

# **Supporting Information for**

## **Adsorbed Sulfamethoxazole Exacerbates the Effects of Polystyrene (~2 μm) on Gut Microbiota and the Antibiotic Resistome of a Soil Collembolan**

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### **Materials and Methods**

#### **Quality Control and Quality Assurance of Sulfamethoxazole Determination**

Strict quality assurance and quality control (QA/QC) were conducted during the analytical procedures. Limits of detection (LOD) of sulfamethoxazole was determined as the lowest concentration resulting in a signal-to-noise (S/N) ratio of 3. The limit of quantification (LOQ) was calculated with an S/N ratio of 10. Concentrations below the LOQ were defined as zero

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during statistical analyses. A solvent blank, a procedural blank, and standards were run successively for each batch to validate background and instrument performance. The selected sulfamethoxazole of interest was not detected in the blanks.

### **Carbon and Nitrogen Stable Isotope Analysis**

The dried collembolan samples were stored at 4 °C until further analysis. They were weighed and analyzed for <sup>13</sup>C and <sup>15</sup>N isotope signatures using a Flash EA 2000 Series Elemental Analyzer connected via a Conflo IV to a DeltaV Advantage isotope ratio mass spectrometer (FLASH-EADELTA-V, Thermo Finnigan, Waltham, MA). Quality control consisted of determining an internal reference (fish muscle tissue) every 10 samples. Overall precision of the <sup>13</sup>C and <sup>15</sup>N measurement was < 0.10‰. The study used the dX notation which denotes the deviation from the reference in parts per thousand (‰) to express <sup>13</sup>C and <sup>15</sup>N isotope natural abundance and was calculated using the following formula,

$$dX = ((R_{sample} - R_{reference})/R_{reference}) * 1000$$

where  $R_{sample}$ , mean <sup>15</sup>N/<sup>14</sup>N or <sup>13</sup>C/<sup>12</sup>C of the sample, and  $R_{reference} = ^{15}\text{N}/^{14}\text{N}$  or <sup>13</sup>C/<sup>12</sup>C of the reference.

The labelled abundance of the <sup>15</sup>N isotope was expressed

directly using atom% <sup>15</sup>N

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Table S2. Information on 296 genes detected in the gene chip.

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exposure

## Figures

Figure S1. Images of fluorescently labeled polystyrene microbeads of 2.0-2.9 $\mu$ m diameters ingested by soil collembolan. Image (A) was the control (0% microplastics in food). Image (B) shows that the fluorescently labeled polystyrene microbeads are localized at microplastics treated collembolan guts (1% microplastics in food).

Figure S2. The effect of polystyrene exposure on collembolan biomass (dry weight per collembolan, DW per collembolan) (One way-ANOVA test,  $F(2, 9) = 1.689$ ,  $P = 0.262$ ). The experiment was designed as CK (0% polystyrene in food), MH (1% polystyrene without sulfamethoxazole in the food), MA (1% polystyrene with sulfamethoxazole in the food).

Figure S3 Antibiotic resistance gene types detected in collembolan guts with different treatments based on the mechanism of resistance.

Figure S4 Bacterial communities in collembolan guts in response to different treatments at a family level.

Figure S5. Variable importance plot of the Random Forest regression model for the prediction of collembolan  $\delta$  13C -gut microbiota and  $\delta$  15N -gut microbiota correlation with different diet treatments includes the variables are ranked on the basis of their importance for the percentage of increase of mean square error (%IncMSE) during the random forest classification routine.

## Total:

### Number of tables: 3

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**Number of figures: 5**

**Number of pages: 34**

**Table S1.** The initial and final concentration of SMZ in solutions in the 6 hour microplastics sorption experiment.

Treatment	Concentration (ng/mL)	
	Initial concentration	Final concentration
CK	No Peak	No Peak
MH	No Peak	No Peak
MA	1793.5	1677.5

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**Table S2.** Information of 296 genes detected in the gene chip.

Number	Gene Name	Forward Primer	Reverse Primer	Classification
1	16S rRNA	GGGTTGCCTCGTTGC	ATGGYTGTCGTCAGCTCGTG	
2	aac	CCCTGCGTTGTGGCTATGT	TTGGCCACGCCAATCC	Aminoglycoside
3	aac(6')I1	GACCGGATTAAGGCCGATG	CTTGCCTTGATATTCAAGTTTTATAACCA	Aminoglycoside
4	aac(6')-Ib(aka aacA4)-01	GTTTGAGAGGAAGGTACCGTAA	GAATGCCTGGCGTGTGTGA	Aminoglycoside
5	aac(6')-Ib(aka aacA4)-02	CGTCGCCGAGCAACTTG	CGGTACCTGCCTCTCAAACC	Aminoglycoside
6	aac(6')-Ib(aka aacA4)-03	AGAACGACGCCGACACTT	GCTCTCCATTCAAGCATTGCA	Aminoglycoside
7	aac(6')-II	CGACCCGACTCCGAACAA	GCACGAATCCTGCCTCTCA	Aminoglycoside
8	aac(6')-Iy	GCTTGCGGATGCCTCAAT	GGAGAACAAAAATACCTCAAGGAAA	Aminoglycoside
9	aacA/aphD	AGAGCCTGGGAAGATGAAGTTT	TTGATCCATACCATAGACTATCTCATCA	Aminoglycoside
10	aacC	CGTCACTTATTCGATGCCCTTAC	GTCGGGCGCGGCATA	Aminoglycoside
11	aacC1	GGTCGTGAGTTCGGAGACGTA	GCAAGTTCCCGAGGTAATCG	Aminoglycoside

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12	aacC2	ACGGCATTCTCGATTGCTT	CCGAGCTTCACGTAAGCATT	Aminoglycoside
13	aacC4	CGGCGTGGGACACGAT	AGGGAACCTTGCCATCAACT	Aminoglycoside
14	aadA-01	GTTGTGCACGACGACATCATT	GGCTCGAAGATACTGCAAGAA	Aminoglycoside
15	aadA-02	CGAGATTCTCCGCGCTGTA	GCTGCCATTCTCCAATTGC	Aminoglycoside
16	aadA1	AGCTAAGCGCGAACTGCAAT	TGGCTCGAAGATACTGCAA	Aminoglycoside
17	aadA-1-01	AAAAGCCGAAGAGGAACTTG	CATCTTCACAAAGATGTTGCTGTCT	Aminoglycoside
18	aadA-1-02	CGGAATTGAAAAAACTGATCGAA	ATACCGGCTGTCCGTCATT	Aminoglycoside
19	aadA2-01	ACGGCTCCGCAGTGGAT	GGCCACAGTAACCAACAAATCA	Aminoglycoside
20	aadA2-02	CTTGTCTGCATGACGACATC	TCGAAGATACCCGCAAGAATG	Aminoglycoside
21	aadA2-03	CAATGACATTCTTGCAGGGTATC	GACCTACCAAGGCAACGCTATG	Aminoglycoside
22	aadA5-01	ATCACGATCTTGCAGTTGCT	CTGCGGATGGGCCTAGAAG	Aminoglycoside
23	aadA5-02	GTTCTTGCTCTTGCCTGCATT	GATGCTCGGCAGGCAAAC	Aminoglycoside
24	aadA9-01	CGCGGCAAGCCTATCTTG	CAAATCAGCGACCGCAGACT	Aminoglycoside

