Supplementary material

1. Soil characterisation

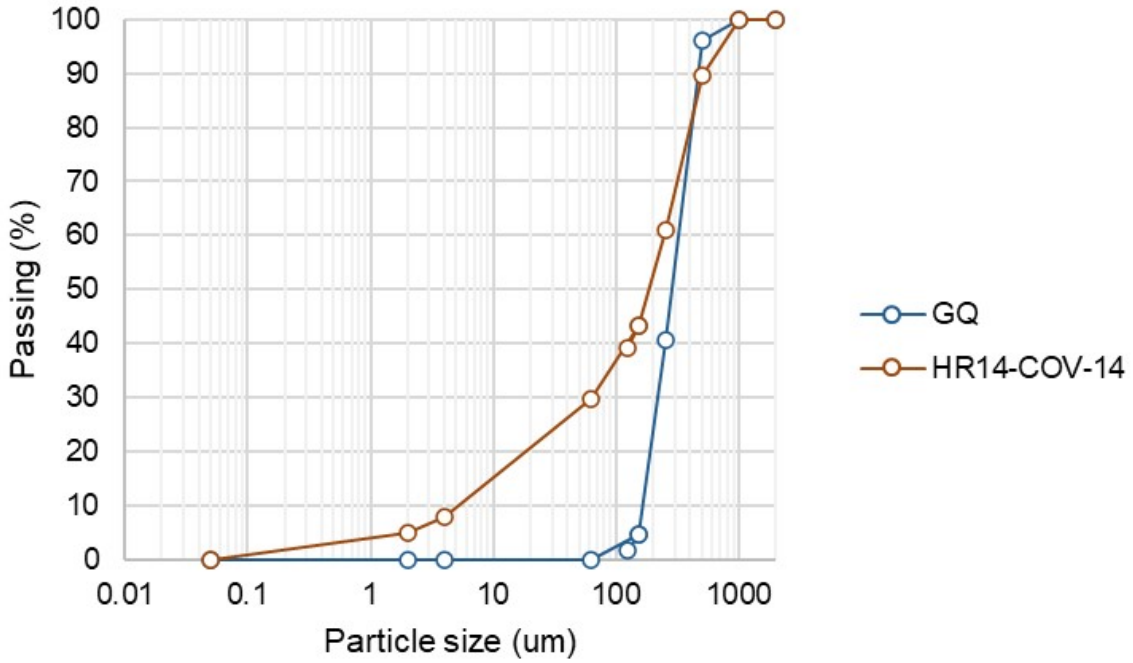

Figure S 1 Particle size distribution curves of quarry sand (GQ) and polluted soil (COV14) determined by laser diffraction on three replicates of <2 mm soil fractions.

Table S 1 Analysis of particle size distribution curves from Figure S 1.

Sample ID	Sand (1000-63 um)	Silt (63-2 um)	Clay (<2 um)	Cu	Cc
GQ	100	0	0	1.72	0.98
HR14-COV-14	70.35	24.92	4.7	42.96	3.04

Table S 2 COV14 Soil total carbon and isotopic δ13C composition analysed with a Picarro Combustion Module Cavity Ring-Down Spectroscopy (CM-CRDS) system (CM by NC Technologies, G2201-i CDRS) interfaced by a Caddy Continuous Flow Interface (A2100) on five analytical replicates.

Sample ID	weight (mg)	C measured (mg)	**d13C-corrected**	**Wt%-C (g/100g)**	dry weight (mg)	**Wt%-C (g/100g)**
COV-14/1	3.28	0.16	**-26.6**	**4.9**	2.53	6.341984
COV-14/2	6.03	0.21	**-26.2**	**3.4**	4.64	4.478789
COV-14/3	4.42	0.22	**-25.8**	**4.9**	3.40	6.385915

