

Antibiotic Resistance in the Collembolan Gut Microbiome

Accelerated by the Nonantibiotic Drug Carbamazepine

Yi-Fei Wang,^{†,‡} Min Qiao,^{*,†,‡} Dong Zhu,^{†,‡} Yong-Guan Zhu,^{†,‡,§}

[†] State Key Laboratory of Urban and Regional Ecology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing 100085, China.

[‡] University of Chinese Academy of Sciences, 19A Yuquan Road, Beijing 100049, China.

[§] Key Laboratory of Urban Environment and Health, Institute of Urban Environment, Chinese Academy of Sciences, 1799 Jimei Road, Xiamen 361021, China.

Contents

Figures

Figure S1. The Shannon indices and Coverage (mean \pm SE, n = 4) of bacterial community in the gut of *F. candida*.

Figure S2. The fold change of intI-1(clinic) abundance in treatments compared with control.

Figure S3. The detected number of ARGs and MGEs in the gut of *F. candida*.

Figure S4. Mortality (mean \pm SE, n = 4) of *F. candida* exposed to individual CBZ (0.04, 0.4, 4 and 40 $\mu\text{g g}^{-1}$), individual TC (10 $\mu\text{g g}^{-1}$), and variable CBZ with fixed TC after 28 days. Asterisks indicate statistically significant differences from the control treatment (* $P < 0.05$, ** $P < 0.01$).

Figure S5. Juvenile number (mean \pm SE, n = 4) of *F. candida* in each treatment after 28 days exposure by individual CBZ (0.04, 0.4, 4 and 40 $\mu\text{g g}^{-1}$), individual TC (10 $\mu\text{g g}^{-1}$), and variable CBZ with fixed TC.

Tables

Table S1. Information of 296 genes detected in the gene chip.

Table S2. Analysis of variance for the effect of pharmaceuticals on the relative abundance and β -diversity of ARGs and MGEs in *F. candida* guts.

Table S3. Pearson Correlation between the abundance of MGEs and ARGs.

Table S4. Analysis of variance for the effect of pharmaceuticals on the β -diversity of *F. candida* gut microbiota.

Table S5. Analysis of variance for the effect of pharmaceuticals on the mortality of *F. candida* based on two-way ANOVA.

Total:

Number of tables: 5

Number of figures: 5

Number of pages: 28

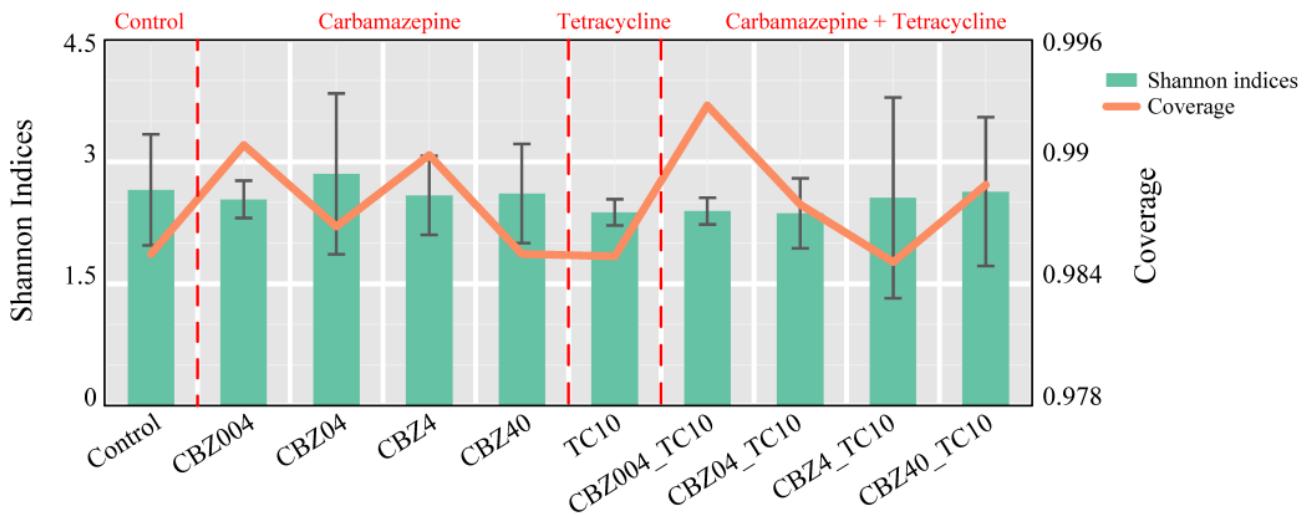


Figure S1. The Shannon indices and Coverage (mean \pm SE, n = 4) of bacterial community in the gut of *F. candida*.

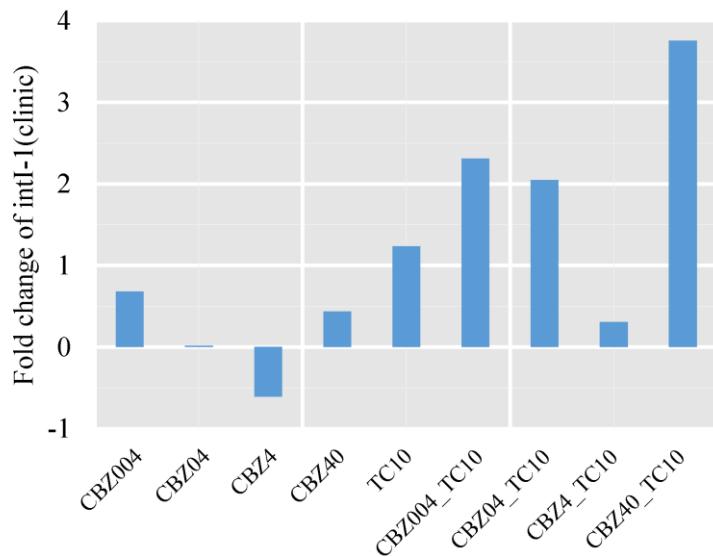


Figure S2. The fold change of intI-1(clinic) abundance in treatments compared with control (fold change = (the abundance of intI-1(clinic) in treatment - the abundance of intI-1(clinic) in control) / the abundance of intI-1(clinic) in control).

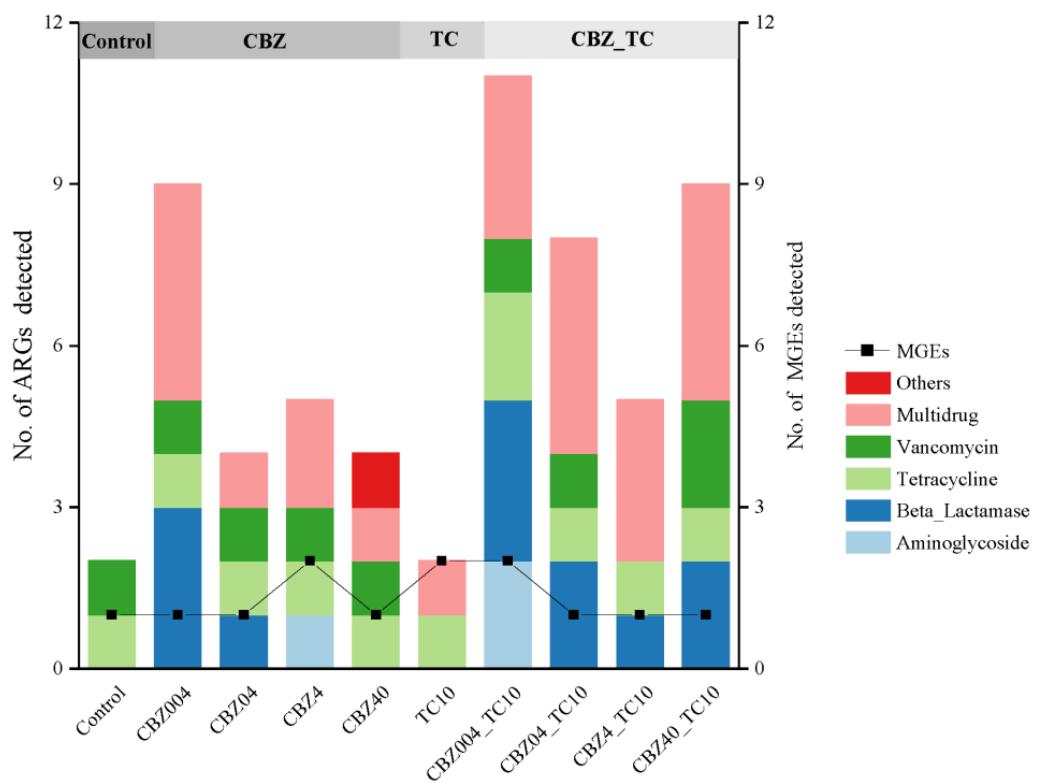


Figure S3. The detected number of ARGs and MGEs in the gut of *F. candida*.