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25	aadA9-02	GGATGCACGCTTGGATGAA	CCTCTAGCGGCCGGAGTATT	Aminoglycoside
26	aadD	CCGACAACATTCTACCATCCTT	ACCGAACCGCTCGTCGTATA	Aminoglycoside
27	aadE	TACCTTATTGCCCTTGAAGAGTTA	GGAACATATGCCCTTTAATTCTACAATCT	Aminoglycoside
28	acrA-01	CAACGATCGGACGGGTTTC	TGGCGATGCCACCGTACT	Multidrug
29	acrA-02	GGTCTATCACCCCTACCGCCTATC	GCGCGCACGAACATACC	Multidrug
30	acrA-03	CAGACCCGCATCGCATATT	CGACAATTTCGCGCTCATG	Multidrug
31	acrA-04	TACTTTCGCGGCCATCTTC	CGTGCACGAACGAACAT	Multidrug
32	acrA-05	CGTGCACGAACGAACA	ACTTTGCACGCCATCTTC	Multidrug
33	acrB-01	AGTCGGTGTTCGCCGTTAAC	CAAGGAAACGAACGCAATACC	Multidrug
34	acrF	GCGGCCAGGCACAAAAA	TACGCTCTCCCACGGTTTC	Multidrug
35	acrR-01	GCGCTGGAGACACGACAAC	GCCTTGCTGCGAGAACAAA	Multidrug
36	acrR-02	GATGATACCCCCTGCTGTGAGA	ACCAAACAAGAACGCAAGAA	Multidrug
37	adeA	CAGTCGAGCGCCTATTCTG	CGCCCTGACCGACCAAT	Multidrug

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38	ampC/blaDHA	TGGCCGCAGCAGAAAGA	CCGTTTATGCACCCAGGAA	Beta_Lactamase
39	ampC-01	TGGCGTATCGGGTCAATGT	CTCCACGGGCCAGTTGAG	Beta_Lactamase
40	ampC-02	GCAGCACGCCCGTAA	TGTACCCATGATGCGCGTACT	Beta_Lactamase
41	ampC-04	TCCGGTGACGCGACAGA	CAGCACGCCGGTGAAAGT	Beta_Lactamase
42	ampC-05	CTGTCGAGCTGGTTCTATAAGTAAA	CAGTATCTGGTCACCGGATCGT	Beta_Lactamase
43	ampC-06	CCGCTCAAGCTGGACCATAC	CCATATCCTGCACGTTGGTTT	Beta_Lactamase
44	ampC-07	CCGCCCAGAGCAAGGACTA	GCTCGACTTCACGCCGTAAG	Beta_Lactamase
45	ampC-09	CAGCCGCTGATGAAAAAATATG	CAGCGAGCCCACTCGA	Beta_Lactamase
46	aph	TTTCAGCAAGTGGATCATGTTAAAAT	CCAAGCTGTTCCACTGTTTTC	Aminoglycoside
47	aph(2')-Id-01	TGAGCAGTATCATAAGTTGAGTGAAAG	GACAGAACATCAATCTCTATGGAATG	Aminoglycoside
48	aph(2')-Id-02	TAAGGATATACCGACAGTTTGAAA	TTAATCCCTCTTCATACCAATCCATA	Aminoglycoside
49	aph6ia	CCCATCCCATGTGTAAGGAAA	GCCACCGCTTCTGCTGTAC	Aminoglycoside
50	aphA1(aka kanR)	TGAACAAGTCTGGAAAGAAATGCA	CCTATTAAATTCCCCTCGTCAAAAA	Aminoglycoside

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51	bacA-01	CGGCTTCGTGACCTCGTT	ACAATGCGATACCAGGCAAAT	Others
52	bacA-02	TTCCACGACACGATTAAGTCATTG	CGGCTCTTCGGCTTCAG	Others
53	bla1	GCAAGTTGAAGCGAAAGAAAAGA	TACCA GTATCAATCGCATATA CACCTAA	Beta_Lactamase
54	bla-ACC-1	CACACAGCTGATGGCTTATCTAAAA	AATAAACGCGATGGGTTCCA	Beta_Lactamase
55	blaCMY	CCGCGGC GAAATTAAGC	GCCACTGTTGCCTGTCAGTT	Beta_Lactamase
56	blaCMY2-01	AAAGCCTCAT GGGTGCATAAA	ATAGCTTTGTTGCCAGCATCA	Beta_Lactamase
57	blaCMY2-02	GCGAGCAGCCTGAAGCA	CGGATGGGCTTGT CCTCTTT	Beta_Lactamase
58	blaCTX-M-01	GGAGGCGTGACGGCTTT	TTCAGTGC GATCCAGACGAA	Beta_Lactamase
59	blaCTX-M-02	GCCGCGGTGCTGAAGA	ATCGGATTATA GTTAACCAGGT CAGATT	Beta_Lactamase
60	blaCTX-M-03	CGATACCACCA CGCCGTTA	GCATTGCCAACGTCAGATT	Beta_Lactamase
61	blaCTX-M-04	CTTGGCGTTGCGCTGAT	CGTTCATCGGCACGGTAGA	Beta_Lactamase
62	blaCTX-M-05	GCGATAACGTGGCGATGAAT	GTCGAGACGGAACGTTTCGT	Beta_Lactamase
63	blaCTX-M-06	CACAGTTGGTGACGTGGCTAA	CTCCGCTGCCGGTTTATC	Beta_Lactamase

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64	blaGES	GCAATGTGCTAACGTTCAAG	GTGCCTGAGTCAATTCTTCAAAG	Beta_Lactamase
65	blaIMP-01	AACACGGTTGGTGGTCTTGTA	GCGCTCCACAAACCAATTG	Beta_Lactamase
66	blaIMP-02	AAGGCAGCATTCCCTCTCATTTC	GGATAGATCGAGAATTAAGCCACTCT	Beta_Lactamase
67	bla-L1	CACCGGGTTACCAGCTGAAG	GCGAAGCTGCGCTTGTAGTC	Beta_Lactamase
68	blaMOX/blaCMY	CTATGTCAATGTGCCGAAGCA	GGCTTGTCCCTTTCGAATAGC	Beta_Lactamase
69	blaOCH	GGCGACTTGC GCCGTAT	TTTCTGCTCGGCCATGAG	Beta_Lactamase
70	blaOKP	GCCGCCATCACCATGAG	GGTGACGTTGTCACCGATCTG	Beta_Lactamase
71	blaOXA1/blaOXA30	CGGATGGTTGAAGGGTTATTAT	TCTTGGCTTTATGCTTGATGTTAA	Beta_Lactamase
72	blaOXA10-01	CGCAATTATCGGCCTAGAAACT	TTGGCTTCCGTCCCATT	Beta_Lactamase
73	blaOXA10-02	CGCAATTATCGGCCTAGAAACT	TTGGCTTCCGTCCCATT	Beta_Lactamase
74	blaOXY	CGTTCAGGCGGCAGGTT	GCCGCGATATAAGATTGAGAATT	Beta_Lactamase
75	blaPAO	CGCCGTACAACCGGTGAT	GAAGTAATGCGGTTCTCCTTCA	Beta_Lactamase
76	blaPER	TGCTGGTTGCTGTTTGTGA	CCTGCGCAATGATAGCTTCAT	Beta_Lactamase

