**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. Na₂EDTA (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

<table>
<thead>
<tr>
<th>Parent</th>
<th>Product</th>
<th>SRE Collision Energy</th>
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<tr>
<td>Ofloxacin</td>
<td>362</td>
<td>261.5</td>
</tr>
<tr>
<td></td>
<td></td>
<td>318.3</td>
</tr>
<tr>
<td>Ofloxacin-d3</td>
<td>365</td>
<td>261.5</td>
</tr>
<tr>
<td></td>
<td></td>
<td>321.3</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>445</td>
<td>410.3</td>
</tr>
<tr>
<td></td>
<td></td>
<td>427.7</td>
</tr>
</tbody>
</table>

**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, Waldbronn, 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>
<thead>
<tr>
<th>Continent/Country</th>
<th>Rivers</th>
<th>Antibiotic Concentration (ng L\textsuperscript{-1})</th>
<th>OFL MIN</th>
<th>OFL MAX</th>
<th>TET MIN</th>
<th>TET MAX</th>
</tr>
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<td></td>
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<td>180</td>
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<td>BDL</td>
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<td>NA</td>
<td></td>
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<td>NA</td>
<td>11700</td>
<td>NA</td>
<td>25500</td>
<td></td>
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<td>NA</td>
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<td>Rivers of Ghana</td>
<td>NA</td>
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<td>3 South Africa</td>
<td>Rivers of Durban</td>
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<td>1 Australia</td>
<td>Australian Rivers</td>
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<td>NA</td>
<td>NA</td>
<td>80</td>
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</tbody>
</table>

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

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

<table>
<thead>
<tr>
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<th>influent pH</th>
<th>effluent pH</th>
<th>change of pH</th>
</tr>
</thead>
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<tr>
<td>Control</td>
<td>7.15</td>
<td>7.30</td>
<td>0.15</td>
</tr>
<tr>
<td>Tetracycline</td>
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<td>7.39</td>
<td>0.29</td>
</tr>
<tr>
<td>Ofloxacin</td>
<td>7.2</td>
<td>7.42</td>
<td>0.22</td>
</tr>
<tr>
<td>Mixture</td>
<td>7.24</td>
<td>7.44</td>
<td>0.20</td>
</tr>
<tr>
<td>Control-R</td>
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<td>7.32</td>
<td>0.32</td>
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<tr>
<td>Tetracycline-R</td>
<td>7.05</td>
<td>7.39</td>
<td>0.34</td>
</tr>
<tr>
<td>Ofloxacin-R</td>
<td>7.02</td>
<td>7.37</td>
<td>0.35</td>
</tr>
<tr>
<td>Mixture-R</td>
<td>7.14</td>
<td>7.41</td>
<td>0.27</td>
</tr>
</tbody>
</table>

### 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).

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

<table>
<thead>
<tr>
<th>Phylum</th>
<th>C vs O</th>
<th>C vs T</th>
<th>C vs OT</th>
<th>CR vs OR</th>
<th>CR vs TR</th>
<th>CR vs OTR</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Proteobacteria</strong></td>
<td>0</td>
<td>9.92E-19</td>
<td>0</td>
<td>7.35E-220</td>
<td>1.93E-08</td>
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<td><strong>Actinobacteria</strong></td>
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<td>0</td>
<td>2.47E-215</td>
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<td><strong>Bacteroidetes</strong></td>
<td>1.93E-93</td>
<td>2.33E-308</td>
<td>2.23E-17</td>
<td>1.51E-35</td>
<td>9.26E-35</td>
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<td><strong>Planctomycetes</strong></td>
<td>7.12E-43</td>
<td>0.033</td>
<td>1.65E-68</td>
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<td><strong>Firmicutes</strong></td>
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<td>3.73E-09</td>
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<td>6.47E-18</td>
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<td><strong>Chlamydiae</strong></td>
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<td>Janthinobacteriu m</td>
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<td>Ensifer</td>
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<td>1.58E-83</td>
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<td>1.49E-91</td>
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<td>Arthrobacter</td>
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<td>0</td>
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<td>Rhizobium</td>
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<td>0.0001</td>
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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).

<table>
<thead>
<tr>
<th>Genus (%)</th>
<th>Control</th>
<th>OFL</th>
<th>TET</th>
<th>OT</th>
<th>Control-R</th>
<th>OFL-R</th>
<th>TET-R</th>
<th>OT-R</th>
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</thead>
<tbody>
<tr>
<td><em>Pseudomonas</em></td>
<td>13.17</td>
<td>5.37</td>
<td>51.99</td>
<td>75.43</td>
<td>14</td>
<td>16.3</td>
<td>43.5</td>
<td>38.87</td>
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<tr>
<td><em>Janthinobacterium</em></td>
<td>1.86</td>
<td>2.92</td>
<td>2.37</td>
<td>0.62</td>
<td>17.17</td>
<td>24.84</td>
<td>20.88</td>
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<tr>
<td><em>Ensifer</em></td>
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<td>5.01</td>
<td>3.03</td>
<td>1.05</td>
<td>10.93</td>
<td>13.63</td>
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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).

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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).

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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).

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<th>OFL</th>
<th>TET</th>
<th>OT</th>
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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).