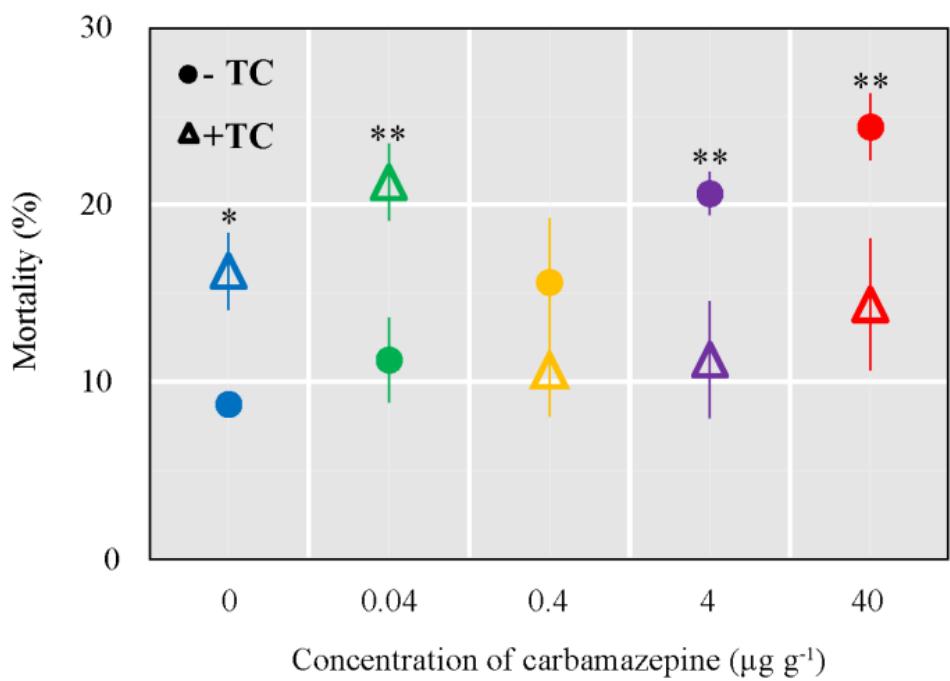


Figure S4. Mortality (mean \pm SE, n = 4) of *F. candida* exposed to individual CBZ (0.04, 0.4, 4 and 40 $\mu\text{g g}^{-1}$), individual TC (10 $\mu\text{g g}^{-1}$), and variable CBZ with fixed TC after 28 days. Asterisks indicate statistically significant differences from the control treatment (* $P < 0.05$, ** $P < 0.01$).

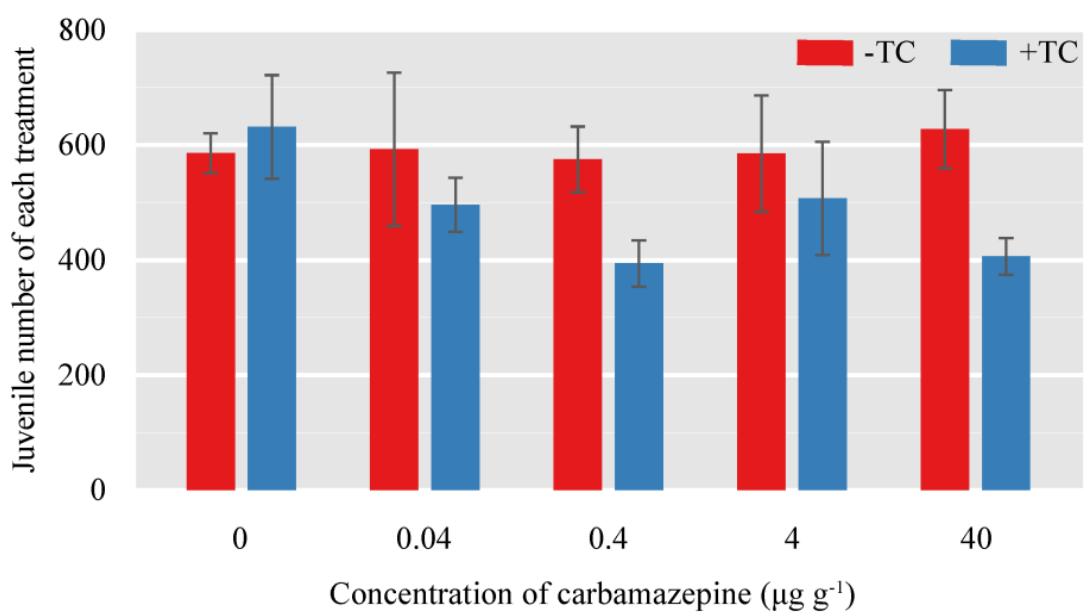


Figure S5. Juvenile number (mean \pm SE, n = 4) of *F. candida* in each treatment after 28 days exposure by individual CBZ (0.04, 0.4, 4 and 40 $\mu\text{g g}^{-1}$), individual TC (10 $\mu\text{g g}^{-1}$), and variable CBZ with fixed TC.

Table S1. Information of 296 genes detected in the gene chip.

Number	Gene Name	Forward Primer	Reverse Primer	Classification	Mechanism (full name)
1	16S rRNA	GGGTTGCGCTCGTTGC	ATGGYTGTCGTCAAGCTCGTG		
2	aac	CCCTGCGTTGTGGCTATGT	TTGGCCACGCCAATCC	Aminoglycoside	antibiotic deactivate
3	aac(6')I1	GACCGGATTAAGGCCGATG	CTTGCCTTGATATTCAAGTTTATAACCA	Aminoglycoside	antibiotic deactivate
4	aac(6')-Ib(aka aacA4)-01	GTTTGAGAGGAAGGTACCGTAA	GAATGCCTGGCGTGTGTTGA	Aminoglycoside	antibiotic deactivate
5	aac(6')-Ib(aka aacA4)-02	CGTCGCCGAGCAAATTG	CGGTACCTGCCTCTCAAACC	Aminoglycoside	antibiotic deactivate
6	aac(6')-Ib(aka aacA4)-03	AGAACGACGCCGACACTT	GCTCTCCATTCAAGCATTGCA	Aminoglycoside	antibiotic deactivate
7	aac(6')-II	CGACCCGACTCCGAACAA	GCACGAATCCTGCCTCTCA	Aminoglycoside	antibiotic deactivate
8	aac(6')-Iy	GCTTGCGGATGCCTCAAT	GGAGAACAAAAACACCTCAAGGAAA	Aminoglycoside	antibiotic deactivate
9	aacA/aphD	AGAGCCTGGAAAGATGAAGTT	TTGATCCATACCATAGACTATCTCATCA	Aminoglycoside	antibiotic deactivate
10	aacC	CGTCACTTATTGATGCCCTTAC	GTCGGCGCGGCATA	Aminoglycoside	antibiotic deactivate
11	aacC1	GGTCGTGAGTCGGAGACGTA	GCAAGTTCCCAGGTAATCG	Aminoglycoside	antibiotic deactivate
12	aacC2	ACGGCATTCTCGATTGCTTT	CCGAGCTTCACGTAAGCATT	Aminoglycoside	antibiotic deactivate
13	aacC4	CGGCGTGGGACACGAT	AGGGAACCTTGCCATCAACT	Aminoglycoside	antibiotic deactivate
14	aadA-01	GTTGTGCACGACGACATCAIT	GGCTCGAAGATACTGCAAGAA	Aminoglycoside	antibiotic deactivate
15	aadA-02	CGAGATTCTCCGCGCTGTA	GCTGCCATTCTCCAATTGC	Aminoglycoside	antibiotic deactivate