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77	blaPSE	TTGTGACCTATTCCCTGTAATAGAA	TGCGAAGCACGCATCATC	Beta_Lactamase
78	blaROB	GCAAAGGCATGACGATTGC	CGCGCTGTTGTCGCTAAA	Beta_Lactamase
79	blaSFO	CCGCCGCCATCCAGTA	GGGCCGCCAAGATGCT	Beta_Lactamase
80	blaSHV-01	TCCCATGATGAGCACCTTAAA	TTCGTCACCGGCATCCA	Beta_Lactamase
81	blaSHV-02	CTTCCCAGATGAGCACCTTT	TCCTGCTGGCGATAGTGGAT	Beta_Lactamase
82	blaTEM	AGCATCTTACGGATGGCATGA	TCCTCCGATCGTTGTCAGAAGT	Beta_Lactamase
83	blaTLA	ACACTTGCCATTGCTGTTATGT	TGCAAATTCCGGCAATAATCTTT	Beta_Lactamase
84	blaVEB	CCCGATGCAAAGCGTTATG	GAAAGATTCCCTTATCTATCTCAGACAA	Beta_Lactamase
85	blaVIM	GCACTTCTCGCGGAGATTG	CGACGGTGATGCGTACGTT	Beta_Lactamase
86	blaZ	GGAGATAAAGTAACAAATCCAGTTAGATATGA	TGCTTAATTTCATTTGCGATAAG	Beta_Lactamase
87	carB	GGAGTGAGGCTGACCGTAGAACG	ATCGGCGAAACGCACAAA	MLSB
88	catA1	GGGTGAGTTCACCAAGTTTGATT	CACCTTGTGCCTTGCCTATA	Others
89	catB3	GCACTCGATGCCTTCCAAAA	AGAGCCGATCCAAACGTCAT	Others

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90	catB8	CACTCGACGCCTTCCAAG	CCGAGCCTATCCAGACATCATT	Others
91	ceoA	ATCAACACGGACCAGGACAAG	GGAAAGTCCGCTCACGATGA	Multidrug
92	cepA	AGTTGCGCAGAACAGTCCTCTT	TCGTATCTGCCCGTCGATAAT	Beta_Lactamase
93	cfiA	GCAGCGTTGCTGGACACA	GTTCGGGATAAACGTGGTGACT	Beta_Lactamase
94	cfr	GCAAAATTCAAGAGCAAGTTACGAA	AAAATGACTCCAACCTGCTTTAT	Others
95	cfxA	TCATTCCCTCGTTCAAGTTTCAGA	TGCAGCACCAAGAGGGAGATGT	Beta_Lactamase
96	cIntI-1(class1)	GGCATCCAAGCAGCAAG	AAGCAGACTTGACCTGA	Integron
97	cmeA	GCAGCAAAGAAGAAGCACCAA	AGCAGGGTAAGTAAACTAAGTGGTAAATCT	Multidrug
98	cmlA1-01	TAGGAAGCATCGGAACGTTGAT	CAGACCGAGCACGACTGTTG	Chloramphenicol
99	cmlA1-02	AGGAAGCATCGGAACGTTGA	ACAGACCGAGCACGACTGTTG	Chloramphenicol
100	cmr	CGGCATCGTCAGTGGATT	CGGTTCCGAAAAAGATGGAA	Multidrug
101	cmx(A)	GCGATGCCATCCTCTGT	TCGACACGGAGCCTTGGT	Chloramphenicol
102	cphA-01	GCGAGCTGCACAAGCTGAT	CGGCCAGTCGCTCTTC	Beta_Lactamase

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103	cphA-02	GTGCTGATGGCGAGTTCTG	GGTGTGGTAGTTGGTGTGATCAC	Beta_Lactamase
104	dfrA1	GGAATGCCCTGATATTCCA	AGTCTTGCCTCCAACCAACAG	Sulfonamide
105	dfrA12	CCTCTACCGAACCGTCACACA	GCGACAGCGTTGAAACAACTAC	Sulfonamide
106	emrD	CTCAGCAGTATGGTGGTAAGCATT	ACCAGGCGCCGAAGAAC	Multidrug
107	ereA	CCTGTGGTACGGAGAATTCATGT	ACCGCATTGCTTGCTT	MLSB
108	ereB	GCTTTATTCAGGAGGCGGAAT	TTTTAAATGCCACAGCACAGAAC	Others
109	erm(34)	GCGCGTTGACGACGATT	TGGTCATACTCGACGGCTAGAAC	MLSB
110	erm(35)	TTGAAAACGATGTTGCATTAAGTCA	TCTATAATCACAACTAACCAACTTGAACGT	MLSB
111	erm(36)	GGCGGACCGACTTGCAT	TCTGCCTTGACGACGGTTAC	MLSB
112	ermA	TTGAGAAGGGATTGCGAAAAG	ATATCCATCTCCACCATTAAATAGTAAACC	MLSB
113	ermA/ermTR	ACATTTACCAAGGAACTTGTGGAA	GTGGCATGACATAAACCTTCATCA	MLSB
114	ermB	TAAAGGGATTAAACGACGAAACT	TTTATACCTCTGTTGTTAGGAAATTGAA	MLSB
115	ermC	TTTGAAATCGGCTCAGGAAAA	ATGGTCTATTCAATGGCAGTTACG	MLSB

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116	ermF	CAGCTTGTTAACATTACGAA	AAATTCTAAAATCACAACCGACAA	MLSB
117	ermJ/ermD	GGACTCGGCAATGGTCAGAA	CCCCGAAACGCAATATAATGTT	MLSB
118	ermK-01	GTTTGATATTGGCATTGTCAGAGAAA	ACCATTGCCGAGTCCACTTT	MLSB
119	ermK-02	GAGCCGCAAGCCCCTTT	GTGTTTCATTGACGCCGGAGTAA	MLSB
120	ermT-01	GTTCACTAGCACTATTTAATGACAGAAGT	GAAGGGTGTCTTTAATACAATTAACGA	MLSB
121	ermT-02	GTAAAATCCCTAGAGAATACTTCATCCA	TGAGTGATATTTGAAGGGTGTCTT	MLSB
122	ermX	GCTCAGTGGTCCCCATGGT	ATCCCCCGTCAACGTTT	MLSB
123	ermY	TTGTCTTGAAAGTGAAGCAACAGT	TAACGCTAGAGAACGATTGTATTGAG	MLSB
124	fabK	TTTCAGCTCAGCACTTGGTCAT	AAGGCATCTTTTCAGCCAGTTC	Others
125	floR	ATTGTCTTCACGGTGTCCGTTA	CCCGCATGTCGTCGAAC	Multidrug
126	folA	CGAGCAGTTCCCTGCCAAAG	CCCAGTCATCCGGTTCATC	Sulfonamide
127	fosB	TCACTGTAACTAATGAAGCATTAGACCAT	CCATCTGGATCTGTAAAGTAAAGAGATC	Others
128	fosX	GATTAAGCCATATCACTTAATTGTGAAAG	TCTCCTTCCATAATGCAAATCCA	Others

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129	fox5	GGTTGCCGCTGCAGTTC	GCGGCCAGGTGACCAA	Beta_Lactamase
130	imiR	CCGGACTAGAGCTTCATGTAAGC	CCCACGCGGTACTCTTGTAAA	Others
131	intI-1(clinic)	CGAACGAGTGGCGGAGGGTG	TACCCGAGAGCTTGGCACCCA	Integron
132	IS613	AGGTCGGACTCAATGCAACA	TTCAGCACATACCGCCTTGAT	Transposase
133	lmrA-01	TCGACGTGACCGTAGTGAACA	CGTGACTACCCAGGTGAGTTGA	MLSB
134	lnuA-01	TGACGCTAACACACACTCAAAAA	TTCATGCTTAAGTTCCATACGTGAA	MLSB
135	lnuB-01	TGAACATAATCCCCTCGTTAAAGAT	TAATTGCCCTGTTCATCGTAAATAA	MLSB
136	lnuB-02	AAAGGAGAAGGTGACCAATACTCTGA	GGAGCTACGTCAAACAAACCAGTT	MLSB
137	lnuC	TGGTCAATATAACAGATGTAAACCAGATT	CACCCCAGCCACCATCAA	MLSB
138	marR-01	GCGGCGTACTGGTGAAGCTA	TGCCCTGGTCGTTGATGA	Multidrug
139	matA/mel	TAGTAGGCAAGCTCGGTGTTGA	CCTGTGCTATTTAACGCCTTGTTC	MLSB
140	mdet11	ATACAGCAGTGGATATTGGTTAATTGT	TGCATAAGGTGAATGTTCCATGA	Multidrug
141	mdtA	CCTAACGGGCGTGACTTCA	TTCACCTGTTCAAGGGTCAA	MLSB

