

Supporting materials for

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Table S1 Physicochemical parameters of soil samples in 30°C incubator.

Groups	Parameters									
	pH	ITC (mg/kg)	SOM (%)	SMC (%)	TOC (%)	TN (%)	Ca (Wt%)	Cu (Wt%)	Mg (Wt%)	Na (Wt%)
B30-O1	6.17	54.67	6.98	31.13	8.12	0.69	0.25	0.0041	0.37	0.061
B30-O2	6.36	56.36	6.96	31.06	8.12	0.75	0.25	0.0047	0.35	0.067
B30-O3	6.25	55.52	7.00	31.18	8.12	0.73	0.24	0.0048	0.37	0.064
B30-T1	6.07	-	9.20	12.16	9.85	0.89	0.30	0.0060	0.40	0.34
B30-T2	6.14	-	9.13	12.08	9.85	0.90	0.30	0.0056	0.37	0.31
B30-T3	6.11	-	9.19	12.13	9.85	0.87	0.31	0.0065	0.41	0.29
Y30-O1	4.20	36.10	4.42	26.63	1.6	0.21	0.90	0.020	0.47	0.094
Y30-O2	4.19	35.88	4.49	26.75	1.6	0.20	0.89	0.026	0.48	0.098
Y30-O3	4.15	35.67	4.45	26.70	1.6	0.21	0.92	0.020	0.48	0.091
Y30-T1	6.10	-	6.71	8.19	2.34	0.31	0.89	0.023	0.50	0.39
Y30-T2	6.05	-	6.74	8.16	2.34	0.29	0.90	0.026	0.52	0.35
Y30-T3	6.04	-	6.72	8.22	2.34	0.30	0.88	0.021	0.52	0.40

ITC: initial tetracycline concentration; SOM: soil organic matter; SMC: soil moisture content; TOC: total carbon; TN: total nitrogen. B30-O and Y30-O stand for original soil

samples, B30-T and Y30-T stand for soil samples collected on day 65.

Table S2 Primers used in this study.

Gene name	Forward primer	Reverse primer	Classification	Mechanism
<i>16S rRNA</i>	GGGTTGCGCTCGTTGC	ATGGYTGTCGTCAGCTCGTG	na	na
<i>intI-1</i>	CGAACGAGTGGCGGAGGGTG	TACCCGAGAGCTTGGCACCCA	Integron	integrase
<i>intI2</i>	TGCTTTTCCACCCCTTACC	GACGGCTACCCTCTGTTATCTC	Integron	integrase
<i>tnpA-01</i>	CATCATCGGACGGACAGAATT	GTCGGAGATGTGGGTGTAGAAAGT	Transposase	transposase
<i>tnpA-02</i>	GGGCGGGTCGATTGAAA	GTGGGCGGGATCTGCTT	Transposase	transposase
<i>tnpA-03</i>	AATTGATGCGGACGGCTTAA	TCACCAAACGTGTTATGGAGTCGTT	Transposase	transposase
<i>tnpA-04</i>	CCGATCACGGAAGCTCAAG	GGCTCGCATGACTTCGAATC	Transposase	transposase
<i>tnpA-05</i>	GCCGCACTGTCGATTTTATC	GCGGGATCTGCCACTTCTT	Transposase	transposase
<i>tnpA-07</i>	GAAACCGATGCTACAATATCCAATT	CAGCACCGTTTGCAGTGTAAG	Transposase	transposase
<i>Tp614</i>	GGAAATCAACGGCATCCAGTT	CATCCATGCGCTTTTGTCTCT	Transposase	transposase
<i>IS613</i>	AGGTTCGGA CTCAATGCAACA	TTCAGCACATAACGCCTTGAT	Transposase	transposase
<i>tet(32)</i>	CCATTACTTCGGACAACGGTAGA	CAATCTCTGTGAGGGCATTAAACA	Tetracycline	cellular protection
<i>tet(34)</i>	CTTAGCGCAAACAGCAATCAGT	CGGTGATACAGCGCGTAAACT	Tetracycline	other/unknown
<i>tet(36)-01</i>	AGAATACTCAGCAGAGGTCAGTTCCT	TGGTAGGTCGATAACCCGAAAAT	Tetracycline	cellular protection
<i>tet(36)-02</i>	TGCAGGAAAGACCTCCATTACAG	CTTTGTCCACACTTCCACGTACTATG	Tetracycline	cellular protection
<i>tetA-02</i>	CTCACCAGCCTGACCTCGAT	CACGTTGTTATAGAAGCCGCATAG	Tetracycline	efflux pump
<i>tetB-01</i>	AGTGCGCTTTGGATGCTGTA	AGCCCCAGTAGCTCCTGTGA	Tetracycline	efflux pump
<i>tetB-02</i>	GCCCAGTGCTGTTGTTGTCAT	TGAAAGCAAACGGCCTAAATACA	Tetracycline	efflux pump
<i>tetC-02</i>	ACTGGTAAGGTAAACGCCATTGTC	ATGCATAAACCCAGCCATTGAGTAAG	Tetracycline	efflux pump
<i>tetD-02</i>	TGTCATCGCGCTGGTGATT	CATCCGCTTCCGGGAGAT	Tetracycline	efflux pump
<i>tetE</i>	TTGGCGCTGTATGCAATGAT	CGACGACCTATGCGATCTGA	Tetracycline	efflux pump
<i>tetG-01</i>	TCAACCATGCCCATTCTGA	TGGCCCCGGCAATCATG	Tetracycline	efflux pump
<i>tetG-02</i>	CATCAGCGCCGGTCTTATG	CCCCATGTAGCCGAACCA	Tetracycline	efflux pump