16	aadA1	AGCTAAGCGCGAACTGCAAT	TGGCTCGAAGATAACCTGCAA	Aminoglycoside	antibiotic deactivate
17	aadA-1-01	AAAAGCCGAAGAGGAACTTG	CATCTTCACAAAGATGTTGCTGTCT	Aminoglycoside	antibiotic deactivate
18	aadA-1-02	CGGAATTGAAAAAAACTGATCGAA	ATACCGGCTGTCCGTCATTT	Aminoglycoside	antibiotic deactivate
19	aadA2-01	ACGGCTCCGCAGTGGAT	GGCCACAGTAACCAACAAATCA	Aminoglycoside	antibiotic deactivate
20	aadA2-02	CTTGTGCGTGCATGACGACATC	TCGAAGATAACCGCAAGAATG	Aminoglycoside	antibiotic deactivate
21	aadA2-03	CAATGACATTCTGCGGGTATC	GACCTACCAAGGCAACGCTATG	Aminoglycoside	antibiotic deactivate
22	aadA5-01	ATCACGATCTTGCATTTGCT	CTGCGGATGGGCCTAGAAG	Aminoglycoside	antibiotic deactivate
23	aadA5-02	GTTCTTGCTCTTGCTCGCATT	GATGCTCGGCAGGCCAAC	Aminoglycoside	antibiotic deactivate
24	aadA9-01	CGCGGCAAGCCTATCTT	CAAATCAGCGACCGCAGACT	Aminoglycoside	antibiotic deactivate
25	aadA9-02	GGATGCACGCTTGGATGAA	CCTCTAGCGGCCGGAGTATT	Aminoglycoside	antibiotic deactivate
26	aadD	CCGACAACATTCTACCATCCTT	ACCGAAGCGCTCGTCGTATA	Aminoglycoside	antibiotic deactivate
27	aadE	TACCTTATTGCCCTTGGAAAGAGTTA	GGAACATATGTCCTTTAATTCTACAATCT	Aminoglycoside	antibiotic deactivate
28	acrA-01	CAACGATCGGACGGTTTC	TGGCGATGCCACCGTACT	Multidrug	efflux pump
29	acrA-02	GGTCTATCACCCCTACCGCCTATC	GCGCGCACGAACATACC	Multidrug	efflux pump
30	acrA-03	CAGACCCGCATCGCATATT	CGACAATTTCGCGCTCATG	Multidrug	efflux pump
31	acrA-04	TACTTTCGCGGCCATCTTC	CGTGCACGAACGAACAT	Multidrug	efflux pump
32	acrA-05	CGTGCACGAACGAACA	ACTTTGCACGCCATCTTC	Multidrug	efflux pump

33	acrB-01	AGTCGGTGTTCGCCGTTAAC	CAAGGAAACGAACGCAATACC	Multidrug	efflux pump
34	acrF	GCGGCCAGGCACAAAAA	TACGCTTCCCACGGTTTC	Multidrug	efflux pump
35	acrR-01	GCGCTGGAGACACGACAAC	GCCTTGCTGCGAGAACAAA	Multidrug	efflux pump
36	acrR-02	GATGATACCCCCTGCTGTGAGA	ACCAAACAAGAAGCGCAAGAA	Multidrug	efflux pump
37	adeA	CAGTTCGAGCGCCTATTCTG	CGCCCTGACCGACCAAT	Multidrug	efflux pump
38	ampC/blaDHA	TGGCCGCAGCAGAAAGA	CCGTTTTATGCACCCAGGAA	Beta_Lactamase	antibiotic deactivate
39	ampC-01	TGGCGTATCGGGTCAATGT	CTCCACGGGCCAGTTGAG	Beta_Lactamase	antibiotic deactivate
40	ampC-02	GCAGCACGCCCGTAA	TGTACCCATGATGCGCGTACT	Beta_Lactamase	antibiotic deactivate
41	ampC-04	TCCGGTGACGCGACAGA	CAGCACGCCGGTGAAAGT	Beta_Lactamase	antibiotic deactivate
42	ampC-05	CTGTTGAGCTGGTTCTATAAGTAAA	CAGTATCTGGTCACCGGATCGT	Beta_Lactamase	antibiotic deactivate
43	ampC-06	CCGCTCAAGCTGGACCATAAC	CCATATCCTGCACGTTGGTTT	Beta_Lactamase	antibiotic deactivate
44	ampC-07	CCGCCCAGAGCAAGGACTA	GCTCGACTTCACGCCGTAAG	Beta_Lactamase	antibiotic deactivate
45	ampC-09	CAGCCGCTGATGAAAAAATATG	CAGCGAGCCCACCTCGA	Beta_Lactamase	antibiotic deactivate
46	aph	TTTCAGCAAGTGGATCATGTTAAAAT	CCAAGCTTTCCACTGTTTTC	Aminoglycoside	antibiotic deactivate
47	aph(2')-Id-01	TGAGCAGTATCATAAGTTGAGTAAAAG	GACAGAACATCAATCTATGGAATG	Aminoglycoside	antibiotic deactivate
48	aph(2')-Id-02	TAAGGATATACCGACAGTTGGAAA	TTTAATCCCTCTTCATACCAATCCATA	Aminoglycoside	antibiotic deactivate
49	aph6ia	CCCATCCCATGTGTAAGGAAA	GCCACCGCTCTGCTGTAC	Aminoglycoside	antibiotic deactivate

50	aphA1(aka kanR)	TGAACAAGTCTGGAAAGAAATGCA	CCTATTAATTCCCCCTCGTAAAAAA	Aminoglycoside	antibiotic deactivate
51	bacA-01	CGGCTTCGTGACCTCGTT	ACAATGCGATACCAGGCAAAT	Others	antibiotic deactivate
52	bacA-02	TTCCACGACACGATTAAGTCATTG	CGGCTCTTCGGCTTCAG	Others	antibiotic deactivate
53	bla1	GCAAGTTGAAGCGAAAGAAAAGA	TACCACTATCAATCGCATACACCTAA	Beta_Lactamase	antibiotic deactivate
54	bla-ACC-1	CACACAGCTGATGGCTTATCTAAAA	AATAAACCGCGATGGGTTCCA	Beta_Lactamase	antibiotic deactivate
55	blaCMY	CCGC GGCGAAATTAAGC	GCCACTGTTGCCTGTCAGTT	Beta_Lactamase	antibiotic deactivate
56	blaCMY2-01	AAAGCCTCAT GGGTGCATAAA	ATAGCTTTGTTGCCAGCATCA	Beta_Lactamase	antibiotic deactivate
57	blaCMY2-02	GCGAGCAGCCTGAAGCA	CGGATGGGCTTGCCTCTT	Beta_Lactamase	antibiotic deactivate
58	blaCTX-M-01	GGAGGC GTGACGGCTTT	TTCAGTGCATCCAGACGAA	Beta_Lactamase	antibiotic deactivate
59	blaCTX-M-02	GCCGCGGTGCTGAAGA	ATCGGATTATAGTTAACCAGGTCAGATT	Beta_Lactamase	antibiotic deactivate
60	blaCTX-M-03	CGATACCACCA CGCCGTTA	GCATTGCCAACGTCAGATT	Beta_Lactamase	antibiotic deactivate
61	blaCTX-M-04	CTTGGCGTTGCGCTGAT	CGTTCATCGGCACGGTAGA	Beta_Lactamase	antibiotic deactivate
62	blaCTX-M-05	GCGATAACGTGGCGATGAAT	GTCGAGACGGAACGTTTCGT	Beta_Lactamase	antibiotic deactivate
63	blaCTX-M-06	CACAGTTGGTGACGTGGCTTAA	CTCCGCTGCCGGTTTATC	Beta_Lactamase	antibiotic deactivate
64	blaGES	GCAATGTGCTAACGTTCAAG	GTGCCTGAGTCAATTCTTCAAAG	Beta_Lactamase	antibiotic deactivate
65	blaIMP-01	AACACGGTTGGTGGTTCTTGT A	GCGCTCCACAAACCAATTG	Beta_Lactamase	antibiotic deactivate
66	blaIMP-02	AAGGCAGCATT CCTCTCATTT	GGATAGATCGAGAATTAAGCCACTCT	Beta_Lactamase	antibiotic deactivate

