacteria_WOR-1	1,58	
Berkelbacteria	1,16	1,00
Burkholderiales	17,65	30,23
Dehalococcoidia_SAR202_clade	1,02	
Enterobacterales	1,25	
Methylomirabilales	3,55	
Myxococcota_bacteriap25	6,21	1,34
Nitrososphaeria_unknown	1,30	
Nitrospirales	6,18	
Nitrospirota_4-29-1		2,92
Nitrospirota_unknown		2,66
Parcubacteria_unknown		1,73
Pseudomonadales	2,60	2,56
Rhizobiales	9,84	1,75
Rokubacterales	4,00	1,30
Sphingobacterales	2,52	
Sphingomonadales	5,80	1,62
Staphylococcales	1,15	1,05
Tenderiales	2,24	
Thermodesulfovibrionia_uncultured		5,00
Unassigned	1,39	2,27
Vicinamibacterales	4,56	1,27
Woesearchaeales	5,49	7,01
other	14,99	22,70

Table S10. Microbial community structure comparison of Southern wells, during water treatment and in the supply system. Relative abundance of sequences at phylum level. Phyla with abundance below 1% are indicated as “other”.

Phylum	South well	water treatment	supply system
Acidobacteriota	2,77	9,34	
Actinobacteriota	1,62	1,61	
Bacteria_DTB120	1,36		
Bacteria_RCP2-54	1,48		
Bacteroidota	1,17		
Bdellovibrionota		7,21	
Chloroflexi	4,57		
Crenarchaeota	1,65		
Cyanobacteria		1,93	
Firmicutes	1,79	3,21	
Methyloirabilota	2,13		
Myxococcota	1,46		
Nanoarchaeota	7,01		
Nitrospirota	11,95	5,68	
Patescibacteria	5,11		
Proteobacteria	47,35	69,82	98,23
Unassigned	2,27		
Verrucomicrobiota	1,37		
other	4,95	1,20	1,77

Table S11. Microbial community structure comparison of Southern wells, during water treatment and in the supply system. Relative abundance of sequences at order level. Orders with abundance below 1% are indicated as “other”.

Order	South well	water treatment	supply system
Acidiferrobacterales	8,27		2,61
Alphaproteobacteria_uncultured		7,43	
Anaerolineae_RBG-13-54-9	2,46		
Bacteria_DTB120	1,36		
Bacteria_RCP2-54	1,48		
Bdellovibrionales		7,21	
Berkelbacteria	1,00		
Blastocatellales		9,27	
Burkholderiales	30,23	21,72	80,11
Caulobacterales		4,88	
Enterobacterales		1,02	
Methylococcales		1,42	
Myxococcota_bacteriap25	1,34		
Nitrospirales		5,57	
Nitrospirota_4-29-1	2,92		
Nitrospirota_unknown	2,66		
Obscuribacterales		1,93	
Parcubacteria_unknown	1,73		
Pseudomonadales	2,56		
Reyranellales		3,51	1,07
Rhizobiales	1,75	11,12	11,30
Rhodobacterales		1,56	
Rokubacterales	1,30		
Sphingomonadales	1,62	14,16	1,27
Staphylococcales	1,05	2,42	
Thermodesulfovibrionia_uncultured	5,00		
Unassigned	2,27		
Vicinamibacterales	1,27		
Woesearchaeales	7,01		
other	22,70	6,80	3,63