Gene name	Forward primer	Reverse primer	Classification	Mechanism
<i>tetL-01</i>	AGCCCGATTTATTCAAGGAATTG	CAAATGCTTTCCCCCTGTTCT	Tetracycline	efflux pump
<i>tetL-02</i>	ATGGTTGTAGTTGCGCGCTATAT	ATCGCTGGACCGACTCCTT	Tetracycline	efflux pump
<i>tetM-01</i>	CATCATAGACACGCCAGGACATAT	CGCCATCTTTTGCAGAAATCA	Tetracycline	cellular protection
<i>tetM-02</i>	TAATATTGGAGTTTTAGCTCATGTTGATG	CCTCTCTGACGTTCTAAAAGCGTATTAT	Tetracycline	cellular protection
<i>tetO-01</i>	ATGTGGATACTACAACGCATGAGATT	TGCCTCCACATGATATTTTCCT	Tetracycline	cellular protection
<i>tetPA</i>	AGTTGCAGATGTGTATAGTCGTAAACTATCTATT	TGCTACAAGTACGAAAACAAAAGTAGAA	Tetracycline	efflux pump
<i>tetPB-03</i>	TGGGCGACAGTAGGCTTAGAA	TGACCCTACTGAAACATTAGAAATATACCT	Tetracycline	cellular protection
<i>tetQ</i>	CGCCTCAGAAGTAAGTTCATACACTAAG	TCGTTTCATGCGGATATTATCAGAAT	Tetracycline	cellular protection
<i>tetS</i>	TTAAGGACAAACTTTCTGACGACATC	TGTCTCCCATTGTTCTGGTTCA	Tetracycline	cellular protection
<i>tetT</i>	CCATATAGAGGTTCCACCAAAATCC	TGACCCTATTGGTAGTGGTTCTATTG	Tetracycline	cellular protection
<i>tetR-02</i>	CGCGATAGACGCCTTCGA	TCCTGACAACGAGCCTCCTT	Tetracycline	efflux pump
<i>tetR-03</i>	CGCGATGGAGCAAAAGTACAT	AGTGAAAAACCTTGTTGGCATAAAA	Tetracycline	efflux pump
<i>tetW-01</i>	ATGAACATTCCCACCGTTATCTTT	ATATCGGCGGAGAGCTTATCC	Tetracycline	cellular protection
<i>tetX</i>	AAATTTGTTACCGACACGGAAGTT	CATAGCTGAAAAAATCCAGGACAGTT	Tetracycline	other/unknown

Table S3 Physiological and biochemical characteristics of *A. faecalis* S-1 and *A. faecalis* S-2.