67	bla-L1	CACCGGGTTACCAGCTGAAG	GCGAAGCTGCGCTTGTAGTC	Beta_Lactamase	antibiotic deactivate
68	blaMOX/blaCMY	CTATGTCAATGTGCCGAAGCA	GGCTTGTCCCTTTCAATAGC	Beta_Lactamase	antibiotic deactivate
69	blaOCH	GGCGACTTGCGCCGTAT	TTTTCTGCTCGGCCATGAG	Beta_Lactamase	antibiotic deactivate
70	blaOKP	GCCGCCATCACCATGAG	GGTGACGTTGTCAACGATCTG	Beta_Lactamase	antibiotic deactivate
71	blaOXA1/blaOXA30	CGGATGGTTGAAGGGTTATTAT	TCTTGGCTTTATGCTTGATGTTAA	Beta_Lactamase	antibiotic deactivate
72	blaOXA10-01	CGCAATTATCGGCCTAGAAACT	TTGGCTTCCGTCCCATT	Beta_Lactamase	antibiotic deactivate
73	blaOXA10-02	CGCAATTATCGGCCTAGAAACT	TTGGCTTCCGTCCCATT	Beta_Lactamase	antibiotic deactivate
74	blaOXY	CGTTCAGGCGGCAGGTT	GCCGCGATATAAGATTGAGAATT	Beta_Lactamase	antibiotic deactivate
75	blaPAO	CGCCGTACAACCGGTGAT	GAAGTAATGCGGTTCTCCTTCA	Beta_Lactamase	antibiotic deactivate
76	blaPER	TGCTGGTTGCTGTTTGTGA	CCTGCGCAATGATAGCTTCAT	Beta_Lactamase	antibiotic deactivate
77	blaPSE	TTGTGACCTATTCCCTGTAATAGAA	TGCGAAGCACGCATCATC	Beta_Lactamase	antibiotic deactivate
78	blaROB	GCAAAGGCATGACGATTGC	CGCGCTGTTGTCGCTAAA	Beta_Lactamase	antibiotic deactivate
79	blaSFO	CCGCCGCCATCCAGTA	GGGCCGCCAACGATGCT	Beta_Lactamase	antibiotic deactivate
80	blaSHV-01	TCCCCATGATGAGCACCTTAAA	TTCGTCACCGGCATCCA	Beta_Lactamase	antibiotic deactivate
81	blaSHV-02	CTTTCCCATGATGAGCACCTT	TCCTGCTGGCGATAGTGGAT	Beta_Lactamase	antibiotic deactivate
82	blaTEM	AGCATCTTACGGATGGCATGA	TCCTCCGATCGTTGTCAGAACT	Beta_Lactamase	antibiotic deactivate
83	blaTLA	ACACTTGCATTGCTGTTATGT	TGCAAATTGCGCAATAATCTT	Beta_Lactamase	antibiotic deactivate

84	blaVEB	CCCGATGCAAAGCGTTATG	GAAAGATTCCCTTATCTATCTCAGACAA	Beta_Lactamase	antibiotic deactivate
85	blaVIM	GCACTTCTCGCGGAGATTG	CGACGGTGATGCGTACGTT	Beta_Lactamase	efflux pump
86	blaZ	GGAGATAAAGTAACAAATCCAGTTAGATATGA	TGCTTAATTTCATTCGATAAG	Beta_Lactamase	antibiotic deactivate
87	carB	GGAGTGAGGCTGACCGTAGAAG	ATCGGCAGAACGCACAAA	MLSB	antibiotic deactivate
88	catA1	GGGTGAGTTTCACCAGTTTGATT	CACCTTGTGCCTTGCCTATA	Others	antibiotic deactivate
89	catB3	GCACTCGATGCCTTCCAAAA	AGAGCCGATCCAAACGTCAT	Others	efflux pump
90	catB8	CACTCGACGCCTTCCAAAG	CCGAGCCTATCCAGACATCATT	Others	antibiotic deactivate
91	ceoA	ATCAACACGGACCAGGACAAG	GGAAAGTCCGCTCACGATGA	Multidrug	antibiotic deactivate
92	cepA	AGTTGCGCAGAACAGTCCTCTT	TCGTATCTGCCCGTCGATAAT	Beta_Lactamase	antibiotic deactivate
93	cfiA	GCAGCGTTGCTGGACACA	GTTCGGGATAAACGTGGTGACT	Beta_Lactamase	antibiotic deactivate
94	cfr	GCAAAATTCAAGAGCAAGTTACGAA	AAAATGACTCCCCAACCTGCTTTAT	Others	efflux pump
95	cfxA	TCATTCTCGTTCAAGTTTCAGA	TGCAGCACCAAGAGGAGATGT	Beta_Lactamase	efflux pump
96	cIntI-1(class1)	GGCATCCAAGCAGCAAG	AAGCAGACTTGACCTGA	Integron	efflux pump
97	cmeA	GCAGCAAAGAAGAACCAAA	AGCAGGGTAAGTAAACTAAGTGGTAAATCT	Multidrug	efflux pump
98	cmlA1-01	TAGGAAGCATCGAACGTTGAT	CAGACCGAGCACGACTGTTG	Chloramphenicol	efflux pump
99	cmlA1-02	AGGAAGCATCGAACGTTGA	ACAGACCGAGCACGACTGTTG	Chloramphenicol	antibiotic deactivate
100	cmr	CGGCATCGTCAGTGGATT	CGGTTCCGAAAAAGATGGAA	Multidrug	antibiotic deactivate