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142	mdtE/yhiU	CGTCGGCGCACTCGTT	TCCAGACGTTGTACGGTAACCA	Multidrug
143	mecA	GGTTACGGACAAGGTGAAATACTGAT	TGTCTTTAATAAGTGAGGTGCGTTAATA	Beta_Lactamase
144	mefA	CCGTAGCATTGGAACAGCTTT	AAACGGAGTATAAGAGTGCTGCAA	MLSB
145	mepA	ATCGGTCGCTCTCGTTCAC	ATAAAATAGGATCGAGCTGCTGGAT	Multidrug
146	mexA	AGGACAACGCTATGCAACGAA	CCGGAAAGGGCCGAAAT	Multidrug
147	mexD	TTGCCACTGGCTTCATGAG	CACTGCGGAGAACTGTCTGTAGA	Multidrug
148	mexE	GGTCAGCACCGACAAGGTCTAC	AGCTCGACGTACTTGAGGAACAC	Multidrug
149	mexF	CCCGAGAACGCCAAGA	TTGAGTTCGCGGGTGATGA	Multidrug
150	mphA-01	CTGACCGCCTCCGTGTT	GGTGGTGCATGGCGATCT	MLSB
151	mphA-02	TGATGACCCTGCCATCGA	TTCGCGAGCCCCTCTTC	MLSB
152	mphB	CGCAGCGCTTGATCTGTAG	TTACTGCATCCATACGCTGCTT	MLSB
153	mphC	CGTTGAAGTACCGAATTGGAAA	GCTGCGGGTTGCCTGTA	MLSB
154	msrA-01	CTGCTAACACAAAGTACGATTCCAAT	TCAAGTAAAGTTGTCTTACCTACACCATT	MLSB

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155	msrC-01	TCAGACCGGATCGGTTGTC	CCTATTTTGGAGTCTTCTCTAATGTT	MLSB
156	mtrC-01	GGACGGGAAGATGGTCAA	CGTAGCGTCCGGTTCGAT	Multidrug
157	mtrC-02	CGGAGTCCATCGACCATTG	ATCGTCGGCAAGGAGAAATCA	Multidrug
158	mtrD-02	GGTCGGCACGCTCTGTC	TGAAGAATTGCGCACCACTAC	Multidrug
159	mtrD-03	CCGCCAAGCCGATATAGACA	GGCCGGGTTGCCAAA	Multidrug
160	ndm-1	ATTAGCCGCTGCATTGAT	CATGTCGAGATAGGAAGTG	Beta_Lactamase
161	nimE	TGCGCCAAGATAAGGCATA	GTCGTGAATTGGCAGGTTA	Others
162	nisB	GGGAGAGTTGCCGATGTTGTA	AGCCACTCGTAAAGGGCAAT	Others
163	oleC	CCCGGAGTCGATGTTCGA	GCCGAAGACGTACACGAACAG	MLSB
164	oprD	ATGAAGTGGAGCGCCATTG	GGCCACGGCGAACTGA	Multidrug
165	oprJ	ACGAGAGTGGCGTCGACAA	AAGGCGATCTCGTTGAGGAA	Multidrug
166	pbp	CCGGTGCCATTGGTTAGA	AAAATAGCCGCCCAAGATT	Beta_Lactamase
167	pbp2x	TTTCATAAGTATCTGGACATGGAAGAA	CCAAAGGAAACTTGCTTGAGATTAG	Beta_Lactamase

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168	Pbp5	GGCGAACTTCTAATTAATCCTATCCA	CGCCGATGACATTCTTCTTATCTT	Beta_Lactamase
169	penA	AGACGGTAACGTATAACTTTGAAAGA	GCGTAGCCGGCAATG	Beta_Lactamase
170	pikR1	TCGACATGCGTGACGAGATT	CCGCGAATTAGGCCAGAA	MLSB
171	pikR2	TCGTGGGCCAGGTGAAGA	TTCCCCTGCCGGTGAA	MLSB
172	pmrA	TTTGCAGGTTTGTTCCTAATGC	GCAGAGCCTGATTCTCCTTG	Multidrug
173	pncA	GCAATCGAGGCGGTGTT	TTGCCGCAGCCAATTCA	Others
174	putitive multidrug	AATTTGCCGATTATTGCTGAAA	GATTGTCATCATTGCTTATCACCAA	Multidrug
175	qac	CAATAATAACCGAAATAATAGGGACAAGTT	AATAAGTGTCCCTAGTGTGGCCATAG	Multidrug
176	qacA	TGGCAATAGGAGCTATGGTGT	AAGGTAACACTATTCGGTCAAATC	Multidrug
177	qacA/qacB	TTTAGGCAGCCTCGCTTC	CCGAATCCAATAAAACCAATAA	Multidrug
178	qacEdelta1-01	TCGCAACATCCGCATTA	ATGGATTTCAGAACCCAGAGAAAGAAA	Multidrug
179	qacEdelta1-02	CCCCTCCGCCGTG	CGACCAGACTGCATAAGCAACA	Multidrug
180	qacH-01	GTGGCAGCTATCGCTTGGAT	CCAACGAACGCCACAA	Multidrug

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181	qacH-02	CATCGTCTTGTGGCAGCTA	TGAACGCCAGAACGCTAGTTT	Multidrug
182	qnrA	AGGATTCTCACGCCAGGATT	CCGCTTCATGAAACTGCAA	Others
183	rarD-02	TGACGCATCGCGTGATCT	AAATTTCTGTGGCGTCTGAATC	Multidrug
184	sat4	GAATGGGCAAAGCATAAAAAC TTG	CCGATTGAAACCACAATTATGATA	Others
185	sdeB	CACTACCGCTTCCGCACTTAA	TGAAAAAACGGAAAAGTCCAT	Multidrug
186	spcN-01	AAAAGTTCGATGAAACACGCCTAT	TCCAGTGGTAGTCCCCGAATC	Aminoglycoside
187	spcN-02	CAGAACATCTCCTGAAAAGTTGATGAA	CGCAGACACGCCGAATC	Aminoglycoside
188	speA	GCAAGAGGTATTGCTCAACAAAGA	CAGGGTCACCCTCATAAAGAAAA	Others
189	str	AATGAGTTTGGAGTGTCTAACGTA	AATCAAAACCCCTATTAAAGCCAAT	Aminoglycoside
190	strA	CCGGTGGCATTGAGAAAAAA	GTGGCTAACCTGCGAAAAG	Aminoglycoside
191	strB	GCTCGGT CGTGAGAACAAATCT	CAATT CGGT CGCCT GGT AGT	Aminoglycoside
192	sul1	CAGCGCTATGCGCTCAAG	ATCCCGCTGCGCTGAGT	Sulfonamide
193	sul2	TCATCTGCCAAACTCGTCGTTA	GTCAAAGAACGCCGCAATGT	Sulfonamide