	<i>A. faecalis</i> S-1	<i>A. faecalis</i> S-2
Gram staining	-	-
Catalase	+	+
H ₂ S production	-	-
Gelatinase	+	+
Indole production	-	-
Glucose oxidation	-	-
Mannitol oxidation	-	-
Sorbitol oxidation	-	-
Saccharose oxidation	-	-
Nitrate reduction	-	+
Urease	+	-
Citrate utilization	-	-

Table S4 T-test results of the tetracycline degradation efficiency of *Raoultella* sp. XY-1 and P&R

Paired Samples Statistics					
		Mean	N	Std. Deviation	Std. Error Mean
Pair 1	<i>Raoultella</i> sp.	.605748277	11	.2859941610	.0862304840
	XY-1				
	P&R	.502032382	11	.2655104110	.0800544011

Paired Samples Correlations				
		N	Correlation	Sig.
Pair 1	<i>Raoultella</i> sp. XY-1 and P&R	11	.975	.000

Paired Samples Test									
		Paired Differences					t	df	Sig. (2-tailed)
		Mean	Std. Deviation	Std. Error Mean	95% Confidence Interval of the Difference				
					Lower	Upper			
Pair 1	<i>Raoultella</i> sp. XY-1 -P&R VAR00001	.1037158950	.0644729374	.0194393221	.0604023865	.1470294040	5.335	10	.000

Table S5 Indices of soil bacterial community richness and diversity.

Samples	No. of Sequences	OTUs	Chao 1	Ace	Shannon	Simpson	Coverage
B30-O1	38088	1502	1712.726	1718.129	3.885821	0.171023	0.984361
B30-O2	63002	669	1689.65	1672.525	3.278787	0.244169	0.991197
B30-O3	32588	1989	2227.659	2207.8	5.940959	0.00735	0.987827
B30-T1	38164	1911	2169.637	2232.485	5.323721	0.032242	0.980816
B30-T2	27314	1682	2147.487	2172.489	5.297233	0.036417	0.985208
B30-T3	32585	1732	447.3333	497.9402	2.635249	0.182368	0.997535
Y30-O1	40978	279	2330.004	2320.722	5.813801	0.011814	0.988573
Y30-O2	36803	1835	2323.447	2365.471	5.377903	0.036664	0.986715
Y30-O3	41918	1906	1051.763	1382.523	3.361916	0.111696	0.995667
Y30-T1	26281	1328	1881.782	1902.021	4.187993	0.144345	0.990356
Y30-T2	40958	1579	2401.783	2394.934	6.082472	0.00644	0.984841
Y30-T3	41806	1357	1886.55	1900.988	4.988859	0.025033	0.98892

B30-O and Y30-O stand for original soil samples, and B30-T and Y30-T stand for soil samples collected on day 65.

