Text S1 Analyses of antibiotics

To quantify the concentrations of the antibiotics, water samples (500 mL) were filtered through 0.45 μm glass microfiber filters (Shanghai Sunggong Technology Co., Ltd.; Shanghai, China). The pH of water samples was adjusted to 3 using formic acid. Na_2EDTA (0.4 g) was added to the solution. After that water samples were loaded onto Waters Oasis HLB cartridges (500 mg, 6 mL), which were preconditioned sequentially with 5 mL of methanol and 5 mL of ultrapure water, at a flow rate of 8 mL/min. The cartridges were rinsed with 5 mL of 5% methanol aqueous solution and 5 mL of ultrapure water, then dried under vacuum. Antibiotics were eluted with 5 mL of methanol, and the eluent was concentrated under a gentle stream of nitrogen to dryness. The extract was redissolved with 1.0 mL methanol and analyzed.

The target antibiotics were analyzed by high-performance liquid chromatography–tandem mass spectrometry (HPLC-MS/MS). The HPLC separation was conducted using a Thermo TSQ Quantum Access Max (Thermo Scientific, USA) equipped with an Agilent Zorbax Eclipse XDB-C18 column (4.6 × 100 mm, 5μm). The column was maintained at 30 °C during sample analysis. The mobile phase consisted of Mobile Phase A (acetonitrile) and Mobile Phase B (0.1% formic acid in ultrapure water). The flow rate was kept at 0.3 mL/min, and the injection volume was 25 μL. The separation of antibiotics was achieved with the following gradient program: 0 - 2 min, 15 % A; 3 - 5 min, 15 % - 60 % A; 6 - 8 min, 60 % - 15 % A. Mass spectrometric analyses were performed using an Agilent 6410 triple quadrupole mass spectrometer equipped with an electrospray ionization source that operated in the positive ionization mode. More information on mass spectrometry condition, fragment ions for identification and quantification were listed in supplementary material including Table S1.

Mass spectrometric analyses were performed by an Agilent 6410 triple quadrupole mass spectrometer equipped with an electrospray ionization source that operated in the positive ionization mode. The nebulizer pressure was set to 40 psi and the flow rate of drying gas was set to 3 L/min. The capillary and nozzle voltages were 4000 and 0 V, respectively. The flow rate and temperature of the sheath gas were 8 L/min and 350 °C, respectively. Sample acquisition was performed in the multiple reaction monitoring (MRM) mode, by recording two MRM per compound. The detailed fragment ions parameters are shown in Table S1. Internal standard method was selected for quantification throughout with standard curves of 7-point ranging from 5 ng/mL to 500 ng/mL based

on the surrogate standard. The coefficient (R^2) of standard curves for all these antibiotics were 0.99 for OFL and 0.97 for TET.

Table S1 The fragment ions parameters

	Parent	Product	SRE Collision Energy
Ofloxacin	362	261.5	27
		318.3	17
Ofloxacin-d3	365	261.5	27
		321.3	17
Tetracycline	445	410.3	20
		427.7	7

Text S2 DNA extraction, amplification and sequencing

Genomic DNA was extracted using the E.Z.N.A.® Tissue DNA kit (Omega Bio-tek, Norcross, GA, U.S.). DNA integrity and purity were monitored on 1% agarose gels. DNA concentration and purity were measured using the spectrophotometer (UVP, USA) at the same time. 16S rRNA genes of V3-V4 region were amplified used 341F/805R primer for the bacterial communities. Primers were synthesized by Qubit® 3.0 (Invitrogen, Carlsbad, CA, USA). PCR reactions, containing 15 μl 2x Premix Taq (Vazyme, Biotech Co.,Ltd, China), 1 μl each primer(10 μM) and DNA (20 ng/μl) template in a volume of 30 μl, were amplified by thermocycling: 3 min at 95°C for initialization; 5 cycles of 20 s denaturation at 94°C, 20 s annealing at 55°C, and 30 s extension at 72°C; followed by 5 min final elongation at 72°C. 3 replicates per sample and each PCR products of the same sample were mixed, the PCR instrument was T100TM Thermal Cyeler (Bio-Rad Laboratory, USA). Then, the PCR products were detected by 1% agarose gel electrophoresis and purified using the MagicPure Size Selection DNA Beads (Transgen, Beijing, China) according to the manufacturer's instructions. Sequencing libraries were generated using NEBNext® Ultra™ DNA Library Prep Kit for Illumina® (New England Biolabs, MA, USA) following manufacturer's recommendations and index codes were added. The library quality was assessed on the Qubit@ 2.0 Fluorometer (Thermo Fisher Scientific, MA, USA) and Agilent Bioanalyzer 2100 system (Agilent Technologies, Waldbron, Germany). At last, the library was sequenced on an Illumina MiSeq300 platform (Shanghai Sunggong Technology Co., Ltd.; Shanghai, China) and 200 bp paired-end reads were generated.

Table S2 Antibiotic concentrations of ofloxacin and tetracycline in rivers across the continents.[1]

