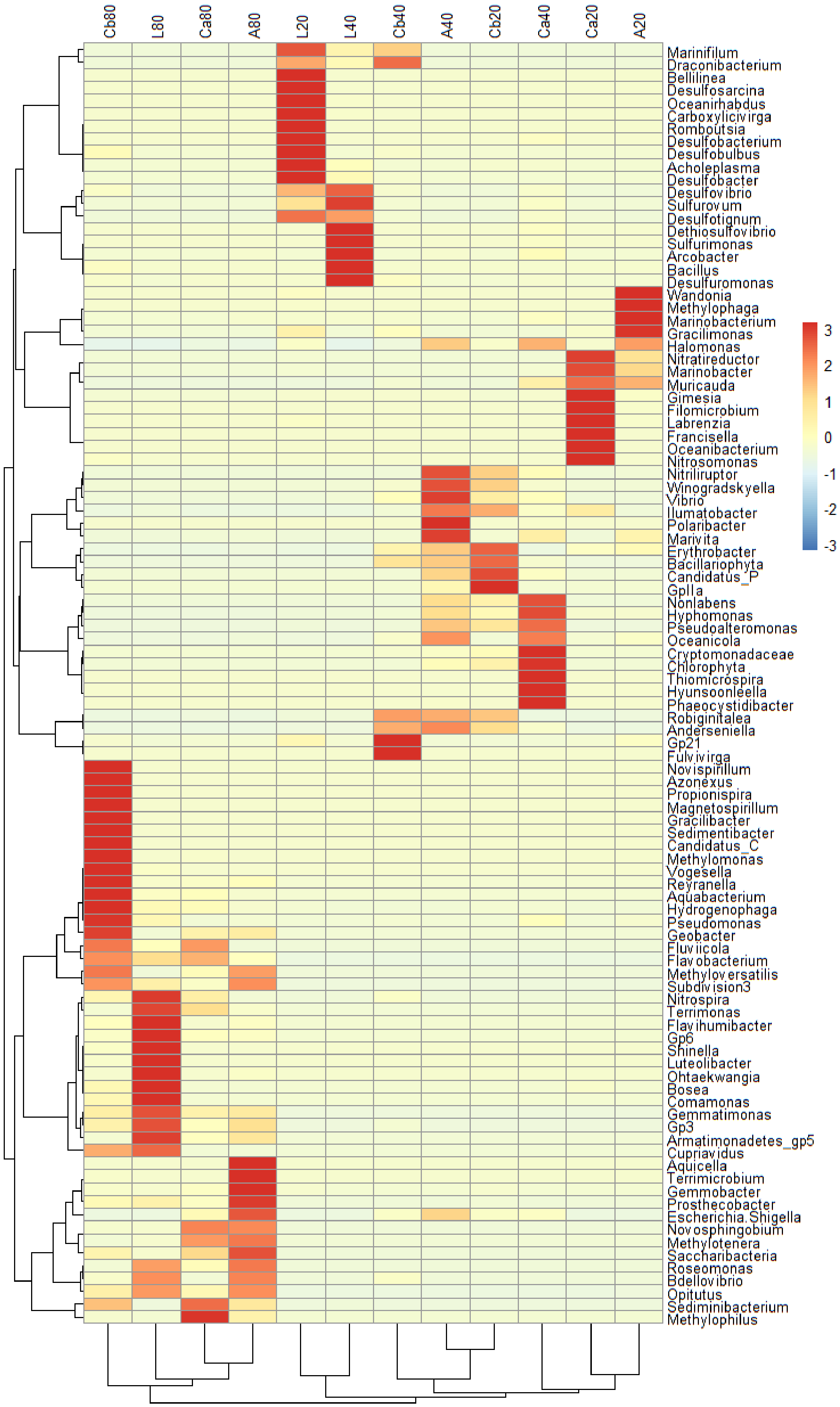

Figure S1. Biodegradation of sulfamethoxazole (SMX) by bacterial strains A12 and L (with fish pond sediment) in aerobic and anaerobic readdition experiments, respectively. Major microbial communities in aerobic and anaerobic experiments with or without bacterial strains A12 and L.

Table S1. Aerobic SA degradation rate constants (*k*) and half-lives ($t_{1/2}$) in Figure 1A.

Treatment	*k* (1/d)	$t_{1/2}$ (d)	R^2
SMX 20 mg/L	0.1052 ± 0.00526	4.75 ± 0.23	0.986
SMX 2 mg/L	0.1328 ± 0.00664	3.76 ± 0.19	0.982
SMZ 20 mg/L	0.0022 ± 0.00011	227.27 ± 11.36	0.909
SMZ 2 mg/L	0.0006 ± 0.00003	833.33 ± 41.66	0.917
SDM 20 mg/L	0.0009 ± 0.00005	555.55 ± 27.77	0.902
SDM 2 mg/L	0.0014 ± 0.00007	357.14 ± 17.85	0.907

R^2: the coefficient of determination.

Table S2. Anaerobic SA degradation rate constants (*k*) and half-lives ($t_{1/2}$) in Figure 1B.