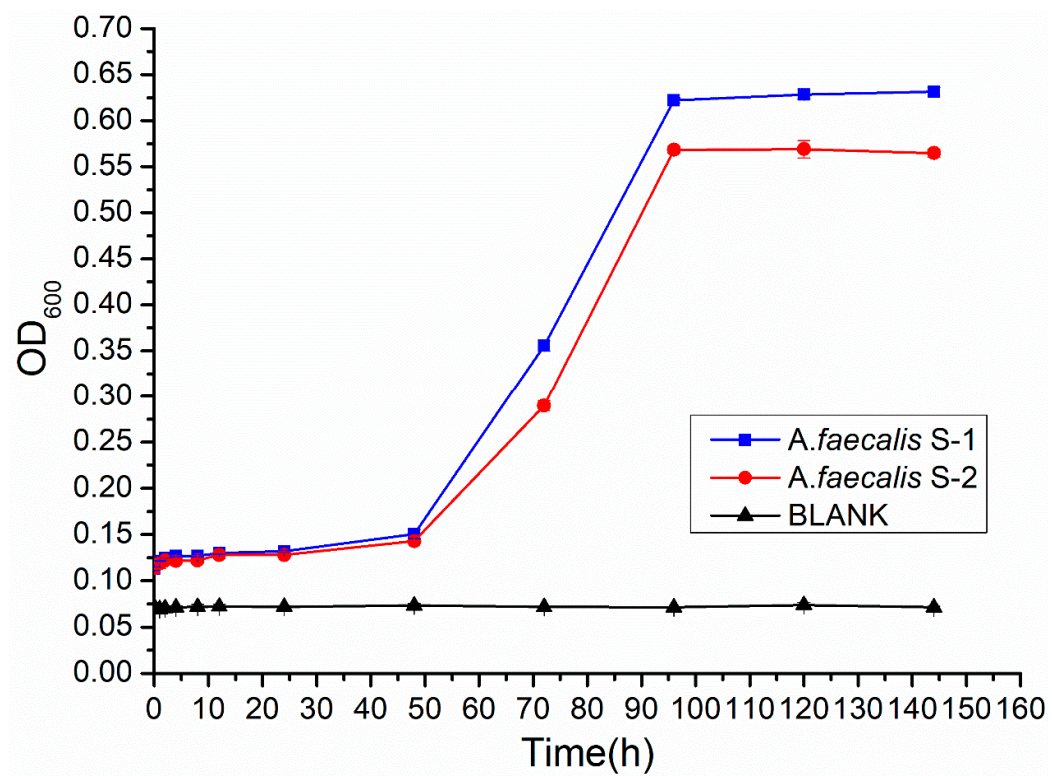


Figure S1. Growth curves of *A. faecalis* S-1 and *A. faecalis* S-2 in the mineral medium with 50 mg/L TC.

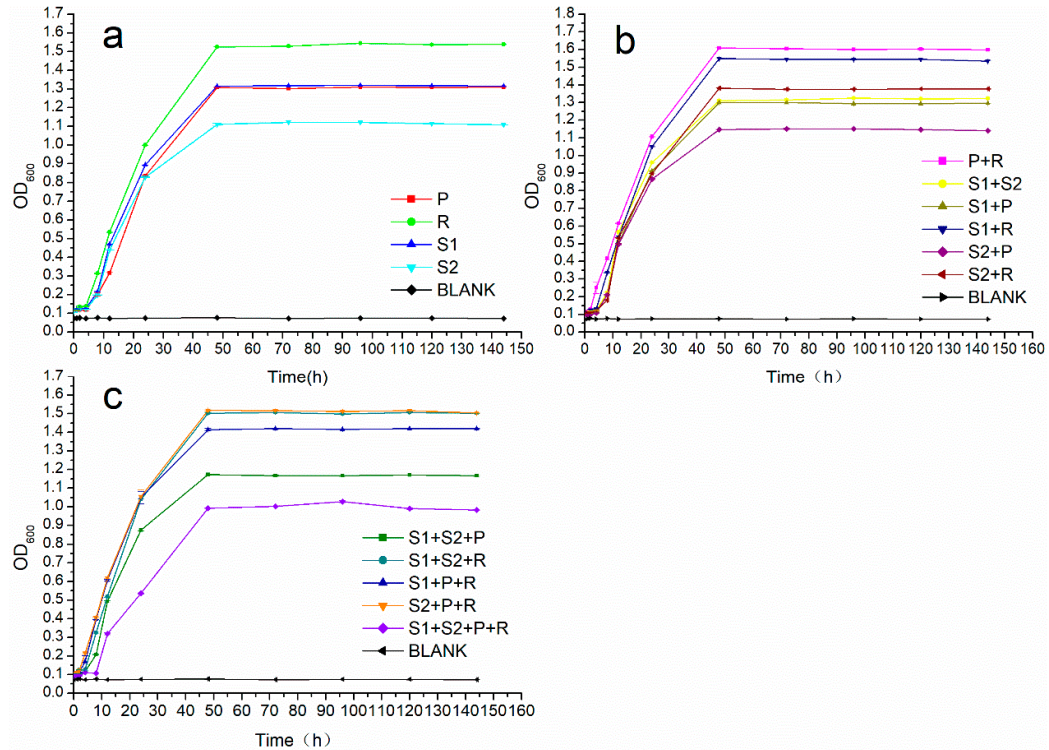


Figure S2. Growth curves of bacteria in the LB medium with 50 mg/L TC: (a) growth curves of the 4 strains, (b) and (c) growth curves of all constructed bacterial consortia. S1: *A. faecalis* S-1; S2: *A. faecalis* S-2; P: *Pandoraea* sp. XY-2; R: *Raoultella* sp. XY-1.