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194	sulA/folP-01	CAGGCTCGTAAATTGATAGCAGAAG	CTTCCTTGCAGATCGCTTT	Sulfonamide
195	sulA/folP-03	CACGGCTTCGGCTCATGT	TGCCATCCTGTGACTAGCTACGT	Sulfonamide
196	tet(32)	CCATTACTTCGGACAACGGTAGA	CAATCTCTGTGAGGGCATTAAACA	Tetracycline
197	tet(34)	CTTAGCGCAAACAGCAATCAGT	CGGTGATACAGCGCGTAAACT	Tetracycline
198	tet(35)	ACCCCATGACGTACCTGTAGAGA	CAACCCACACTGGCTACCAGTT	Tetracycline
199	tet(36)-01	AGAATACTCAGCAGAGGTCACTTCCT	TGGTAGGTCGATAACCCGAAAAT	Tetracycline
200	tet(36)-02	TGCAGGAAAGACCTCCATTACAG	CTTGTCACACTTCCACGTACTATG	Tetracycline
201	tet(37)	GAGAACGTTGAAAAGGTGGTGAA	AACCAAGCCTGGATCAGTCTCA	Tetracycline
202	tetA-01	GCTGTTGTTCTGCCGGAAA	GGTTAAGTTCTTGAACGCAAAC	Tetracycline
203	tetA-02	CTCACCAAGCCTGACCTCGAT	CACGTTGTTATAGAACGCCGATAG	Tetracycline
204	tetB-01	AGTGCCTTGGATGCTGTA	AGCCCCACTAGCTCCTGTGA	Tetracycline
205	tetB-02	GCCCAGTGCTGTTGTGTCAT	TGAAAGCAAACGGCCTAAATACA	Tetracycline
206	tetC-01	CATATCGCAATACATGCGAAAAA	AAAGCCGGTAAATAGCAA	Tetracycline

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207	tetC-02	ACTGGTAAGGTAAACGCCATTGTC	ATGCATAAACAGCCATTGAGTAAG	Tetracycline
208	tetD-01	TGCCCGCTTGATTACACA	CACCA GTGATCCC GGAGATAA	Tetracycline
209	tetD-02	TGTCATCGCGCTGGTGATT	CATCCGCTTCCGGGAGAT	Tetracycline
210	tetE	TTGGCGCTGTATGCAATGAT	CGACGACCTATGCGATCTGA	Tetracycline
211	tetG-01	TCAACCATTGCCGATTCGA	TGGCCCGGCAATCATG	Tetracycline
212	tetG-02	CATCAGCGCCGGTCTTATG	CCCCATGTAGCCGAACCA	Tetracycline
213	tetH	TTGGGTCATCTTACCAGCATTAA	TTGCGCATTATCATCGACAGA	Tetracycline
214	tetJ	GGGTGCCGCATTAGATTACCT	TCGTCCAATGTAGAGCATCCATA	Tetracycline
215	tetK	CAGCAGTCATTGGAAAATTATCTGATTATA	CCTTGTACTAACCTACCAAAAATCAAATA	Tetracycline
216	tetL-01	AGCCCGATTATTCAAGGAATTG	CAAATGCTTCCCCCTGTTCT	Tetracycline
217	tetL-02	ATGGTTGTAGTTGCGCGCTATAT	ATCGCTGGACCGACTCCTT	Tetracycline
218	tetM-01	CATCATAGACACGCCAGGACATAT	CGCCATCTTGCAGAAATCA	Tetracycline
219	tetM-02	TAATATTGGAGTTTAGCTCATGTTGATG	CCTCTCTGACGTTCTAAAGCGTATTAT	Tetracycline

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220	tetO-01	ATGTGGATACTACAACGCATGAGATT	TGCCTCCACATGATATTTTCCT	Tetracycline
221	tetPA	AGTTGCAGATGTGTATAGTCGAAACTATCTATT	TGCTACAAGTACGAAAACAAAACAGAA	Tetracycline
222	tetPB-01	ACACCTGGACACGCTGATT	ACCGTCTAGAACGCGGAATG	Tetracycline
223	tetPB-02	TGATACACCTGGACACGCTGAT	CGTCCAAAACGCGGAATG	Tetracycline
224	tetPB-03	TGGGCGACAGTAGGCTTAGAA	TGACCCTACTGAAACATTAGAAATATACCT	Tetracycline
225	tetPB-04	AGTGGTGCAAATACTGAAAAAGTTGT	TTTGTTCCTTCGTTGGACAGA	Tetracycline
226	tetPB-05	CTGAAGTGGAGCGATCATTCC	CCCTCAACGGCAGAAATAACTAA	Tetracycline
227	tetQ	CGCCTCAGAAGTAAGTTCATACACTAAG	TCGTTCATGCGGATATTATCAGAAT	Tetracycline
228	tetR-02	CGCGATAGACGCCTTCGA	TCCTGACAACGAGCCTCCTT	Tetracycline
229	tetR-03	CGCGATGGAGCAAAAGTACAT	AGTAAAAAACCTTGTGGCATAAAA	Tetracycline
230	tetS	TTAAGGACAAACTTCTGACGACATC	TGTCTCCCATTGTTCTGGTTCA	Tetracycline
231	tetT	CCATATAGAGGTTCCACCAAATCC	TGACCCTATTGGTAGTGGTTCTATTG	Tetracycline
232	tetU-01	GTGGCAAAGCAACGGATTG	TGCGGGCTTGCAAAACTATC	Tetracycline

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233	tetV	GCGGGAACGACGATGTATATC	CCGCTATCTCACGACCATGAT	Tetracycline
234	tetX	AAATTGTTACCGACACGGAAGTT	CATAGCTAAAAAATCCAGGACAGTT	Tetracycline
235	tnpA-01	CATCATCGGACGGACAGAATT	GTCGGAGATGTGGGTGTAGAAAGT	Transposase
236	tnpA-02	GGCGGGTCGATTGAAA	GTGGGCAGGATCTGCTT	Transposase
237	tnpA-03	AATTGATGCGGACGGCTTAA	TCACCAAACGTGTTATGGAGTCGTT	Transposase
238	tnpA-04	CCGATCACGGAAAGCTCAAG	GGCTCGCATGACTTCGAATC	Transposase
239	tnpA-05	GCCGCACTGTCGATTTTATC	GCGGGATCTGCCACTTCTT	Transposase
240	tnpA-07	GAAACCGATGCTACAATATCCAATT	CAGCACCGTTGCAGTGTAAG	Transposase
241	tolC-01	GGCCGAGAACCTGATGCA	AGACTTACGCAATTCCGGGTTA	Multidrug
242	tolC-02	CAGGCAGAGAACCTGATGCA	CGCAATTCCGGGTTGCT	Multidrug
243	tolC-03	GCCAGGCAGAGAACCTGATG	CGCAATTCCGGGTTGCT	Multidrug
244	Tp614	GGAAATCAACGGCATCCAGTT	CATCCATGCGCTTTGTCTCT	Transposase
245	ttgA	ACGCCAATGCCAACGATT	GTCACGGCGCAGCTTGA	Multidrug