	Continent/Country	Rivers	Antibiotic Concentration (ng L^{-1})			
			OFL		TET	
	ASIA		MIN	MAX	MIN	MAX
1	India	Isaka-Nakkavagu	180	10000	NA	NA
2	India	Gomti River	BDL	BDL	NA	NA
3	China	Hai River System	NA	11700	NA	25500
4	China	Songhua River	0.01	1.8	NA	NA
5	China	Beijiang River	ND	36.7	NA	NA
6	China	Huangpu River	ND	28.5	ND	54.3
7	China	Huangpu River	NA	16.14	NA	ND
8	China	Haihe River	ND	10.5	NA	NA
9	China	Nanming River	NA	NA	NA	6800
10	China	Pearl River	ND	1560	ND	72.6
11	China	Beijing River	0.34	990	NA	NA
12	China	Wangyang River	NA	11735	NA	25538
13	Iran	Kan River	NA	NA	NA	NA
14	Iran	Firozabad River	NA	NA	NA	NA
	AFRICA					
1	Kenya	Nairobi River Basin	NA	NA	NA	NA
2	Ghana	Rivers of Ghana	NA	NA	11	30
3	South Africa	Rivers of Durban	NA	NA	NA	NA
	EUROPE					
1	Poland	Reda River	NA	NA	NA	NA
2	Poland	Reda River	NA	NA	NA	NA
3	Poland	Drweca River	NA	NA	16	34
4	Spain	Ter River	86	186	NA	NA
5	Luxembourg	Alzette River	NA	NA	1	8
6	Luxembourg	Mess River	NA	NA	1	7
7	France	Predecelle River	NA	65	NA	7.4
8	France	Charmoise River	NA	231	NA	NA
	AMERICA					
1	USA	Poudre River	NA	NA	ND	102700
2	Cuba	Almendares River	NA	NA	1	155.7
	AUSTRALIA					
1	Australia	Australian Rivers	NA	NA	NA	80

Abbreviations: OFL, Ofloxacin; TET, Tetracycline; NA, Not available; BQL, Below quantification limit; ND, Not detected.

1. Singh R, Singh A P, Kumar S, et al. Antibiotic Resistance in Major Rivers in the World: A Systematic Review on Occurrence, Emergence, and Management Strategies[J]. Journal of Cleaner Production, 2019.

Table S3 pH in CWs (-R indicates the microcosms treated with root exudates, Mixture = the mixture of tetracycline and ofloxacin).

	influent pH	effluent pH	change of pH
Control	7.15	7.30	0.15
Tetracycline	7.1	7.39	0.29
Ofloxacin	7.2	7.42	0.22
Mixture	7.24	7.44	0.20
Control-R	7.00	7.32	0.32
Tetracycline-R	7.05	7.39	0.34
Ofloxacin-R	7.02	7.37	0.35
Mixture-R	7.14	7.41	0.27

Table S4 The relative contribution of the thirteen most common bacterial phylum to the biofilm communities from the eight treatments (OFL = ofloxacin, TET = tetracycline, OT = the mixture of tetracycline and ofloxacin, R indicates the microcosms treated with exudates).

Phylum (%)	Control	OFL	TET	OT	Control-R	OFL-R	TET-R	OT-R
Proteobacteria	62.17	77.01	59.2	88.01	93.38	73.67	97.63	92.45
Actinobacteria	24.23	7.72	15.08	2.66	3.07	11.63	0.48	1.42
Bacteroidetes	3.68	6.63	10.09	4.87	1.72	6.8	0.81	2.9
Planctomycetes	4.1	2.52	4.4	2.02	0.38	0.63	0.17	0.3
Firmicutes	0.68	1.37	1.06	1.1	1.07	2.38	0.56	2.02
Chlamydiae	3.93	0.57	5.22	0.35	0.07	0.08	0.09	0.28
Candidatus Saccharibacteria	0	3.13	0.48	0.01	0	4	0.01	0.01
Parcubacteria	0.38	0.26	2.2	0.44	0.04	0.22	0.08	0.2
unclassified	0.34	0.36	1.04	0.04	0.12	0.17	0.01	0.04
Acidobacteria	0.45	0.22	0.67	0.15	0.05	0.16	0.07	0.2
Verrucomicrobia	0.01	0.15	0.42	0.21	0.08	0.22	0.08	0.08
Nitrospirae	0.01	0.07	0.1	0.14	0	0	0.01	0
Deinococcus-Thermus	0.01	0.01	0.04	0.01	0.01	0.04	0.01	0.1

Table S5 Significant differences (*p* value) between different treatments (O = ofloxacin, T = tetracycline, OT = the mixture of tetracycline and ofloxacin, R indicates the microcosms treated with exudates).

	C vs O	C vs T	C vs OT	CR vs OR	CR vs TR	CR vs OTR
Phylum						
Proteobacteria	0	9.92E-19	0	0	7.35E-220	1.93E-08
Actinobacteria	0	3.74E-248	0	0	2.47E-215	2.058E-11
Bacteroidetes	1.93E-93	2.33E-308	2.23E-17	2.72E-322	1.51E-35	9.26E-35
Planctomycetes	7.12E-43	0.033	1.65E-68	3.48E-7	4.34E-10	0.036
Firmicutes	1.58E-25	3.73E-09	1.59E-10	4.94E-51	6.47E-18	2.67E-33
Chlamydiae	3.41E-306	2.62E-19	6.59E-319	0.80	0.35	2.04E-15
Genus						
Pseudomonas	0	0	0	0	4.44E-46	0
Janthinobacterium	8.34E-08	6.53E-24	5.47E-60	1.32E-43	4.17E-87	4.98E-49
Ensifer	1.06E-283	1.58E-83	0	0.504	1.49E-91	7.67E-42
Arthrobacter	0	1.08E-252	0	0	9.39E-218	6.10E-78
Rhizobium	0	6.89E-44	0	0	9.75E-270	0
Rhizobacter	0.781	6.20E-70	0.0001	2.50E-32	0	0

Table S6 The relative contribution of the thirty-five most common bacterial genus to the biofilm communities from the eight treatments (OFL = ofloxacin, TET = tetracycline, OT = the mixture of tetracycline and ofloxacin, R indicates the microcosms treated with exudates).