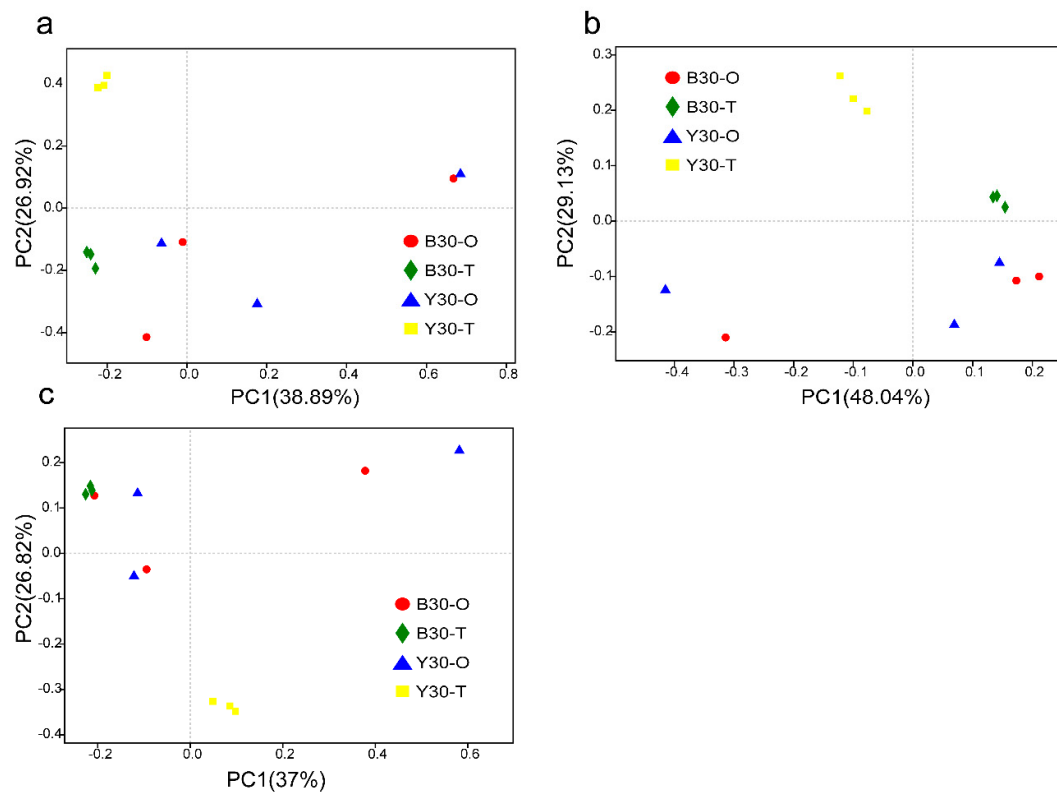


Figure S3. Principal coordinate analysis showing the distribution pattern of the bacterial communities:

(a) is based on Bray-Curtis distance; (b) is based on weighted unifracs distance; (c) is based on unweighted unifracs distance. B30-O and Y30-O stand for original soil samples, and B30-T and Y30-T stand for soil samples collected on day 65.

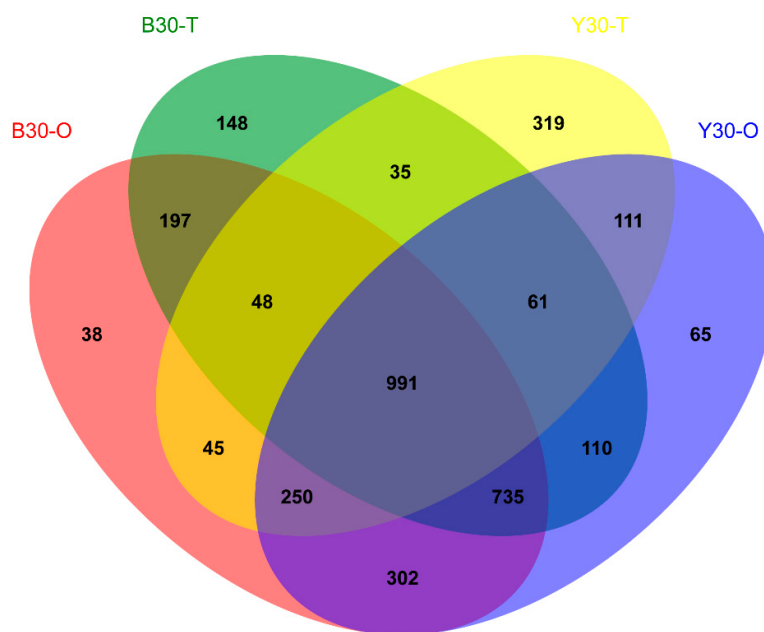


Figure S4. Venn diagram of the specific and shared OTUs in all soil samples. B30-O and Y30-O stand for original soil samples, B30-T and Y30-T stand for soil samples collected on day 65.