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246	ttgB	TCGCCCTGGATGTACACCTT	ACCATTGCCGACATCAACAAC	Multidrug
247	vanA	AAAAGGCTCTGAAAACGCAGTTAT	CGGCCGTTATCTGTAAAAACAT	Vancomycin
248	vanB-01	TTGTCGGCGAACGTGGATCA	AGCCTTTTCCGGCTCGTT	Vancomycin
249	vanB-02	CCGGTCGAGGAACGAAATC	TCCTCCTGCAAAAAAAGATCAAC	Vancomycin
250	vanC-01	ACAGGGATTGGCTATGAACCAT	TGACTGGCGATGATTGACTATG	Vancomycin
251	vanC-03	AAATCAATACTATGCCGGCTTT	CCGACCGCTGCCATCA	Vancomycin
252	vanC1	AGGCGATAGCGGGTATTGAA	CAATCGTCAATTGCTCATTCC	Vancomycin
253	vanC2/vanC3	TTTGACTGTCGGTGCTTGTGA	TCAATCGTTCAGGCAATGG	Vancomycin
254	vanG	ATTGAAATTGGCAGGTATACAGGTTA	TGATTGTCTTGTCCATACATAATGC	Vancomycin
255	vanHB	GAGGTTCCGAGGCGACAA	CTCTCGGCGGCAGTCGTAT	Vancomycin
256	vanHD	GTGGCCGATTATAACCGTCATG	CGCAGGTCAATTCAAGGCAAT	Vancomycin
257	vanRA-01	CCCTTACTCCCACCGAGTTT	TTCGTCGCCCATATCTCAT	Vancomycin
258	vanRA-02	CCACTCCGGCCTTGTCAATT	GCTAACACATTCCCCTGTTT	Vancomycin

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259	vanRB	GCCCTGTCGGATGACGAA	TTACATAGTCGTCTGCCTCTGCAT	Vancomycin
260	vanRC	TGCGGGAAAAACTGAACGA	CCCCCCATACGGTTTGATTA	Vancomycin
261	vanRC4	AGTGCTTGGCTTATCTCGAAAA	TCCGGCAGCATCACATCTAA	Vancomycin
262	vanRD	TTATAATGGCAAGGATGCACTAAAGT	CGTCTACATCCGGAAGCATGA	Vancomycin
263	vanSA	CGCGTCATGCTTCAAAATTCT	TCCGCAGAAAGCTCAATTGTT	Vancomycin
264	vanSB	GCGCGGCAAATGACAAC	TTTGCCATTTATT CGCACTGT	Vancomycin
265	vanSC-02	GCCATCAGCGAGTCTGATGA	CAGCTGGATCGTTTCCTT	Vancomycin
266	vanSE	TGGCCGAAGAAGCAGGAA	CAATAATACTCGTCAAAGGAGTTCTCA	Vancomycin
267	vanTC-01	CACACGCATTTTCCCATCTAG	CAGCCAACAGATCATCAAAACAA	Vancomycin
268	vanTC-02	ACAGTTGCCGCTGGTGAAG	CGTGGCTGGTCGATCAAAA	Vancomycin
269	vanTE	GTGGTGCCAAGGAAGTTGCT	CGTAGCCACCGCAAAAAAAAT	Vancomycin
270	vanTG	CGTGTAGCCGTTCCGTTCTT	CGGCATTACAGGTATATCTGGAAA	Vancomycin
271	vanWB	CGGACAAAGATACCCCCTATAAAG	AAATAGTAAATTGCTCATCTGGCACAT	Vancomycin

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272	vanWG	ACATTTCATTGGCAGCTTGTAC	CCGCCATAAGAGCCTACAATCT	Vancomycin
273	vanXA	CGCTAAATATGCCACTTGGGATA	TCAAAAGCGATTCAAGCCAAC	Vancomycin
274	vanXB	AGGCACAAAATCGAAGATGCTT	GGGTATGGCTCATCAATCAACTT	Vancomycin
275	vanXD	TAAACCGTGTATGGAACGAA	GCGATAGCCGTCCCATAAGA	Vancomycin
276	vanYB	GGCTAAAGCGGAAGCAGAAA	GATATCCACAGCAAGACCAAGCT	Vancomycin
277	vanYD-01	AAGGCATAACCCTGACTGTCA	ATTGCCGGACGGAAGCA	Vancomycin
278	vanYD-02	CAAACGGAAGAGAGGGTCACTTACA	CGGACGGTAATAGGGACTGTT	Vancomycin
279	vatB-01	GGAAAAAGCAACTCCATCTCTGA	TCCTGGCATAACAGTAACATTCTGA	MLSB
280	vatB-02	TTGGGAAAAAGCAACTCCATCT	CAATCCACACATCATTCCAACA	MLSB
281	vatC-01	CGGAAATTGGGAAACGATGTT	GCAATAATAGCCCCGTTCTTA	MLSB
282	vatC-02	CGATGTTGGATTGGACGAGAT	GCTGCAATAATAGCCCCGTT	MLSB
283	vatE-01	GGTGCCATTATCGGAGCAAAT	TTGGATTGCCACCGACAAT	MLSB
284	vatE-02	GACCGTCCTACCAGGGCGTAA	TTGGATTGCCACCGACAATT	MLSB

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285	vgaA-01	CGAGTATTGTGAAAGCAGCTAGTT	CCCGTACCGTTAGAGCCGATA	MLSB
286	vgaA-02	GACGGGTATTGTGAAAGCAA	TTTCCTGTACCATTAGATCCGATAATT	MLSB
287	vgb-01	AGGGAGGGTATCCATGCAGAT	ACCAAATGCGCCCGTTT	MLSB
288	vgbB-01	CAGCCGGATTCTGGTCCTT	TACGATCTCCATTCAATTGGGTAAA	MLSB
289	vgbB-02	ATACGAGCTGCCTAATAAAGGATCTT	TGTGAACCACAGGGCATTATCA	MLSB
290	yceE/mdtG-01	TGGCACAAAATATCTGGCAGTT	TTGTGTGGCGATAAGAGCATTAG	Multidrug
291	yceE/mdtG-02	TTATCTTTCTGCTCACCTTCTTT	GCGTGGTGACAAACAGGCTTA	Multidrug
292	yceL/mdtH-01	TCGGGATGGTGGGCAAT	CGATAACCGAGCCGATGTAGA	Multidrug
293	yceL/mdtH-02	CGCGTGAACCTTAAGTGCTT	AGACGGCTAACCCCCATATAAGCT	Multidrug
294	yceL/mdtH-03	CTGCCGTTAAATGGATGTATGC	ACTCCAGCGGGCGATAGG	Multidrug
295	yidY/mdtL-01	GCAGTTGCATATCGCCTCTC	CTTCCC GGCAAACAGCAT	Multidrug
296	yidY/mdtL-02	TGCTGATCGGGATTCTGATTG	CAGGCGCGACGAACATAAT	Multidrug