Genus (%)	Control	OFL	TET	OT	Control-R	OFL-R	TET-R	OT-R
Pseudomonas	13.17	5.37	51.99	75.43	14	16.3	43.5	38.87
Janthinobacterium	1.86	2.92	2.37	0.62	17.17	24.84	20.88	15.83
Ensifer	8.31	5.01	3.03	1.05	10.93	13.63	10.79	15.29
Arthrobacter	23.63	14.51	7.47	2.56	11.49	1.22	2.88	0.4
Rhizobium	14.54	18.07	5.32	1.52	5.64	5.3	0.95	4.6
unclassified	7.82	13.54	7.39	4.82	4.66	5.09	4.04	2.79
Rhizobacter	0.49	1.73	0.5	0.69	0.93	17.15	0.31	7.29
Gemmobacter	0.59	2.13	0.7	0.72	8.34	3.21	4.45	7.24
Parasegetibacter	0.46	0.49	2.97	3.25	4.9	1.23	0.62	0.01
Sediminibacterium	1.87	5.65	1.54	1.03	0.46	1.34	0.91	0.42
Parachlamydia	3.88	5.11	0.39	0.31	0.08	0.28	0.07	0.08
Saccharibacteria_genera_incertae_sedis	0	0.48	3.13	0.01	4	0.01	0	0.01
Massilia	4.32	1.43	0.29	0.24	0.56	0.23	0.38	0.12
Bradyrhizobium	1.78	1.38	0.47	0.39	1.08	0.59	1.06	0.57
Neorhizobium	0.51	0.83	0.8	0.17	0.26	1.92	0.5	0.91
Hydrogenophaga	1.45	1.71	0.85	0.51	0.17	0.49	0.49	0.25
Vasilyevaea	0.71	1	0.35	0.33	2.18	0.26	0.57	0.38
Brevundimonas	1.31	1.76	0.5	0.4	0.77	0.24	0.24	0.18
Sphingomonas	1.56	1.25	0.37	0.25	0.74	0.44	0.21	0.28
Azohydromonas	0	0.71	0.21	0.63	3.58	0.2	0	0.01
Shinella	0.07	0.04	0.04	0.06	0.21	0.22	3.25	0.41
Pirellula	1.22	0.86	0.93	0.9	0.09	0.12	0.12	0.05
Sphingopyxis	1.12	2.51	0.18	0.17	0.12	0.03	0.18	0.08
Noviherbaspirillum	0.36	0.36	0.17	0.04	0.5	0.91	0.88	0.48
Parcubacteria_genera_incertae_sedis	0.38	2.2	0.26	0.44	0.22	0.2	0.04	0.08
Pseudoxanthomonas	0.01	0.12	1.56	0.42	0.69	0.08	0.1	0.37
Domibacillus	0.27	0.26	0.01	0.01	1.83	0.53	0.34	0.13
Planctopirus	0.99	1.03	0.38	0.15	0.02	0.01	0.11	0.01
Sphingobium	0.07	0.01	0.01	0.02	0.19	1.01	0.37	0.25
Bacillus	0.19	0.43	0.35	0.3	0.17	0.37	0.07	0.06
Pelomonas	0.19	0.45	0.11	0.07	0.27	0.26	0.12	0.31
Mesorhizobium	1.26	0.15	0.08	0.04	0.02	0.04	0.07	0.05
Singulisphaera	0.39	0.86	0.15	0.07	0.07	0.06	0.01	0.02
Devosia	0.38	0.33	0.08	0.05	0.33	0.2	0.03	0.15
Aminobacter	1.15	0.07	0.1	0.02	0.08	0.02	0.03	0
others	3.69	5.24	4.95	2.31	3.25	1.97	1.43	2.02

Table S7 Anosim analyses of different groups (O = ofloxacin, T = tetracycline, OT = the mixture of tetracycline and ofloxacin, R indicates the microcosms treated with root exudates).

Group	Anosim	
No root exudates VS Root exudates	R = 0.2396	P = 0.099
C-T VS O-T VS OR-TR-CR-OTR	R = 0.5000	P = 0.065
C-T VS O-T VS TR-CR VS OTR-OR	R = 0.9304	P = 0.004

Table S8 The distribution of the functional capacities at the level2 of KEGG from all microcosms (OFL = ofloxacin, TET = tetracycline, OT = the mixture of tetracycline and ofloxacin, R indicates the microcosms treated with root exudates).

	Control		OFL		TET		OT		Control-R		OFL-R		TET-R		OT-R	
	abundance	%	abundance	%	abundance	%	abundance	%	abundance	%	abundance	%	abundance	%	abundance	%
Membrane Transport	3.65E+06	14.65	2.88E+06	12.92	3.41E+06	13.39	2.62E+06	12.12	3.72E+06	14.80	3.58E+06	14.50	4.31E+06	14.48	5.08E+06	13.86
Amino Acid Metabolism	2.69E+06	10.78	2.37E+06	10.64	2.74E+06	10.75	2.28E+06	10.53	2.60E+06	10.33	2.58E+06	10.45	3.01E+06	10.14	3.64E+06	9.95
Carbohydrate Metabolism	2.53E+06	10.14	2.10E+06	9.46	2.61E+06	10.24	1.97E+06	9.13	2.26E+06	8.99	2.38E+06	9.63	2.72E+06	9.15	3.40E+06	9.28
Replication and Repair	1.53E+06	6.13	1.40E+06	6.31	1.67E+06	6.56	1.38E+06	6.37	1.46E+06	5.81	1.50E+06	6.07	1.80E+06	6.04	2.30E+06	6.29
Poorly Characterized	1.23E+06	4.94	1.21E+06	5.42	1.23E+06	4.83	1.24E+06	5.74	1.31E+06	5.20	1.23E+06	4.97	1.54E+06	5.19	1.88E+06	5.12
Energy Metabolism	1.31E+06	5.27	1.17E+06	5.25	1.42E+06	5.57	1.11E+06	5.13	1.28E+06	5.08	1.32E+06	5.34	1.57E+06	5.28	2.00E+06	5.47
Cell Motility	8.24E+05	3.31	8.45E+05	3.80	7.93E+05	3.11	9.25E+05	4.27	1.13E+06	4.48	9.82E+05	3.98	1.33E+06	4.49	1.67E+06	4.56
Cellular Processes and Signaling	8.71E+05	3.50	9.18E+05	4.13	8.90E+05	3.49	9.61E+05	4.45	1.04E+06	4.12	9.45E+05	3.82	1.21E+06	4.07	1.49E+06	4.08
Metabolism of Cofactors and Vitamins	9.85E+05	3.95	8.79E+05	3.95	1.05E+06	4.11	8.45E+05	3.91	9.66E+05	3.84	9.83E+05	3.98	1.18E+06	3.96	1.50E+06	4.10
Xenobiotics Biodegradation and Metabolism	1.02E+06	4.10	8.23E+05	3.70	1.00E+06	3.93	7.68E+05	3.55	9.36E+05	3.72	9.32E+05	3.77	1.16E+06	3.90	1.48E+06	4.04
Lipid	9.52E+0	3.82	8.75E+0	3.93	9.75E+0	3.83	8.70E+0	4.02	9.23E+0	3.67	8.83E+0	3.58	1.06E+0	3.58	1.28E+0	3.48