Treatment	*k* (1/d)	$t_{1/2}$ (d)	R^2
SMX 20 mg/L	0.1252 ± 0.00626	3.99 ± 0.19	0.968
SMX 2 mg/L	0.1269 ± 0.00634	3.94 ± 0.18	0.981
SMZ 20 mg/L	0.0036 ± 0.00018	138.88 ± 6.94	0.958
SMZ 2 mg/L	0.0004 ± 0.00002	1250 ± 62.5	0.959
SDM 20 mg/L	0.0023 ± 0.00011	217.39 ± 10.86	0.977
SDM 2 mg/L	0.0021 ± 0.00010	238.09 ± 11.91	0.988

R^2: the coefficient of determination.

Table S3. SMX degradation rate constants (*k*) and half-lives ($t_{1/2}$) in Figure 4.

Strain	*k* (1/d)	$t_{1/2}$ (d)	R^2
Sterilized medium (aerobic)	0.0048 ± 0.00024	104.16 ± 5.21	0.936
A2	0.2989 ± 0.02491	1.67 ± 0.05	0.987
A12	0.4983 ± 0.01494	1.01 ± 0.09	0.975
Sterilized medium (anaerobic)	0.0022 ± 0.00011	227.27 ± 11.36	0.911
M	0.1305 ± 0.00652	3.83 ± 0.19	0.979
L	0.2080 ± 0.01040	2.40 ± 0.12	0.984

The half-live of each treatment (with addition of isolated bacterial strains) was significantly different from the sterilized medium (without addition of isolated bacterial strains) (t-test $P < 0.05$).
R^2: the coefficient of determination.

Table S4. 16S rRNA gene sequence analysed by the NCBI Blast in Figure 5.

Strain	Name	Identity	Accession Number
A2	*Vibrio alginolyticus* strain ATCC 17749	1319/1324 (99%)	NR_118258.1
A12	*Vibrio alginolyticus* strain ATCC 17749	1306/1314 (99%)	NR_118258.1
L	*Pseudomonas pseudoalcaligenes* strain Stanier 63	1267/1285 (99%)	NR_037000.1
M	*Marinobacter pelagius* strain HS225	1285/1299 (99%)	NR_043863.1

Table S5. SMX degradation rate constants (*k*) and half-lives ($t_{1/2}$) in Figure 7.

Strain	*k* (1/d)	$t_{1/2}$ (d)	R^2
Sterilized sediment (aerobic)	0.0028 ± 0.00014	178.57 ± 8.93	0.912
Sediment (aerobic)	0.0148 ± 0.00074	33.78 ± 1.69	0.981
Sediment + A2	0.4258 ± 0.02129	0.67 ± 0.04	0.986
Sediment + A12	0.7378 ± 0.03689	1.17 ± 0.06	0.997
Sterilized sediment (anaerobic)	0.0013 ± 0.00006	384.61 ± 19.23	0.957
Sediment (anaerobic)	0.0822 ± 0.00411	6.08 ± 0.30	0.965
Sediment + M	0.1095 ± 0.00547	4.56 ± 0.23	0.993
Sediment + L	0.1701 ± 0.00851	2.94 ± 0.14	0.981

The half-live of each treatment (with addition of isolated bacterial strains) was significantly different from the sediment and sterilized sediment (without addition of isolated bacterial strains) (t-test $P < 0.05$).
R^2: the coefficient of determination.

Table S6. The aerobic SMX degradation rate constants (k) and half-lives ($t_{1/2}$) following the 3rd and 4th additions of SMX during 81 d of incubation in Figure 8A.

Treatment	With degrading bacteria			Without degrading bacteria		
	k (1/d)	$t_{1/2}$ (d)	R^2	k (1/d)	$t_{1/2}$ (d)	R^2
3rd addition	0.1853 ± 0.0092	2.69 ± 0.13	0.969	0.0335 ± 0.0016	14.9 ± 0.746	0.988
4th addition	0.4299 ± 0.0215	1.16 ± 0.06	0.998	0.024 ± 0.0012	20.8 ± 1.041	0.983

The half-lives of all treatment pairs between with and without bacteria were significantly different (paired t-test $P < 0.05$).
R^2: the coefficient of determination.

Table S7. The anaerobic SMX degradation rate constants (k) and half-lives ($t_{1/2}$) following the 3rd and 4th additions of SMX during 81 d of incubation in Figure 8D.

Treatment	With degrading bacteria			Without degrading bacteria		
	k (1/d)	$t_{1/2}$ (d)	R^2	k (1/d)	$t_{1/2}$ (d)	R^2
3rd addition	0.1605 ± 0.008	3.1 ± 0.15	0.985	0.0087 ± 0.0004	57.4 ± 2.87	0.979
4th addition	0.1023 ± 0.0051	4.9 ± 0.24	0.979	0.0068 ± 0.0003	73.5 ± 3.67	0.981

The half-lives of all treatment pairs between with and without bacteria were significantly different (paired t-test $P < 0.05$).
R^2: the coefficient of determination.