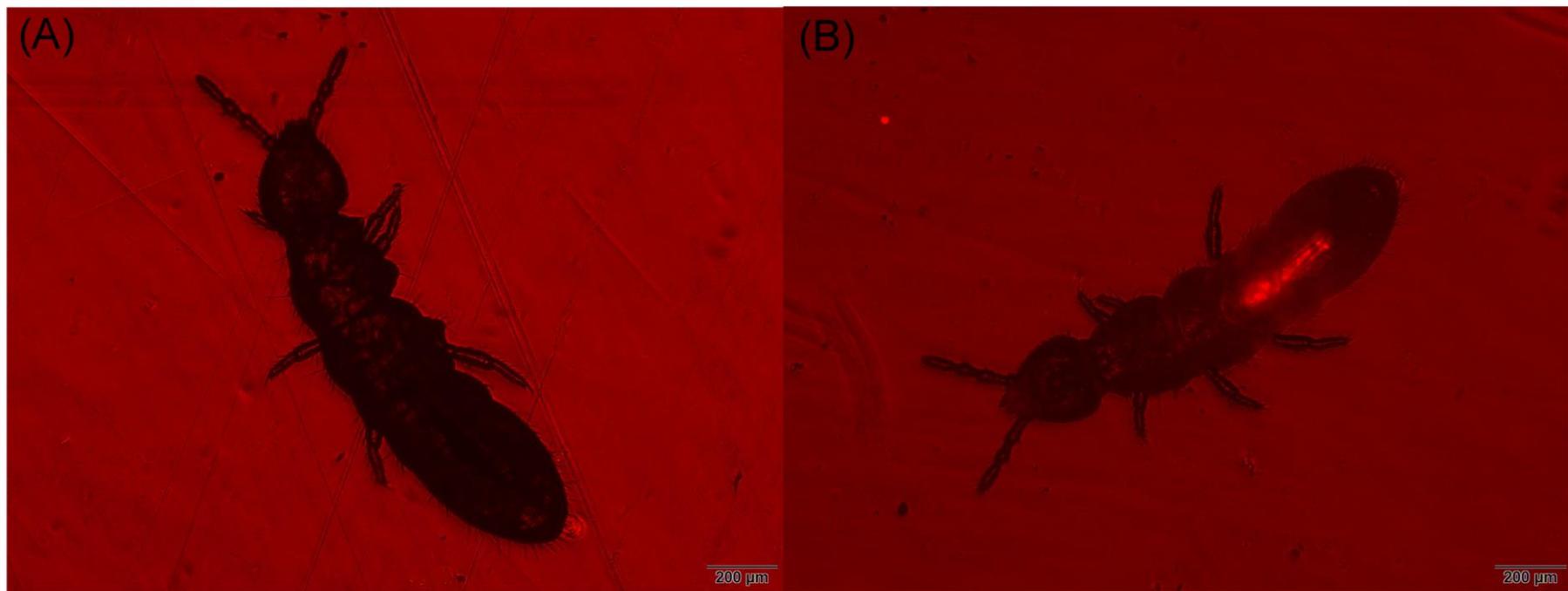
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**Table S3.** The alpha diversity of collembolan gut microbiota in response to microplastic exposure

Treatment	Richness estimates		Diversity estimates
	Observed species	Chao1 index	Shannon index
CK	1286 ± 173 b	2293.86 ± 283.60 b	3.54 ± 0.46 a
MH	1611 ± 140 a	2795.74 ± 254.32 a	4.14 ± 0.53 a
MA	1701 ± 147a	2870.52 ± 161.33 a	3.67 ± 0.11 a

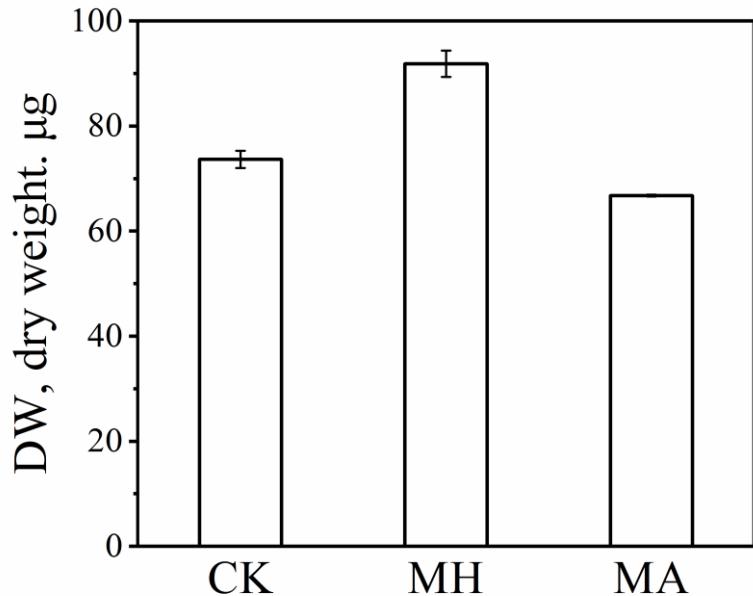
Different letters represent significant differences between food treatments ( $P < 0.05$ , Duncan).

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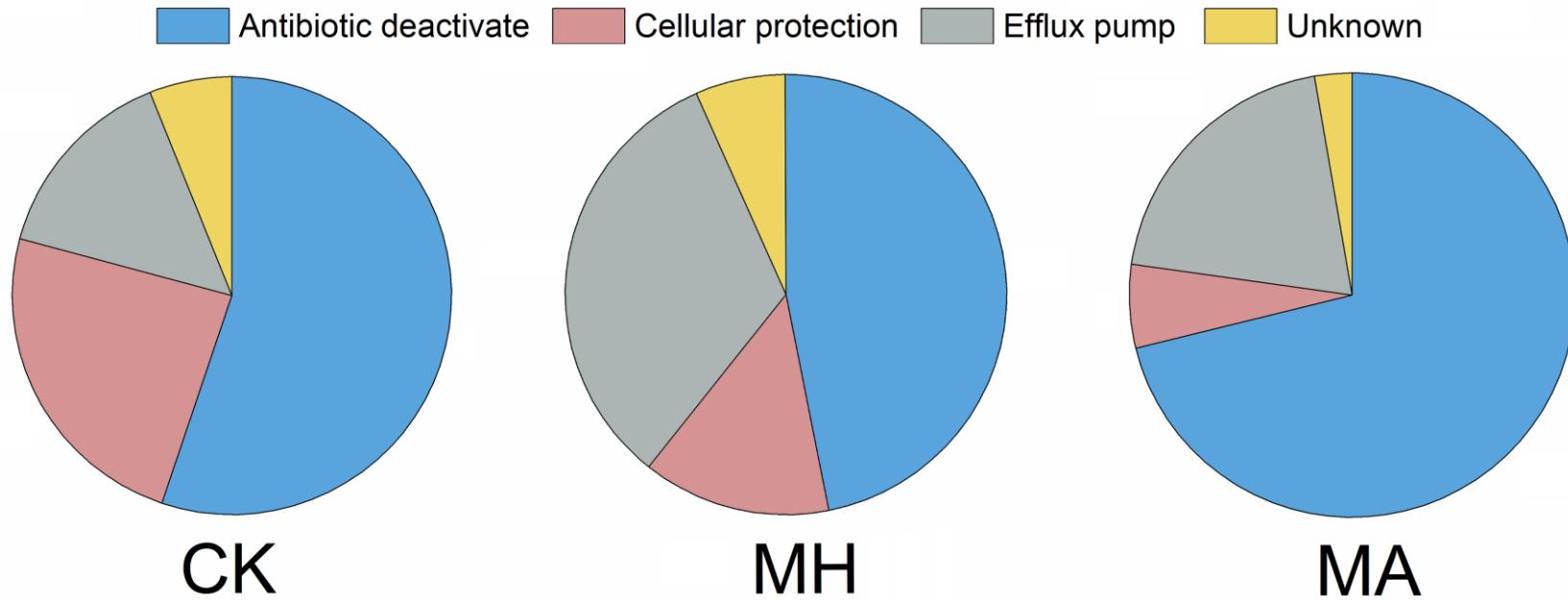
**Figure S1.** Images of fluorescently labeled polystyrene microbeads of 2.0-2.9 $\mu\text{m}$  diameters ingested by soil collembolan. Image (A) was the control (0% microplastics in food). Image (B) shows that the fluorescently labeled polystyrene microbeads are localized at microplastics treated collembolan guts (1% microplastics in food).