Metabolism	5		5		5		5		5		5		6		6	
Translation	8.96E+05	3.60	8.37E+05	3.76	9.98E+05	3.92	8.11E+05	3.75	8.46E+05	3.36	8.74E+05	3.54	1.01E+06	3.40	1.28E+06	3.48
Signal Transduction	5.66E+05	2.27	6.05E+05	2.72	5.66E+05	2.22	6.40E+05	2.96	7.40E+05	2.94	6.52E+05	2.64	8.65E+05	2.91	1.08E+06	2.94
Nucleotide Metabolism	7.58E+05	3.04	6.56E+05	2.95	8.08E+05	3.17	6.24E+05	2.89	7.30E+05	2.90	7.49E+05	3.03	8.64E+05	2.91	1.07E+06	2.91
Metabolism	6.47E+05	2.60	6.00E+05	2.70	6.51E+05	2.56	5.79E+05	2.68	6.88E+05	2.74	6.64E+05	2.69	8.11E+05	2.73	1.04E+06	2.84
Transcription	5.90E+05	2.37	5.25E+05	2.36	5.90E+05	2.32	5.05E+05	2.33	6.08E+05	2.42	5.91E+05	2.39	6.82E+05	2.29	8.23E+05	2.25
Genetic Information Processing	5.64E+05	2.26	5.25E+05	2.36	5.77E+05	2.26	5.37E+05	2.48	5.87E+05	2.33	5.67E+05	2.30	7.25E+05	2.44	8.59E+05	2.35
Folding, Sorting and Degradation	5.00E+05	2.01	4.99E+05	2.24	5.39E+05	2.12	5.06E+05	2.34	5.21E+05	2.07	5.11E+05	2.07	6.16E+05	2.07	7.66E+05	2.09
Metabolism of Other Amino Acids	4.79E+05	1.92	4.24E+05	1.90	4.87E+05	1.91	4.11E+05	1.90	4.92E+05	1.96	4.77E+05	1.93	5.73E+05	1.93	7.00E+05	1.91
Metabolism of Terpenoids and Polyketides	4.99E+05	2.00	4.55E+05	2.04	5.18E+05	2.04	4.54E+05	2.10	4.76E+05	1.89	4.64E+05	1.88	5.63E+05	1.89	6.61E+05	1.80
Enzyme Families	4.10E+05	1.65	3.86E+05	1.73	4.26E+05	1.67	3.76E+05	1.74	4.36E+05	1.73	4.31E+05	1.74	5.06E+05	1.70	6.51E+05	1.78
Glycan Biosynthesis and Metabolism	4.05E+05	1.63	4.29E+05	1.93	4.65E+05	1.83	4.22E+05	1.95	4.25E+05	1.69	4.17E+05	1.69	4.82E+05	1.62	5.99E+05	1.64

Biosynthesis of Other Secondary Metabolites	2.39E+05	0.96	1.95E+05	0.88	2.43E+05	0.95	1.76E+05	0.81	2.11E+05	0.84	2.27E+05	0.92	2.33E+05	0.78	2.75E+05	0.75
Cell Growth and Death	1.80E+05	0.72	1.19E+05	0.54	1.91E+05	0.75	9.86E+04	0.46	1.55E+05	0.62	1.66E+05	0.67	1.86E+05	0.63	2.22E+05	0.61
Infectious Diseases	1.02E+05	0.41	1.06E+05	0.48	1.05E+05	0.41	1.08E+05	0.50	1.25E+05	0.50	1.13E+05	0.46	1.36E+05	0.46	1.55E+05	0.42
Neurodegenerative Diseases	1.08E+05	0.43	8.78E+04	0.39	1.13E+05	0.44	8.59E+04	0.40	1.10E+05	0.44	1.06E+05	0.43	1.34E+05	0.45	1.53E+05	0.42
Endocrine System	7.26E+04	0.29	6.62E+04	0.30	7.80E+04	0.31	6.70E+04	0.31	7.16E+04	0.28	6.83E+04	0.28	8.93E+04	0.30	1.25E+05	0.34
Transport and Catabolism	7.79E+04	0.31	7.18E+04	0.32	8.32E+04	0.33	7.14E+04	0.33	7.16E+04	0.28	7.45E+04	0.30	8.39E+04	0.28	1.02E+05	0.28
Cancers	5.04E+04	0.20	3.38E+04	0.15	5.46E+04	0.21	2.74E+04	0.13	4.47E+04	0.18	4.60E+04	0.19	5.15E+04	0.17	5.72E+04	0.16
Signaling Molecules and Interaction	3.73E+04	0.15	3.79E+04	0.17	4.13E+04	0.16	3.14E+04	0.15	4.35E+04	0.17	4.50E+04	0.18	4.33E+04	0.15	5.78E+04	0.16
Environmental Adaptation	3.46E+04	0.14	3.01E+04	0.14	3.73E+04	0.15	2.94E+04	0.14	3.43E+04	0.14	3.34E+04	0.14	4.25E+04	0.14	5.40E+04	0.15
Nervous System	2.69E+04	0.11	2.75E+04	0.12	2.56E+04	0.10	2.87E+04	0.13	3.07E+04	0.12	2.60E+04	0.11	3.38E+04	0.11	3.54E+04	0.10
Metabolic Diseases	2.04E+04	0.08	1.80E+04	0.08	2.13E+04	0.08	1.70E+04	0.08	2.23E+04	0.09	2.12E+04	0.09	2.46E+04	0.08	3.07E+04	0.08
Circulatory System	1.43E+04	0.06	1.41E+04	0.06	1.54E+04	0.06	1.50E+04	0.07	1.81E+04	0.07	1.55E+04	0.06	2.28E+04	0.08	2.96E+04	0.08
Digestive System	8.40E+03	0.03	7.91E+03	0.04	9.02E+03	0.04	8.42E+03	0.04	1.35E+04	0.05	1.25E+04	0.05	1.55E+04	0.05	2.12E+04	0.06
Immune	1.30E+0	0.05	1.10E+0	0.05	1.40E+0	0.06	1.02E+0	0.05	1.26E+0	0.05	1.13E+0	0.05	1.49E+0	0.05	1.87E+0	0.05

