

**Table S1.** The longitude, latitude and urbanization intensity of the 18 sample plots. RP1-RP6 represent rural plots, SP1-SP6 represent suburban plots, UP1-UP6 represent urban plots. R1, R2, R3 and R4 represent the urbanization intensity at 250 m, 1 km, 2 km and 5 km resolution, respectively.

	Plots	longitude	latitude	R1	R2	R3	R4
RP1	Heimi Park	113.005	28.4447	0	0	0.0048	0
RP2	Shiyan Hu Park	113.0802	28.016	0.0992	0	0	0.4336
RP3	Xiangtan Tangwan Village	112.6568	27.8717	0.0192	0.0352	0	0.0144
RP4	FengShu Ridge	112.8714	27.7983	0.0464	0.0464	0.0064	0.0624
RP5	Zhuzhou Dajin Scenic Spot	113.2528	27.8485	0	0.1424	0	0
RP6	TaoHua Hill	112.8934	28.1805	0.2048	0	0	0.0912
SP1	The jing port Town	112.7781	28.4606	0.5488	0.096	0.1888	0.0384
SP2	DaWang Mountain	112.9123	28.0728	0.4528	0.1824	0.0912	0.0144
SP3	Lion Rock Park	112.7113	28.2379	0.0032	0	0.0528	0.0208
SP4	Changsha Garden Ecological Park	113.0392	28.2958	0.056	0.2496	0.0368	0.0032
SP5	Luojia zui	113.1282	27.9022	0.1072	0.5712	0.2864	0.4704
SP6	The martyr Park	112.9927	28.2095	0.32	0.1136	0.1536	0.5248
UP1	YangHu Wetland	112.9271	28.1284	0.1952	0.0144	0.6544	0.6592
UP2	Changsha Botanical Garden	113.0313	28.1065	0.0832	0.2416	0.3392	0.5664
UP3	Huxiang Park	112.9363	27.8397	0.08	0.5408	0.9264	0.2976
UP4	Juhua Tong Park	112.908	27.8321	0.5952	0.832	0.6464	0.2976
UP5	Baishi Park	112.8933	27.857	0.6	0.9792	0.832	0.7408
UP6	LiYu Leisure Valley	113.0714	27.8377	0.6576	0.152	0.6624	0.1456

**Table S2.** The relative abundance of soil bacterial communities at phylum (top10) and order (top19) ranks (%). RF, SF, UF, RG, SG and UG represent rural forestland, suburban forestland, urban forestland, rural grassland, suburban grassland and urban grassland, respectively. Significant differences ( $p < 0.05$ ) among treatments are shown with different letters. The differences were tested using one-way analysis of variance (ANOVA) and followed by post-hoc Tukey Honestly Significant Difference (HSD) tests for significance.

Taxa		Forestland				Grassland			
		RF	SF	UF	RG	SG	UG		
Phylu		42.75	± 32.13	± 23.71	± 25	± 2.15	20.74	± 20.12	±
m	Acidobacteria	3.45 a	3.72 b	2.71 bc	bc		1.76 c	1.84 c	