101	cmx(A)	GCGATGCCCATCCTCTGT	TCGACACGGAGCCTTGGT	Chloramphenicol	antibiotic deactivate
102	cphA-01	GCGAGCTGCACAAGCTGAT	CGGCCAGTCGCTCTTC	Beta_Lactamase	antibiotic deactivate
103	cphA-02	GTGCTGATGGCGAGTTCTG	GGTGTGGTAGTTGGTGTGATCAC	Beta_Lactamase	efflux pump
104	dfrA1	GGAATGGCCCTGATATTCCA	AGTCTTGCCTCCAACCAACAG	Sulfonamide	antibiotic deactivate
105	dfrA12	CCTCTACCGAACCGTCACACA	GCGACAGCGTTGAAACAACACTAC	Sulfonamide	antibiotic deactivate
106	emrD	CTCAGCAGTATGGTGGTAAGCATT	ACCAGGCGCCGAAGAAC	Multidrug	cellular protection
107	ereA	CCTGTGGTACGGAGAACATGT	ACCGCATTGCTTGCTT	MLSB	cellular protection
108	ereB	GCTTTATTCAGGAGGCGGAAT	TTTTAAATGCCACAGCACAGAAC	Others	cellular protection
109	erm(34)	GCGCGTTGACGACGATT	TGGTCATACTCGACGGCTAGAAC	MLSB	cellular protection
110	erm(35)	TTGAAAACGATGTTGCATTAAGTCA	TCTATAATCACAACTAACCACATTGAAAC	MLSB	cellular protection
111	erm(36)	GGCGGACCGACTTGCAT	TCTGCGTTGACGACGGTTAC	MLSB	cellular protection
112	ermA	TTGAGAAGGGATTGCGAAAAG	ATATCCATCTCCACCATTAATAGTAAACC	MLSB	cellular protection
113	ermA/ermTR	ACATTTACCAAGGAACCTGTGGAA	GTGGCATGACATAAACCTTCATCA	MLSB	cellular protection
114	ermB	TAAAGGGATTTAACGACGAAACT	TTTATACCTCTGTTGTTAGGAAATTGAA	MLSB	cellular protection
115	ermC	TTTGAAATCGGCTCAGGAAAA	ATGGTCTATTCAATGGCAGTTACG	MLSB	cellular protection
116	ermF	CAGCTTGGTTGAACATTACGAA	AAATTCTAAATCACAACCGACAA	MLSB	cellular protection
117	ermJ/ermD	GGACTCGGCAATGGTCAGAA	CCCCGAAACGCAATATAATGTT	MLSB	cellular protection

118	ermK-01	GTTTGATATTGGCATTGTCAGAGAAA	ACCATTGCCGAGTCCACTTT	MLSB	cellular protection
119	ermK-02	GAGCCGCAAGCCCCTTT	GTGTTCATTTGACGCGGAGTAA	MLSB	cellular protection
120	ermT-01	GTTCACTAGCACTATTTAATGACAGAAGT	GAAGGGTGTCTTTAATACAATTAACGA	MLSB	cellular protection
121	ermT-02	GTAAAATCCCTAGAGAACATTTCATCCA	TGAGTGATATTTGAAGGGTGTCTT	MLSB	antibiotic deactivate
122	ermX	GCTCAGTGGTCCCCATGGT	ATCCCCCGTCAACGTTT	MLSB	efflux pump
123	ermY	TTGTCTTGAAAGTGAAGCAACAGT	TAACGCTAGAGAACGATTGTATTGAG	MLSB	antibiotic deactivate
124	fabK	TTTCAGCTCAGCACTTGGTCAT	AAGGCATCTTTCAGCCAGTTC	Others	antibiotic deactivate
125	floR	ATTGTCTTCACGGTGTCCGTTA	CCCGCATGTCGTCGAAC	Multidrug	antibiotic deactivate
126	folA	CGAGCAGTCCCTGCCAAAG	CCCAGTCATCCGGTTCATAATC	Sulfonamide	antibiotic deactivate
127	fosB	TCACTGTAACATGAAGCATTAGACCAT	CCATCTGGATCTGTAAAGTAAAGAGATC	Others	other/unknown
128	fosX	GATTAAGCCATATCACTTAAATTGTGAAAG	TCTCCTCCATAATGCAAATCCA	Others	integrase
129	fox5	GGTTTGCCGCTGCAGTTC	GCGGCCAGGTGACCAA	Beta_Lactamase	integrase
130	imiR	CCGGACTAGAGCTTCATGTAAGC	CCCACGCGGTACTCTTGATAA	Others	integrase
131	intI-1(clinic)	CGAACGAGTGGCGGAGGGTG	TACCCGAGAGCTTGGCACCCA	Integron	integrase
132	IS613	AGGTTCGGACTCAATGCAACA	TTCAGCACATACCGCCTTGAT	Transposase	transposase
133	lmrA-01	TCGACGTGACCGTAGTGAACA	CGTGAACCTCCAGGTGAGTTGA	MLSB	efflux pump
134	InuA-01	TGACGCTAACACACTCAAAAA	TTCATGCTTAAGTCCATACGTGAA	MLSB	antibiotic deactivate

135	InuB-01	TGAACATAATCCCCTCGTTAAAGAT	TAATTGCCCTGTTCATCGTAAATAA	MLSB	antibiotic deactivate
136	InuB-02	AAAGGAGAAGGTGACCAATACTCTGA	GGAGCTACGTCAAACAACCAGTT	MLSB	antibiotic deactivate
137	InuC	TGGTCAATATAACAGATGTAAACCAGATT	CACCCAGCCACCATCAA	MLSB	antibiotic deactivate
138	marR-01	GCGGCGTACTGGTGAAGCTA	TGCCCTGGTCGTTGATGA	Multidrug	efflux pump
139	matA/mel	TAGTAGGCAAGCTCGGTGTTGA	CCTGTGCTATTTAACGCCTGTTCT	MLSB	efflux pump
140	mdeI1	ATACAGCAGTGGATATTGGTTAATTGT	TGCATAAGGTGAATGTTCCATGA	Multidrug	efflux pump
141	mdtA	CCTAACGGCGTGACTTCA	TTCACCTGTTCAAGGGTCAA	MLSB	efflux pump
142	mdtE/yhiU	CGTCGGCGCACTCGTT	TCCAGACGTTGTACGGTAACCA	Multidrug	efflux pump
143	mecA	GGTTACGGACAAGGTGAAATACTGAT	TGTCTTTAATAAGTGAGGTGCGTTAATA	Beta_Lactamase	cellular protection
144	mefA	CCGTAGCATTGGAACAGCTTT	AAACGGAGTATAAGAGTGCTGCAA	MLSB	efflux pump
145	mepA	ATCGGTCCCTTTCGTTCAC	ATAAAATAGGATCGAGCTGCTGGAT	Multidrug	efflux pump
146	mexA	AGGACAACGCTATGCAACGAA	CCGGAAAGGGCCGAAAT	Multidrug	efflux pump
147	mexD	TTGCCACTGGCTTCATGAG	CACTGCGGAGAACTGTCTGTAGA	Multidrug	efflux pump
148	mexE	GGTCAGCACCGACAAGGTCTAC	AGCTCGACGTACTTGAGGAACAC	Multidrug	efflux pump
149	mexF	CCCGCAGAAAGGCCAAGA	TTGAGTTCGCGGGTGTGATGA	Multidrug	efflux pump
150	mphA-01	CTGACGCGCTCCGTGTT	GGTGGTGCATGGCGATCT	MLSB	antibiotic deactivate
151	mphA-02	TGATGACCCCTGCCATCGA	TTCGCGAGCCCCCTCTTC	MLSB	antibiotic deactivate

152	mphB	CGCAGCGCTTGATCTTGTAG	TTACTGCATCCATACGCTGCTT	MLSB	antibiotic deactivate
153	mphC	CGTTGAAGTACCGAATTGGAAA	GCTGCGGTTGCCTGTA	MLSB	antibiotic deactivate
154	msrA-01	CTGCTAACACAAGTACGATTCCAAT	TCAAGTAAAGTTGTCCTACCTACACCATT	MLSB	efflux pump
155	msrC-01	TCAGACCGGATCGGTTGTC	CCTATTTTGAGTCTCTCTAATGTT	MLSB	efflux pump
156	mtrC-01	GGACGGGAAGATGGTCAA	CGTAGCGTCCGGTTCGAT	Multidrug	efflux pump
157	mtrC-02	CGGAGTCCATCGACCATTG	ATCGTCGGCAAGGAGAATCA	Multidrug	efflux pump
158	mtrD-02	GGTCGGCACGCTCTGTC	TGAAGAATTGCGCACCACTAC	Multidrug	efflux pump
159	mtrD-03	CCGCCAAGCCGATATAGACA	GGCCGGGTTGCCAAA	Multidrug	efflux pump
160	ndm-1	ATTAGCCGCTGCATTGAT	CATGTCGAGATAGGAAGTG	Beta_Lactamase	antibiotic deactivate
161	nimE	TGCGCCAAGATAGGGCATA	GTCGTGAATT CGGCAGGTTA	Others	other/unknown
162	nisB	GGGAGAGTTGCCGATGTTGTA	AGCCACTCGTTAAAGGGCAAT	Others	other/unknown
163	oleC	CCCGGAGTCGATGTTGA	GCCGAAGACGTACACGAACAG	MLSB	efflux pump
164	oprD	ATGAAGTGGAGCGCCATTG	GGCCACGGCGAACTGA	Multidrug	efflux pump
165	oprJ	ACGAGAGTGGCGTCGACAA	AAGGCGATCTCGTTGAGGAA	Multidrug	efflux pump
166	pbp	CCGGTGCCATTGGTTAGA	AAAATAGCCGCCCAAGATT	Beta_Lactamase	cellular protection
167	pbp2x	TTTCATAAGTATCTGGACATGGAAGAA	CCAAAGGAAACTTGCTTGAGATTAG	Beta_Lactamase	cellular protection
168	Pbp5	GGCGAACTTCTAATTAATCCTATCCA	CGCCGATGACATTCTTCTTATCTT	Beta_Lactamase	cellular protection