System	4		4		4		4		4		4		4		4	
Immune System Diseases	1.14E+04	0.05	1.01E+04	0.05	1.08E+04	0.04	1.01E+04	0.05	1.23E+04	0.05	1.17E+04	0.05	1.40E+04	0.05	1.76E+04	0.05
Excretory System	9.62E+03	0.04	6.41E+03	0.03	9.34E+03	0.04	5.66E+03	0.03	9.37E+03	0.04	9.23E+03	0.04	1.15E+04	0.04	1.64E+04	0.04
Cardiovascular Diseases	8.54E+03	0.03	3.55E+03	0.02	9.05E+03	0.04	1.77E+03	0.01	6.16E+03	0.02	7.49E+03	0.03	7.39E+03	0.02	6.74E+03	0.02
Sensory System	6.00E+00	0.00	7.00E+00	0.00	3.00E+00	0.00	9.00E+00	0.00	4.00E+00	0.00	5.00E+00	0.00	0.00E+00	0.00	2.00E+00	0.00
Cell Communication	0.00E+00	0.00	0.00E+00	0.00	0.00E+00	0.00	0.00E+00	0.00	0.00E+00	0.00	1.00E+00	0.00	0.00E+00	0.00	0.00E+00	0.00

Table S9 The magnitude of difference of functional composition among antibiotic-treated and control treatments (OFL = ofloxacin, TET = tetracycline, OT = the mixture of tetracycline and ofloxacin, R indicates the microcosms treated with root exudates).

	OFL	TET	OT	OFL-R	TET-R	OT-R
Membrane Transport	-1.726	-1.259	-2.532	-0.298	-0.316	-0.932
Amino Acid Metabolism	-0.142	-0.035	-0.253	0.121	-0.192	-0.376
Carbohydrate Metabolism	-0.683	0.093	-1.018	0.639	0.155	0.285
Replication and Repair	0.173	0.432	0.241	0.263	0.238	0.488
Poorly Characterized	0.478	-0.103	0.804	-0.229	-0.004	-0.073
Energy Metabolism	-0.021	0.300	-0.139	0.261	0.202	0.398
Cell Motility	0.492	-0.192	0.969	-0.507	0.006	0.077
Cellular Processes and Signaling	0.630	-0.003	0.949	-0.301	-0.054	-0.043
Metabolism of Cofactors and Vitamins	-0.002	0.163	-0.044	0.142	0.120	0.263
Xenobiotics Biodegradation and Metabolism	-0.397	-0.162	-0.543	0.053	0.180	0.323
Lipid Metabolism	0.111	0.008	0.204	-0.091	-0.092	-0.184
Translation	0.165	0.320	0.154	0.175	0.035	0.119
Signal Transduction	0.447	-0.052	0.684	-0.304	-0.034	-0.006
Nucleotide Metabolism	-0.091	0.132	-0.154	0.130	0.004	0.012
Metabolism	0.097	-0.042	0.078	-0.048	-0.009	0.100
Transcription	-0.009	-0.052	-0.035	-0.022	-0.122	-0.169
Genetic Information Processing	0.096	0.001	0.220	-0.037	0.104	0.013
Folding, Sorting and Degradation	0.235	0.111	0.333	-0.003	-0.001	0.021
Metabolism of Other Amino Acids	-0.018	-0.009	-0.021	-0.025	-0.029	-0.045
Metabolism of Terpenoids and Polyketides	0.041	0.034	0.097	-0.011	0.002	-0.087
Enzyme Families	0.087	0.026	0.092	0.011	-0.030	0.047
Glycan Biosynthesis and Metabolism	0.303	0.200	0.325	0.000	-0.067	-0.050
others	-0.266	0.089	-0.413	0.080	-0.097	-0.180

Notes: Values = the percentage of the functional capacities in microcosm exposed to antibiotics - the percentage of the functional capacities in control microcosm (Control and Control-R) at the level2 of KEGG.