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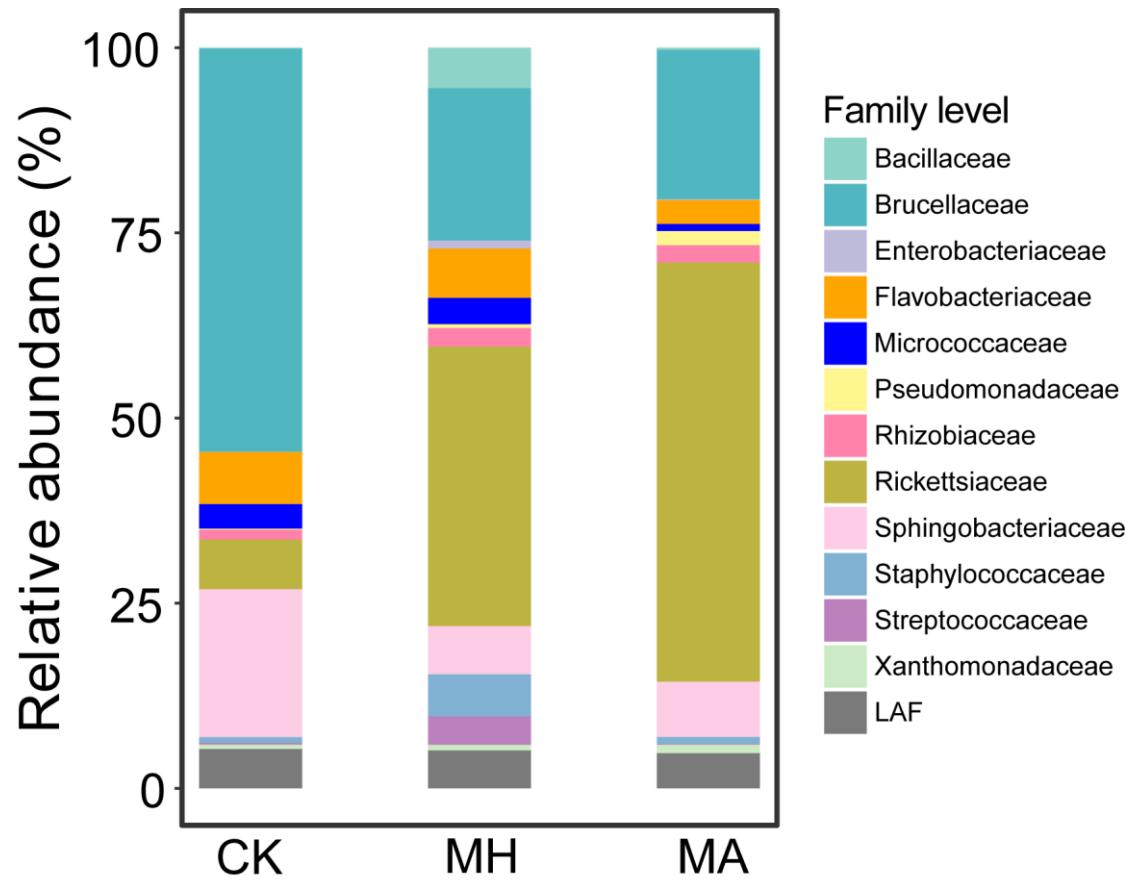
**Figure S2.** The effect of microplastic exposure on collembolan biomass (dry weight per collembolan, DW per collembolan) (ANOVA test,  $F_{(2, 9)} = 1.689$ ,  $P = 0.262$ ). The experiment was designed as CK (0% microplastics in food), MH (1% microplastics without antibiotic in the food), MA (1% microplastics with antibiotic in the food).

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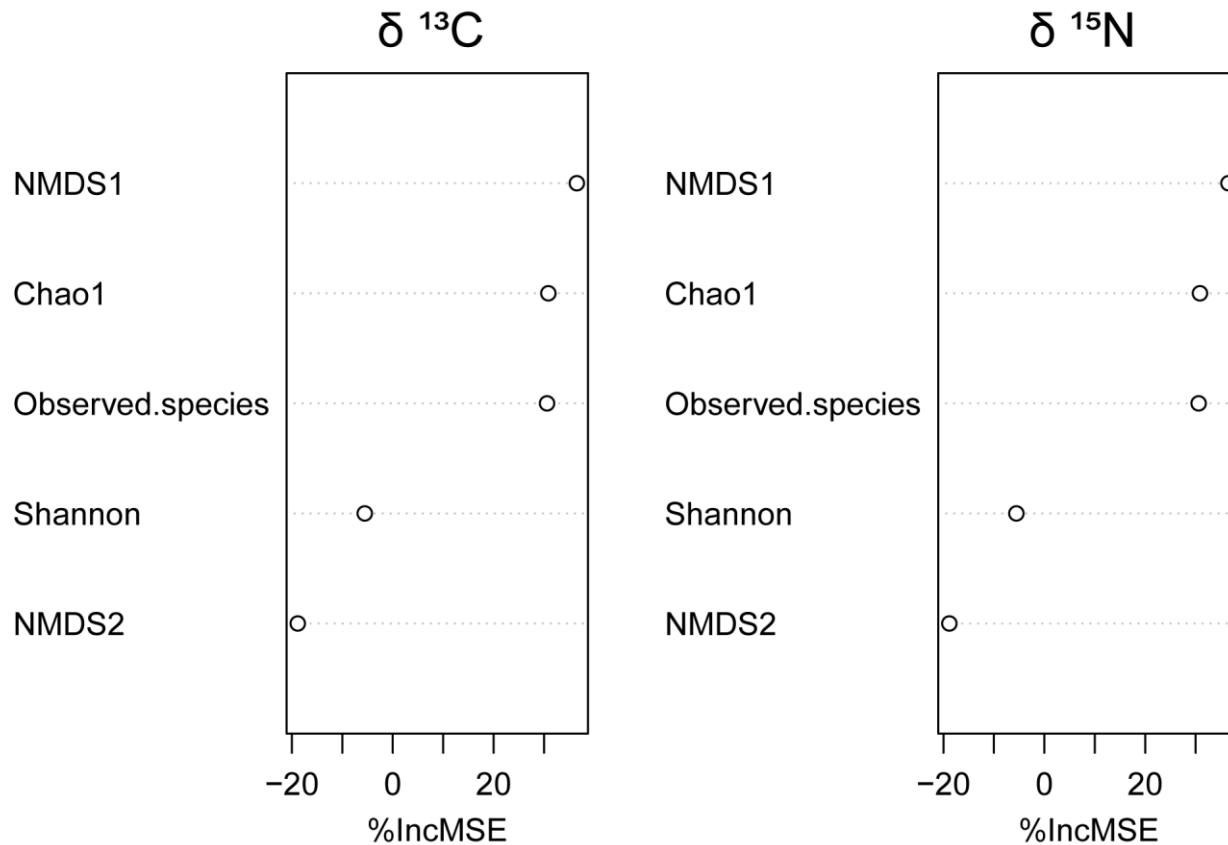
**Figure S3.** Antibiotic resistance gene types detected in collembolan guts with different treatments based on the mechanism of resistance.

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**Figure S4.** Bacterial communities in collembolan guts in response to different treatments at a family level.

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**Figure S5.** Variable importance plot of the Random Forest regression model for the prediction of collembolan  $\delta^{13}\text{C}$ -gut microbiota and  $\delta^{15}\text{N}$ -gut microbiota correlation with different diet treatments includes the variables are ranked on the basis of their importance for the percentage of increase of mean square error (%IncMSE) during the random forest classification routine.

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