169	penA	AGACGGTAACGTATAACTTTTGAAAGA	GCGTAGCCGGCAATG	Beta_Lactamase	cellular protection
170	pikR1	TCGACATGCGTGACGAGATT	CCGCGAATTAGGCCAGAA	MLSB	cellular protection
171	pikR2	TCGTGGGCCAGGTGAAGA	TTCCCTTGCCGGTGAA	MLSB	cellular protection
172	pmrA	TTTGCAGGTTTGTCTTAATGC	GCAGAGCCTGATTCTCCTTG	Multidrug	efflux pump
173	pncA	GCAATCGAGGCGGTGTC	TTGCCGCAGCCAATTCA	Others	other/unknown
174	putative multidrug	AATTTGCCGATTATTGCTGAAA	GATTGTCATCATCGTTATCACCAA	Multidrug	efflux pump
175	qac	CAATAATAACCGAAATAATAGGGACAAGTT	AATAAGTGTCCCTAGTGTGCCATAG	Multidrug	efflux pump
176	qacA	TGGCAATAGGAGCTATGGTGT	AAGGTAACACTATTCGGTCCAAATC	Multidrug	efflux pump
177	qacA/qacB	TTAGGCAGCCTCGCTCA	CCGAATCCAATAAAACCCAATAA	Multidrug	efflux pump
178	qacEdelta1-01	TCGCAACATCCGCATTA	ATGGATTCAGAACAGAGAAAGAAA	Multidrug	efflux pump
179	qacEdelta1-02	CCCCTCCGCCGTGT	CGACCAGACTGCATAAGCAACA	Multidrug	efflux pump
180	qacH-01	GTGGCAGCTATCGCTGGAT	CCAACGAACGCCACAA	Multidrug	efflux pump
181	qacH-02	CATCGTGCTTGTGGCAGCTA	TGAACGCCAGAACGTCTAGTTT	Multidrug	efflux pump
182	qnrA	AGGATTCTCACGCCAGGATT	CCGCTTCAATGAAACTGCAA	Others	other/unknown
183	rarD-02	TGACGCATCGCGTGATCT	AAATTCTGTGGCGTCTGAATC	Multidrug	efflux pump
184	sat4	GAATGGCAAAGCATAAAACTTG	CCGATTGAAACCACAATTATGATA	Others	antibiotic deactivate
185	sdeB	CACTACCGCTCCGCACTTAA	TGAAAAAACGGAAAAGTCCAT	Multidrug	efflux pump

186	spcN-01	AAAAGTCGATGAAACACGCCAT	TCCAGTGGTAGTCCCCGAATC	Aminoglycoside	antibiotic deactivate
187	spcN-02	CAGAATCTCCTGAAAAGTTGATGAA	CGCAGACACGCCGAATC	Aminoglycoside	antibiotic deactivate
188	speA	GCAAGAGGTATTGCTAACAGA	CAGGGTCACCCTCATAAAGAAAA	Others	other/unknown
189	str	AATGAGTTTGAGTGTCAACGTA	AATCAAAACCCATTAAAGCCAAT	Aminoglycoside	antibiotic deactivate
190	strA	CCGGTGGCATTGAGAAAAAA	GTGGCTAACCTGCGAAAAG	Aminoglycoside	antibiotic deactivate
191	strB	GCTCGGTCGTGAGAACATCT	CAATTTCGGTCGCCTGGTAGT	Aminoglycoside	antibiotic deactivate
192	sul1	CAGCGCTATGCGCTCAAG	ATCCCGCTGCGCTGAGT	Sulfonamide	cellular protection
193	sul2	TCATCTGCCAAACTCGTCGTTA	GTCAAAGAACGCCGAATGT	Sulfonamide	cellular protection
194	sulA/folP-01	CAGGCTCGTAAATTGATAGCAGAAG	CTTTCCTTGCATCGCTTT	Sulfonamide	cellular protection
195	sulA/folP-03	CACGGCTTCGGCTCATGT	TGCCATCCTGTGACTAGCTACGT	Sulfonamide	cellular protection
196	tet(32)	CCATTACTTCGGACAACGGTAGA	CAATCTCTGTGAGGGCATTAAACA	Tetracycline	cellular protection
197	tet(34)	CTTAGCGAAACAGCAATCAGT	CGGTGATACAGCGCGTAAACT	Tetracycline	antibiotic deactivate
198	tet(35)	ACCCCAGACGTACCTGTAGAGA	CAACCCACACTGGCTACCAGTT	Tetracycline	other/unknown
199	tet(36)-01	AGAATACTCAGCAGAGGTAGTTCT	TGGTAGGTGATAACCCGAAAT	Tetracycline	cellular protection
200	tet(36)-02	TGCAGGAAAGACCTCCATTACAG	CTTTGTCCACACTTCCACGTACTATG	Tetracycline	cellular protection
201	tet(37)	GAGAACGTTGAAAGGTGGTGAA	AACCAAGCCTGGATCAGTCTCA	Tetracycline	other/unknown
202	tetA-01	GCTGTTGTTCTGCCGGAAA	GGTTAAGTTCTGAACGCAAAC	Tetracycline	efflux pump

203	tetA-02	CTCACCAAGCCTGACCTCGAT	CACGTTGTTAGAAGCCGCATAG	Tetracycline	efflux pump
204	tetB-01	AGTGCCTTGATGCTGTA	AGCCCCAGTAGCTCCTGTGA	Tetracycline	efflux pump
205	tetB-02	GCCCAGTGCTGTTGTCAT	TGAAAGCAAACGGCCTAAATACA	Tetracycline	efflux pump
206	tetC-01	CATATCGCAATACATGCGAAAAA	AAAGCCGCGTAAATAGCAA	Tetracycline	efflux pump
207	tetC-02	ACTGGTAAGGTAAACGCCATTGTC	ATGCATAAACCCAGCCATTGAGTAAG	Tetracycline	efflux pump
208	tetD-01	TGCCCGCTTGATTACACA	CACCAGTGATCCCGGAGATAA	Tetracycline	efflux pump
209	tetD-02	TGTCATCGCGCTGGTGATT	CATCCGCTTCCGGGAGAT	Tetracycline	efflux pump
210	tetE	TTGGCGCTGTATGCAATGAT	CGACGACCTATGCGATCTGA	Tetracycline	efflux pump
211	tetG-01	TCAACCATTGCCGATTCGA	TGGCCCGGCAATCATG	Tetracycline	efflux pump
212	tetG-02	CATCAGCGCCGGTCTTATG	CCCCATGTAGCCGAACCA	Tetracycline	efflux pump
213	tetH	TTTGGGTACATCTIACCAGCATTAA	TTGCGCATTATCATGACAGA	Tetracycline	efflux pump
214	tetJ	GGGTGCCGCATTAGATTACCT	TCGTCCAATGTAGAGCATCCATA	Tetracycline	efflux pump
215	tetK	CAGCAGTCATTGGAAAATTATCTGATTATA	CCTTGTACTAACCTACCAAAAATCAAATA	Tetracycline	efflux pump
216	tetL-01	AGCCCGATTATTCAAGGAATTG	CAAATGCTTCCCCCTGTTCT	Tetracycline	efflux pump
217	tetL-02	ATGGTTGTAGTTGCGCGCTATAT	ATCGCTGGACCGACTCCTT	Tetracycline	efflux pump
218	tetM-01	CATCATAGACACGCCAGGACATAT	CGCCATTTTGAGAAATCA	Tetracycline	cellular protection
219	tetM-02	TAATATTGGAGTTTAGCTCATGTTGATG	CCTCTCTGACGTTCTAAAGCGTATTAT	Tetracycline	cellular protection