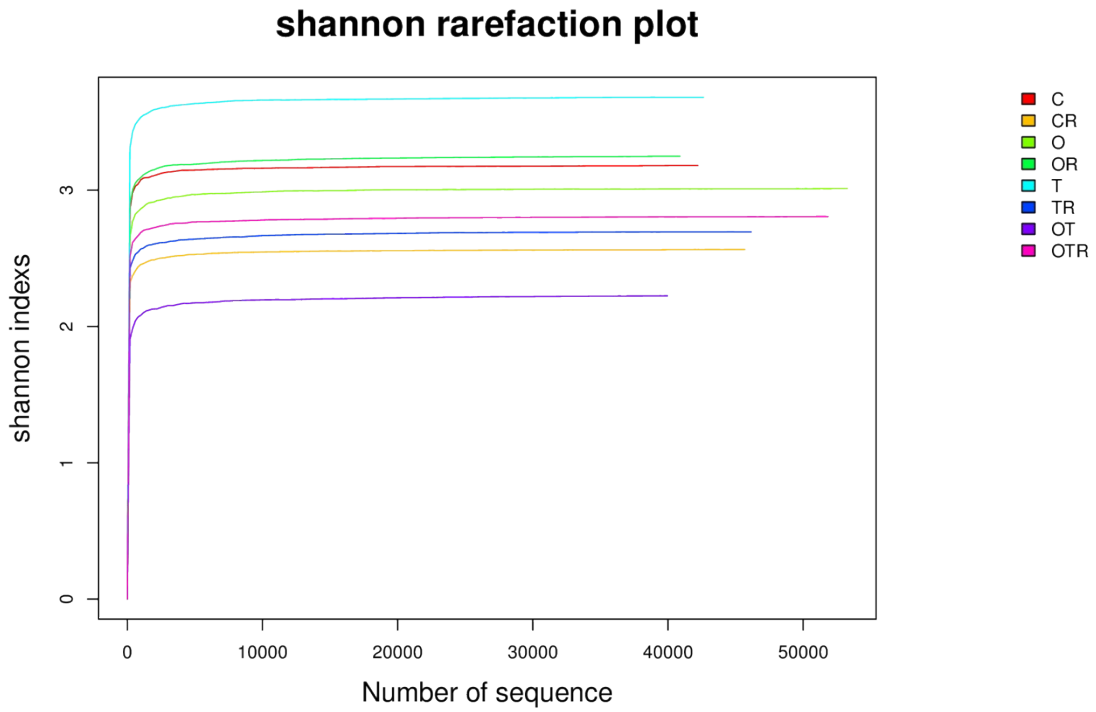

Fig.S1 The rarefaction plots (Shannon) for the biofilm samples from the eight treatments (C = Control, O = ofloxacin, T = tetracycline, OT = the mixture of tetracycline and ofloxacin, R indicates the microcosms treated with exudates). Sample rarefaction using Alpha_Diversity.py was run on the data and the sequences per biofilm sample was plotted. The rarefaction curves are done with OTUs from Mothur. The rarefaction analysis indicates that all biofilm samples was close to being saturated.