Orde r	Proteobacteria	26.7 ± 1.86 ab	29.41 ± 2.22 ab	32.02 ± 1.87 a	32.12 ± 2.89 a	32.09 ± 2.65 a	33.12 ± 2.57 a
	Chloroflexi	9.82 ± 2.31 ab	12.63 ± 13.6 ± 2.2 a	11.34 ± 1.28 a	12.08 ± 1.67 a	15.17 ± 1.27 a	1.87 a
	Actinobacteria	8.43 ± 0.9 ab	10.47 ± 2.08 a	9.69 ± 1.56 ab	5.58 ± 0.94 b	12.17 ± 1.8 a	10.14 ± 1.47 ab
	Verrucomicrobia	4.59 ± 0.69 ab	3.74 ± 0.62 b	5.11 ± 0.75 ab	6.67 ± 0.82 a	5.84 ± 0.73 ab	5.3 ± 0.63 ab
	Bacteroidetes	2.51 ± 0.51 b	3.08 ± 0.46 b	7.28 ± 0.95 a	6.04 ± 1.19 a	5.58 ± 0.81 a	6 ± 0.67 a
	Gemmatimonadetes	2.12 ± 0.6 b	2.35 ± 0.42 ab	4.07 ± 0.59 ab	4.5 ± 1.12 a	4.46 ± 0.68 a	3.85 ± 0.46 ab
	Latescibacteria	0.17 ± 0.07 c	0.84 ± 0.32 bc	1.46 ± 0.44 ab	1.03 ± 0.99 bc	1.35 ± 0.23 ab	1.69 ± 0.26 a
	Nitrospirae	0.35 ± 0.11 c	0.68 ± 0.23 bc	1.25 ± 0.34 b	3.2 ± 0.24 a	0.91 ± 0.37 b	0.65 ± 0.39 b
	Planctomycetes	0.61 ± 0.08 c	0.65 ± 0.11 bc	0.63 ± 0.09 bc	0.96 ± 0.16 abc	1.06 ± 0.19 ab	1.16 ± 0.17 a
	Acidobacteriales	16.77 ± 2.08 a	9.03 ± 1.66 bc	4.62 ± 1.45 cd	9.45 ± 1.92 b	4.6 ± 1.03 cd	3.69 ± 1.19 d
	Acidobacteriia_Subgroup_2	15.27 ± 0.65a	13.09 ± 0.37a	5.14 ± 0.48b	4.91 ± 1.16b	5.33 ± 1.99b	1.88 ± 0.75c
	Solibacterales	7.51 ± 2.53a	5.07 ± 2.75b	4.26 ± 1.99b	4.97 ± 0.67ab	3.36 ± 0.53b	2.85 ± 0.68b
	Rhizobiales	7 ± 0.68a	5 ± 0.79a	5.85 ± 0.94a	6.13 ± 0.73a	4.57 ± 0.24a	4.87 ± 0.36b
	Ktedonobacterales	5.74 ± 0.51a	3.78 ± 1.1ab	2.45 ± 0.44b	2.55 ± 1.36b	2.5 ± 0.98b	1.52 ± 1.6b
	Elsterales	4.64 ± 0.33a	4.24 ± 0.27ab	1.75 ± 0.25b	1.43 ± 0.85bc	1.87 ± 0.78b	0.96 ± 0.39c
	Frankiales	3.77 ± 0.6a	2.84 ± 0.69ab	1.58 ± 0.41bc	0.89 ± 0.23bc	1.41 ± 0.75bc	0.85 ± 0.16c
	Pedosphaerales	3.11 ± 1.84b	2.86 ± 1b	3.26 ± 0.64b	4.81 ± 0.15a	3.76 ± 0.3a	3.47 ± 0.18a
	Betaproteobacteriales	2.73 ± 0.16c	7.03 ± 0.13bc	10.18 ± 0.15a	8.57 ± 0.6bc	9.7 ± 0.53ab	11.29 ± 0.45a

	2.23	±			0.96	±	1.07	±	0.6	±	0.58	±
Micropepsales	0.32a		1.3 ± 0.23a		0.21a		1.09a		1.37a		1.43a	
	2.11	±	2.28	±	3.97	±	4.46	±	4.28	±	3.74	±
Gemmatimonadales	0.49b		0.48ab		0.53ab		0.22a		0.14a		0.17ab	
Gammaproteobacteria	1.79	±			0.77	±	0.79	±	0.79	±	0.58	±
	0.6a		1.11 ± 0.4a		0.58ab		1.07bc		0.66bc		0.45c	
			2.83	±			4.56	±	5.47	±	5.53	±
Myxococcales	1.5 ± 0.28c		0.56bc		3.88 ± 0.5b		0.17a		0.17a		0.09a	
	1.31	±	0.65	±			1.32	±	1.49	±	1.14	±
Chthoniobacterales	0.54b		1.75b		1.4 ± 1.58b		0.63b		0.59a		0.46b	
	1.3	±			2.54	±			0.97	±	1.06	±
Sphingomonadales	0.16b		1.53 ± 0.3b		0.27a		1.17 ± 0.3b		0.27b		0.36b	
	1.08	±	1.12	±			2.06	±	2.03	±		
Chitinophagales	0.47b		0.34b		4.17 ± 0.3a		0.44b		0.57b		2.83 ± 0.5b	
	1.01	±	0.86	±	0.83	±	0.61	±	0.46	±	0.59	±
Caulobacterales	0.36a		0.2ab		0.43ab		0.25b		0.71b		0.26b	
	0.86	±	1.44	±	1.46	±	1.25	±	2.97	±	1.69	±
Gaiellales	0.27c		0.2bc		0.64bc		0.82ab		0.44a		0.29ab	
	0.44	±			1.44	±			1.93	±	1.6	±
Cytophagales	0.18b		0.75 ± 0.2b		0.37a		2.22 ± 0.3a		0.4a		0.16ab	

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