220	tetO-01	ATGTGGATACTACAACGCATGAGATT	TGCCTCCACATGATACTTTCCCT	Tetracycline	cellular protection
221	tetPA	AGTTGCAGATGTGTAGTCGAAACTATCTATT	TGCTACAACTACGAAAACAAAAGTAGAA	Tetracycline	efflux pump
222	tetPB-01	ACACCTGGACACGCTGATTTT	ACCGTCTAGAACGCGGAATG	Tetracycline	cellular protection
223	tetPB-02	TGATACACCTGGACACGCTGAT	CGTCCAAAACGCGGAATG	Tetracycline	cellular protection
224	tetPB-03	TGGGCGACAGTAGGCTTAGAA	TGACCCCTACTGAAACATTAGAAATACCT	Tetracycline	cellular protection
225	tetPB-04	AGTGGTGCAAATACTGAAAAAGTTGT	TTTGGTCCTTCGTTGGACAGA	Tetracycline	cellular protection
226	tetPB-05	CTGAAGTGGAGCGATCATTCC	CCCTCAACGGCAGAAATAACTAA	Tetracycline	cellular protection
227	tetQ	CGCCTCAGAAGTAAGTTCATACACTAAG	TCGTTCATGCGGATATTACAGAAT	Tetracycline	cellular protection
228	tetR-02	CGCGATAGACGCCCTCGA	TCCTGACAACGAGCCTCCTT	Tetracycline	efflux pump
229	tetR-03	CGCGATGGAGCAAAAGTACAT	AGTGAAAAACCTTGTGGCATAAAA	Tetracycline	efflux pump
230	tetS	TTAAGGACAAACTTCTGACGACATC	TGTCTCCCATTGTTCTGGTTCA	Tetracycline	cellular protection
231	tetT	CCATATAGAGGTTCCACCAAATCC	TGACCCATTGGTAGTGGTTCTATTG	Tetracycline	cellular protection
232	tetU-01	GTGGCAAAGCAACGGATTG	TGCGGGCTTGCAAAACTATC	Tetracycline	other/unknown
233	tetV	GCGGAACGACGATGTATATC	CCGCTATCTCACGACCATGAT	Tetracycline	efflux pump
234	tetX	AAATTTGTTACCGACACGGAAGTT	CATAGCTGAAAAATCCAGGACAGTT	Tetracycline	other/unknown
235	tnpA-01	CATCATCGGACGGACAGAATT	GTCGGAGATGTGGGTGTAGAAAGT	Transposase	transposase
236	tnpA-02	GGGCGGGTCGATTGAAA	GTGGGCGGGATCTGCTT	Transposase	transposase

237	tnpA-03	AATTGATGCGGACGGCTTAA	TCACCAAACTGTTATGGAGTCGTT	Transposase	transposase
238	tnpA-04	CCGATCACGGAAAGCTCAAG	GGCTCGCATGACTTCGAATC	Transposase	transposase
239	tnpA-05	GCCGCACTGTCGATTTTATC	GCGGGATCTGCCACTTCTT	Transposase	transposase
240	tnpA-07	GAAACCGATGCTACAATATCCAATT	CAGCACCGTTGCAGTGAAAG	Transposase	transposase
241	tolC-01	GGCCGAGAACCTGATGCA	AGACTTACGCAATTCCGGGTTA	Multidrug	efflux pump
242	tolC-02	CAGGCAGAGAACCTGATGCA	CGCAATTCCGGGTTGCT	Multidrug	efflux pump
243	tolC-03	GCCAGGCAGAGAACCTGATG	CGCAATTCCGGGTTGCT	Multidrug	efflux pump
244	Tp614	GGAAATCAACGGCATCCAGTT	CATCCATGCGTTTGTCTCT	Transposase	transposase
245	ttgA	ACGCCAATGCCAACGATT	GTCACGGCGCAGCTGA	Multidrug	efflux pump
246	ttgB	TCGCCCTGGATGTACACCTT	ACCATTGCCGACATCAACAAAC	Multidrug	efflux pump
247	vanA	AAAAGGCTCTGAAAACGCAGTTAT	CGGGCCGTTATCTTGAAAAACAT	Vancomycin	cellular protection
248	vanB-01	TTGTCGGCGAAGTGGATCA	AGCCTTTTCCGGCTCGTT	Vancomycin	cellular protection
249	vanB-02	CCGGTCGAGGAACGAAATC	TCCTCCTGCAAAAAAGATCAAC	Vancomycin	cellular protection
250	vanC-01	ACAGGGATTGGCTATGAACCAT	TGACTGGCGATGATTGACTATG	Vancomycin	cellular protection
251	vanC-03	AAATCAATACTATGCCGGCTTT	CCGACCGCTGCCATCA	Vancomycin	cellular protection
252	vanC1	AGGCGATAGCGGGTATTGAA	CAATCGTCAATTGCTCATTCC	Vancomycin	cellular protection
253	vanC2/vanC3	TTTGAUTGTCGGTGCTTGTGA	TCAATCGTTTCAGGCAATGG	Vancomycin	cellular protection

254	vanG	ATTGAAATTGGCAGGTATAACAGGTTA	TGATTGTCTTGTCCATACATAATGC	Vancomycin	cellular protection
255	vanHB	GAGGTTCCGAGGCACAA	CTCTCGCGGCAGTCGTAT	Vancomycin	cellular protection
256	vanHD	GTGGCCGATTATAACCGTCATG	CGCAGGTCAATTCAAGGCAAT	Vancomycin	cellular protection
257	vanRA-01	CCCTTACTCCCACCGAGTTT	TTCGTCGCCCATATCTCAT	Vancomycin	cellular protection
258	vanRA-02	CCACTCCGGCCTTGTCAATT	GCTAACACATTCCCTTGTTTT	Vancomycin	cellular protection
259	vanRB	GCCCTGTCGGATGACGAA	TTACATAGTCGTCTGCCTCTGCAT	Vancomycin	cellular protection
260	vanRC	TGCGGGAAAAACTGAACGA	CCCCCCATACGGTTTGATTA	Vancomycin	cellular protection
261	vanRC4	AGTGCTTGGCTTATCTCGAAAA	TCCGGCAGCAGCACATCTAA	Vancomycin	cellular protection
262	vanRD	TTATAATGGCAAGGATGCACTAAAGT	CGTCTACATCCGGAAGCATGA	Vancomycin	cellular protection
263	vanSA	CGCGTCATGCTTCAAAATTCA	TCCGCAGAAAGCTCAATTGTT	Vancomycin	cellular protection
264	vanSB	GCGCGGCAAATGACAAC	TTTGCCATTATTATCGCACTGT	Vancomycin	cellular protection
265	vanSC-02	GCCATCAGCGAGTCTGATGA	CAGCTGGATCGTTTCCTT	Vancomycin	cellular protection
266	vanSE	TGGCCGAAGAAGCAGGAA	CAATAATACTCGTCAAAGGAGTTCTCA	Vancomycin	cellular protection
267	vanTC-01	CACACGCACTTTTCCCATCTAG	CAGCCAACAGATCATAAAACAA	Vancomycin	cellular protection
268	vanTC-02	ACAGTTGCCGCTGGTGAAG	CGTGGCTGGTCGATCAAAA	Vancomycin	cellular protection
269	vanTE	GTGGTGCCAAGGAAGTTGCT	CGTAGCCACCGCAAAAAAAAT	Vancomycin	cellular protection
270	vanTG	CGTGTAGCCGTTCCGTTCTT	CGGCATTACAGGTATATCTGGAAA	Vancomycin	cellular protection