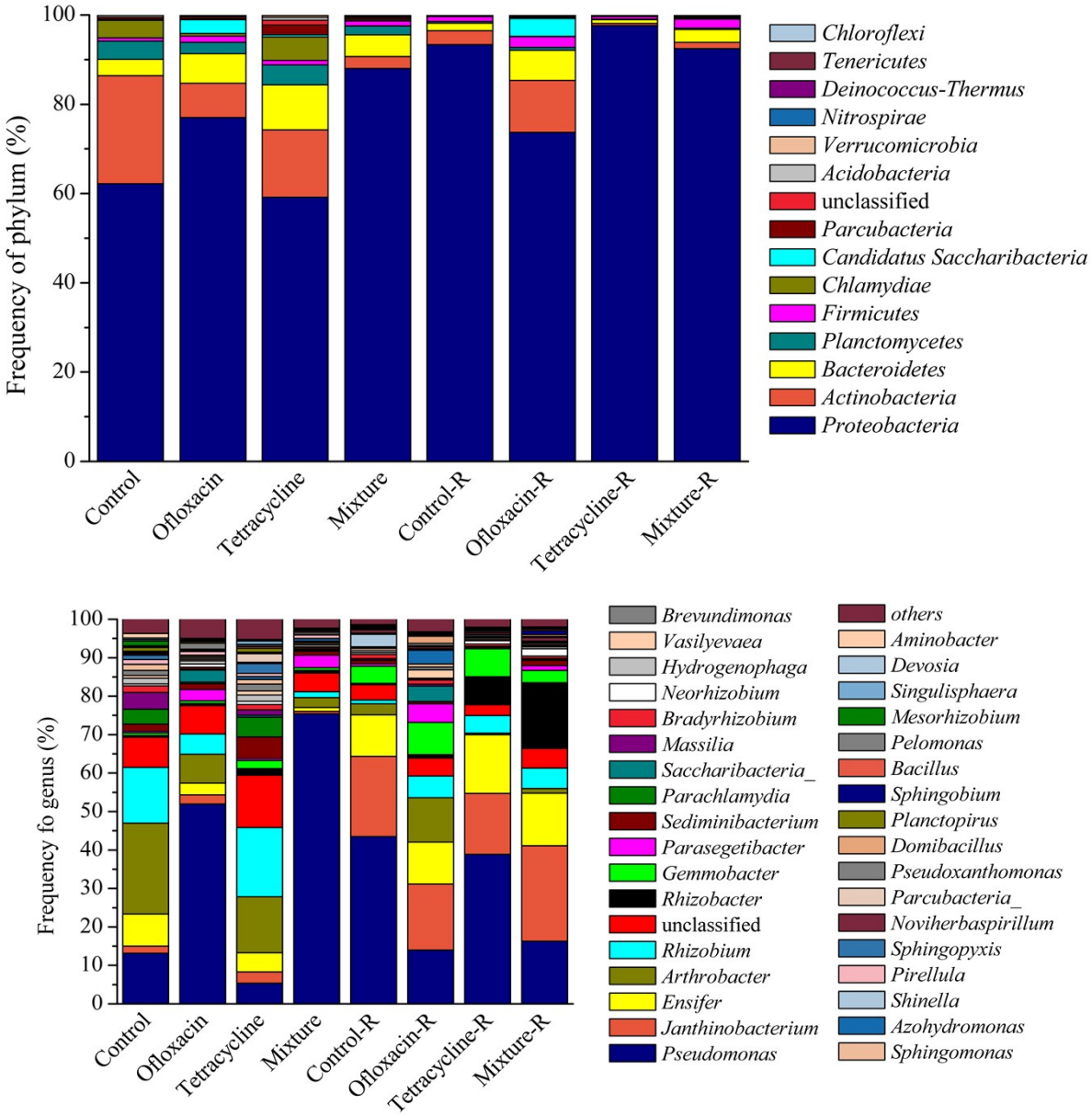

Fig.S2 Relative abundance of the different bacterial phyla (a) and genera (b) in different treated microcosms (-R indicates the microcosms treated with root exudates, Mixture= the mixture of tetracycline and ofloxacin)

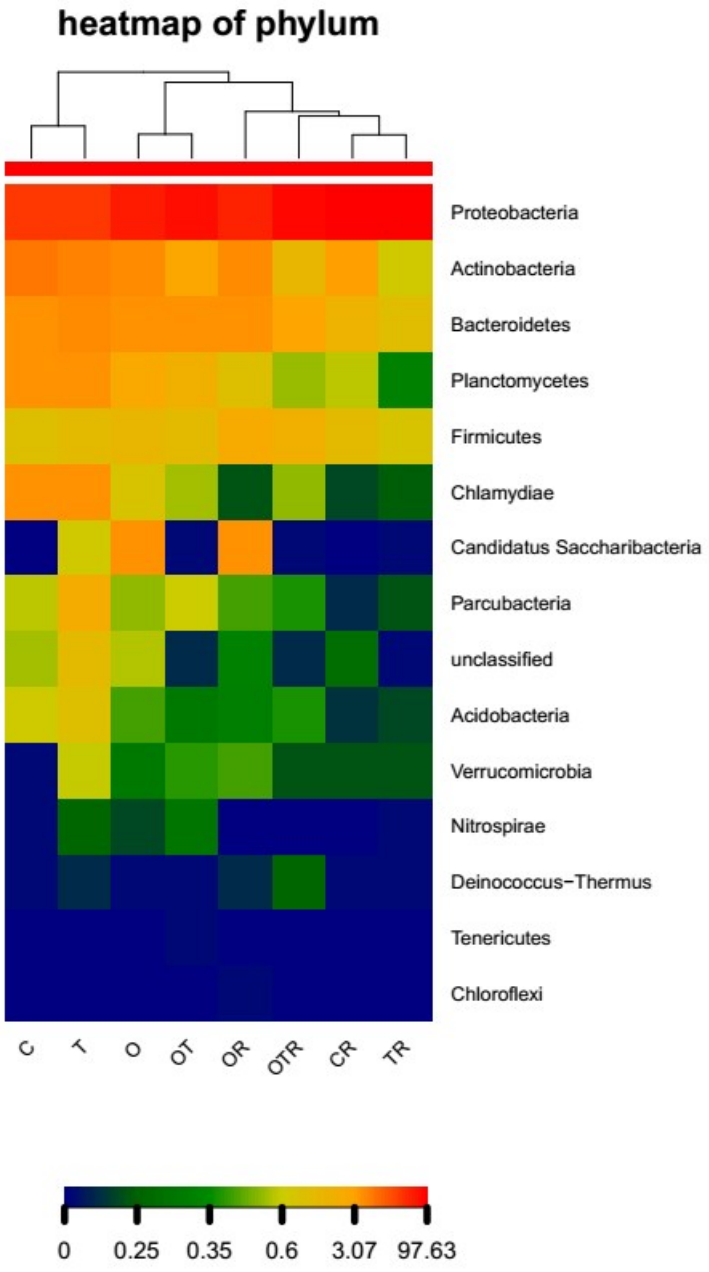

Fig.S3 Heatmap analysis of the biofilm communities at the phylum level from the eight treatments (OFL = ofloxacin, TET = tetracycline, OT = the mixture of tetracycline and ofloxacin, R indicates the microcosms treated with exudates).

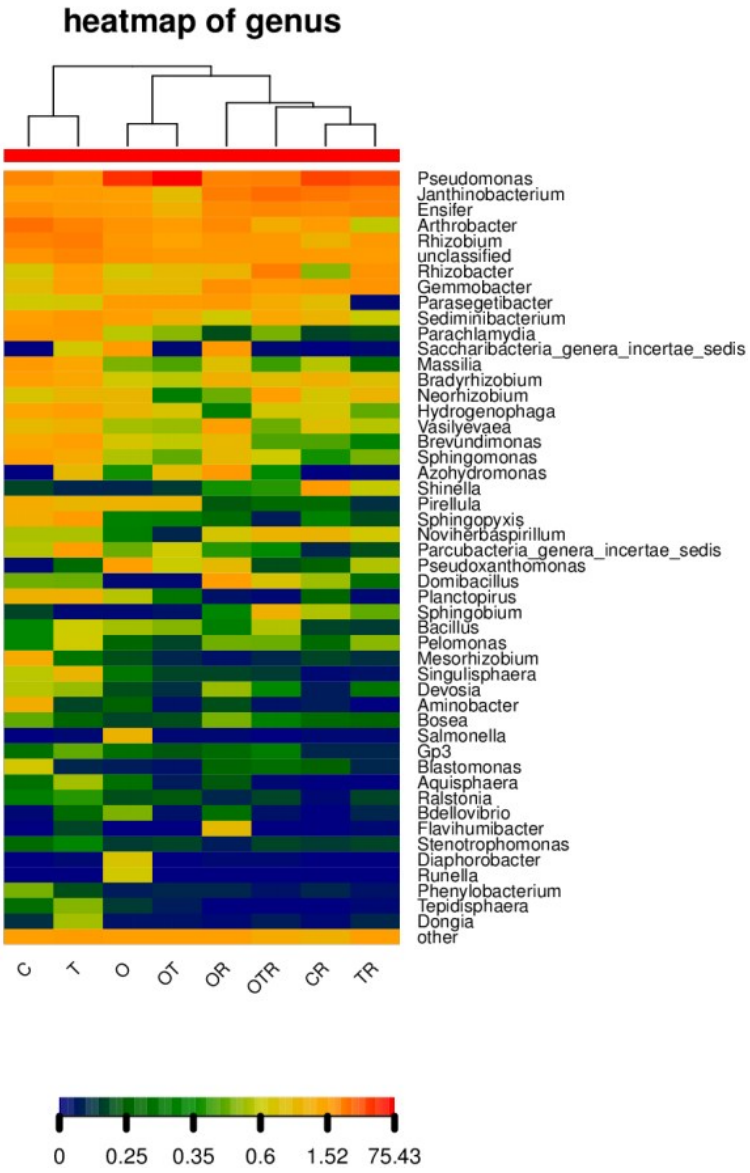

Fig.S4 Heatmap analysis of the biofilm communities at the genus level from the eight treatments (OFL = ofloxacin, TET = tetracycline, OT = the mixture of tetracycline and ofloxacin, R indicates the microcosms treated with exudates).

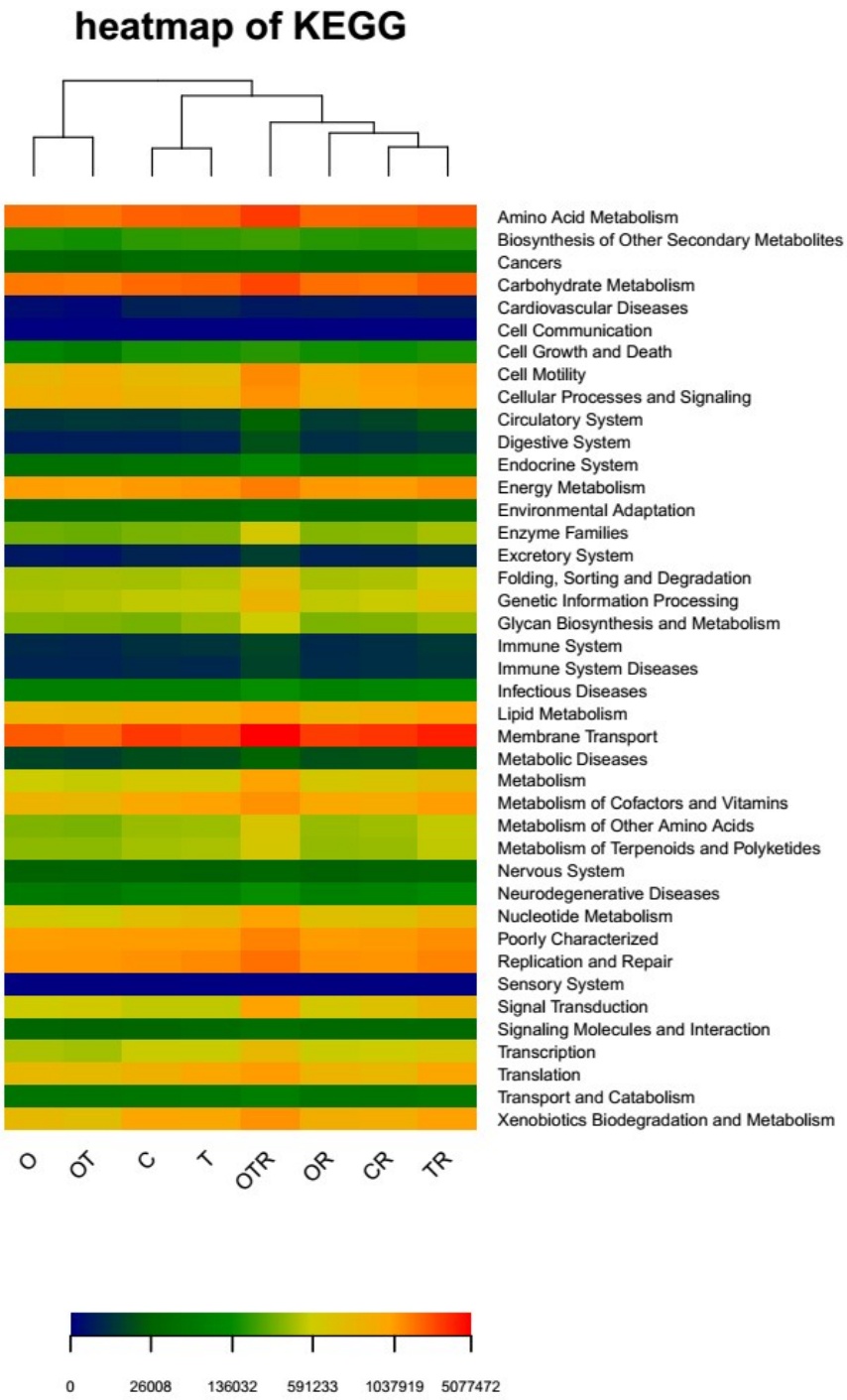

Fig.S5 Heatmap analysis of the functional capacities at the level2 of KEGG from the eight treatments (OFL = ofloxacin, TET = tetracycline, OT = the mixture of tetracycline and ofloxacin, R indicates the microcosms treated with exudates).

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