271	vanWB	CGGACAAAGATACCCCCTATAAAG	AAATAGTAAATTGCTCATCTGGCACAT	Vancomycin	cellular protection
272	vanWG	ACATTTCATTGGCAGCTGTAC	CCGCCATAAGAGCCCTACAATCT	Vancomycin	cellular protection
273	vanXA	CGCTAAATATGCCACTTGGGATA	TCAAAAGCGATTCAAGCCAAC	Vancomycin	cellular protection
274	vanXB	AGGCACAAAATCGAACAGATGCTT	GGGTATGGCTCATCAATCAACTT	Vancomycin	cellular protection
275	vanXD	TAAACCGTGTATGGGAACGAA	GCGATAGCCGTCCCATAAGA	Vancomycin	cellular protection
276	vanYB	GGCTAAAGCGGAAGCAGAAA	GATATCCACAGCAAGACCAAGCT	Vancomycin	cellular protection
277	vanYD-01	AAGGCGATACCCTGACTGTCA	ATTGCCGGACGGAAGCA	Vancomycin	cellular protection
278	vanYD-02	CAAACGGAAGAGAGGTCACCTACA	CGGACGGTAATAGGACTGTT	Vancomycin	cellular protection
279	vatB-01	GGAAAAAGCAACTCCATCTCTGA	TCCTGGCATAACAGTAACATTCTGA	MLSB	antibiotic deactivate
280	vatB-02	TTGGGAAAAGCAACTCCATCT	CAATCCACACATCATTCCAACA	MLSB	antibiotic deactivate
281	vatC-01	CGGAAATTGGAACGATGTT	GCAATAATAGCCCCGTTCTTA	MLSB	antibiotic deactivate
282	vatC-02	CGATGTTGGATTGGACGAGAT	GCTGCAATAATAGCCCCGTTT	MLSB	antibiotic deactivate
283	vatE-01	GGTGCCATTATCGGAGCAAAT	TTGGATTGCCACCGACAAT	MLSB	antibiotic deactivate
284	vatE-02	GACCGTCCTACCAGGCGTAA	TTGGATTGCCACCGACAATT	MLSB	antibiotic deactivate
285	vgaA-01	CGAGTATTGTGGAAAGCAGCTAGTT	CCCGTACCGTTAGAGCCGATA	MLSB	efflux pump
286	vgaA-02	GACGGGTATTGTGGAAAGCAA	TTTCCTGTACCATTAGATCCGATAATT	MLSB	efflux pump
287	vgb-01	AGGGAGGGTATCCATGCAGAT	ACCAAATGCGCCCGTT	MLSB	antibiotic deactivate

288	vgbB-01	CAGCCGGATTCTGGTCCTT	TACGATCTCCATTCAATTGGGTAAA	MLSB	efflux pump
289	vgbB-02	ATACGAGCTGCCTAATAAAGGATCTT	TGTGAACCACAGGGCATTATCA	MLSB	antibiotic deactivate
290	yceE/mdtG-01	TGGCACAAAATATCTGGCAGTT	TTGTGTGGCGATAAGAGCATTAG	Multidrug	efflux pump
291	yceE/mdtG-02	TTATCTGTTTCTGCTCACCTTCTTT	GCGTGGTGACAAACAGGCTTA	Multidrug	efflux pump
292	yceL/mdtH-01	TCGGGATGGTGGGCAAT	CGATAACCGAGCCGATGTAGA	Multidrug	efflux pump
293	yceL/mdtH-02	CGCGTGAAACCTTAAGTGCTT	AGACGGCTAAACCCCATAAGCT	Multidrug	efflux pump
294	yceL/mdtH-03	CTGCCGTTAAATGGATGTATGC	ACTCCAGCGGGCGATAGG	Multidrug	efflux pump
295	yidY/mdtL-01	GCAGTTGCATATGCCCTCTC	CTTCCCGGCAAACAGCAT	Multidrug	efflux pump
296	yidY/mdtL-02	TGCTGATCGGGATTCTGATTG	CAGGCGCGACGAACATAAT	Multidrug	efflux pump

Table S2. Analysis of variance for the effect of pharmaceuticals on the relative abundance and β -diversity of ARGs and MGEs in *F. candida* guts based on two-way ANOVA. One asterisk denotes $P < 0.05$, two asterisks denote $P < 0.01$ and three denote $P < 0.001$.

	Relative abundance		NMDS	
	ARGs	MGEs	NMDS1	NMDS2
R ²	0.392	0.555	0.461	0.474
CBZ	F _{4,30} = 2.964 P = 0.036*	F _{4,30} = 3.068 P = 0.031*	F _{4,30} = 2.734 P = 0.001***	F _{4,30} = 6.517 <i>P</i> = 0.054
TC	F _{1,30} = 4.225 P = 0.049*	F _{1,30} = 20.576 P < 0.001***	F _{1,30} = 3.872 <i>P</i> = 0.545	F _{1,30} = 0.536 <i>P</i> = 0.843
CBZ × TC	F _{4,30} = 0.811 <i>P</i> = 0.528	F _{4,30} = 1.145 <i>P</i> = 0.355	F _{4,30} = 0.391 <i>P</i> = 0.789	F _{4,30} = 1.013 P = 0.009**

Table S3. Pearson's Correlation analysis of the relative abundance of MGEs and ARGs. The correlations were calculated with SPSS 20.0. Asterisks indicate statistically significant differences (* $P < 0.05$, ** $P < 0.01$).

	Aminoglycoside	Beta_Lactamase	Tetracycline	Vancomycin	Multidrug	Others	MGEs
Beta_Lactamase	0.109						
Tetracycline	-0.133	0.262					
Vancomycin	-0.069	.625**	.421**				
Multidrug	-0.043	.619**	.344*	.475**			
Others	-0.032	-0.113	0.111	-0.127	0.048		
MGEs	0.131	.657**	.406**	.702**	.474**	-0.071	
Total ARGs	0.055	.767**	.651**	.791**	.774**	-0.004	.853**

Table S4. Analysis of variance for the effect of pharmaceuticals on the β -diversity of *F. candida* gut microbiota based on two-way ANOVA. One asterisk denotes $P < 0.05$, two asterisks denote $P < 0.01$ and three denote $P < 0.001$.

	NMDS1	NMDS2
R ²	0.649	0.261
CBZ	F _{4,30} = 2.973 P = 0.035*	F _{4,30} = 0.543 <i>P</i> = 0.706
TC	F _{1,30} = 28.03 P < 0.001***	F _{1,30} = 0.126 <i>P</i> = 0.725
CBZ × TC	F _{4,30} = 3.885 P = 0.012*	F _{4,30} = 2.073 <i>P</i> = 0.109

Table S5. Analysis of variance for the effect of pharmaceuticals on the mortality of *F. candida* based on two-way ANOVA. One asterisk denotes $P < 0.05$, two asterisks denote $P < 0.01$ and three denote $P < 0.001$.

	Mortality
R ²	0.557
CBZ	$F_{4,30} = 2.973$ $P = 0.078$
TC	$F_{1,30} = 28.03$ $P = 0.40$
CBZ × TC	$F_{4,30} = 3.885$ $P < 0.001^{***}$