COV-14/4	3.19	0.18	**-26.7**	**5.7**	2.46	7.40655
COV-14/5	2.57	0.28	**-26.7**	**11.0**	1.98	14.3195

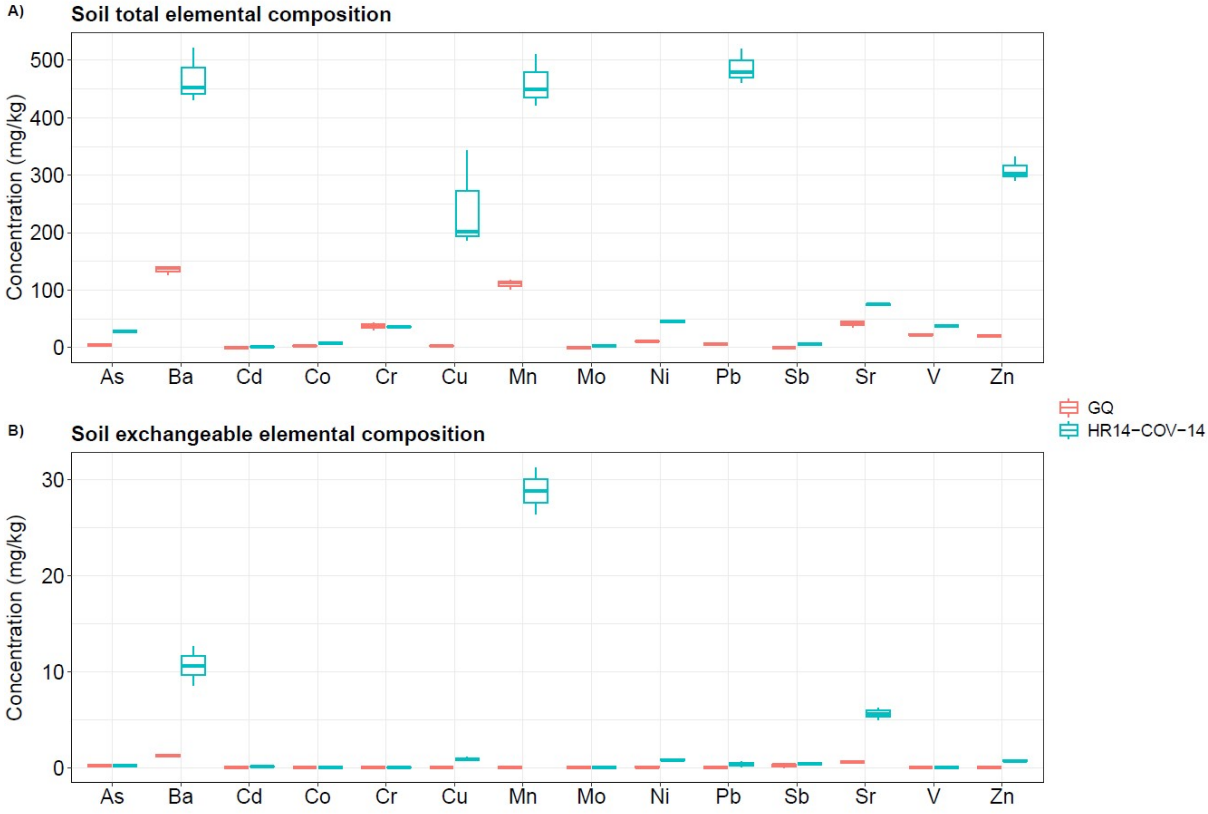

Figure S 2 Total (A) and exchangeable (B) elemental composition of GQ and COV14 soils (n = 3) determined by total soil digestion and step 1 of Tessier et al., (1979) sequential extraction, respectively, and analysed by ICP-OES/MS.

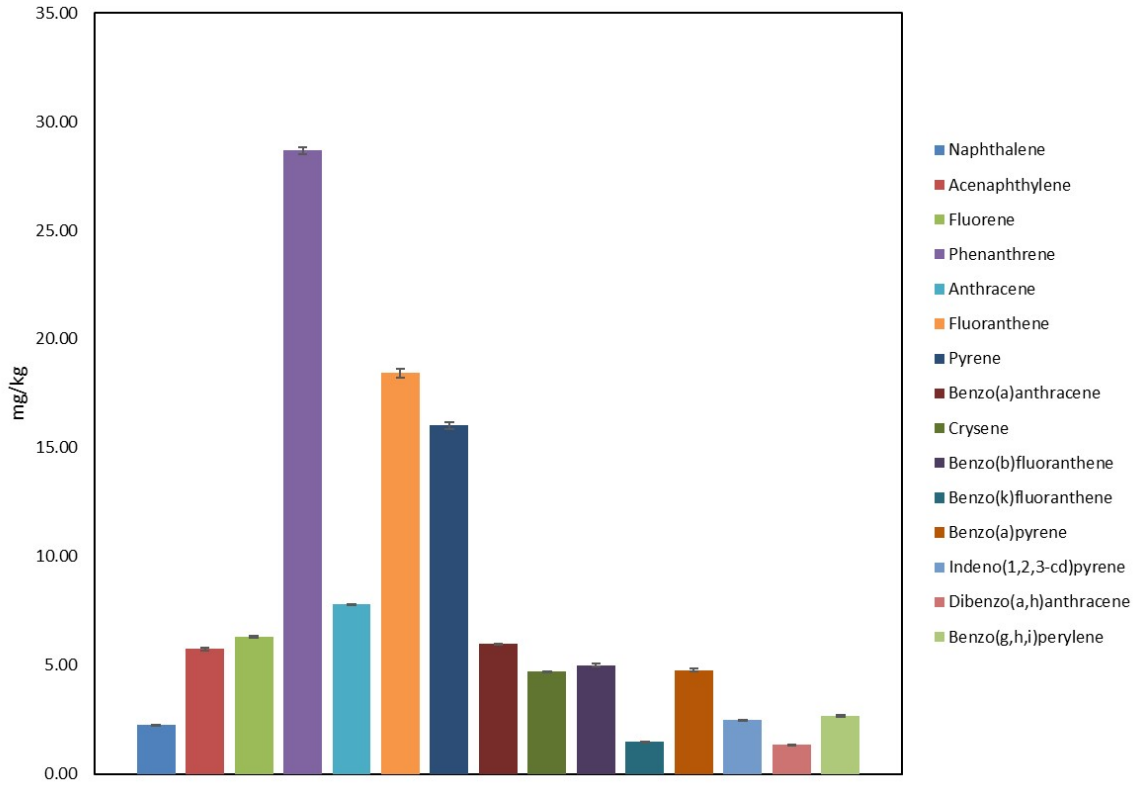

Figure S 3 Polycyclic aromatic hydrocarbon (PAH) concentrations of soil COV14 (n = 3).

2. ureC primer optimisation

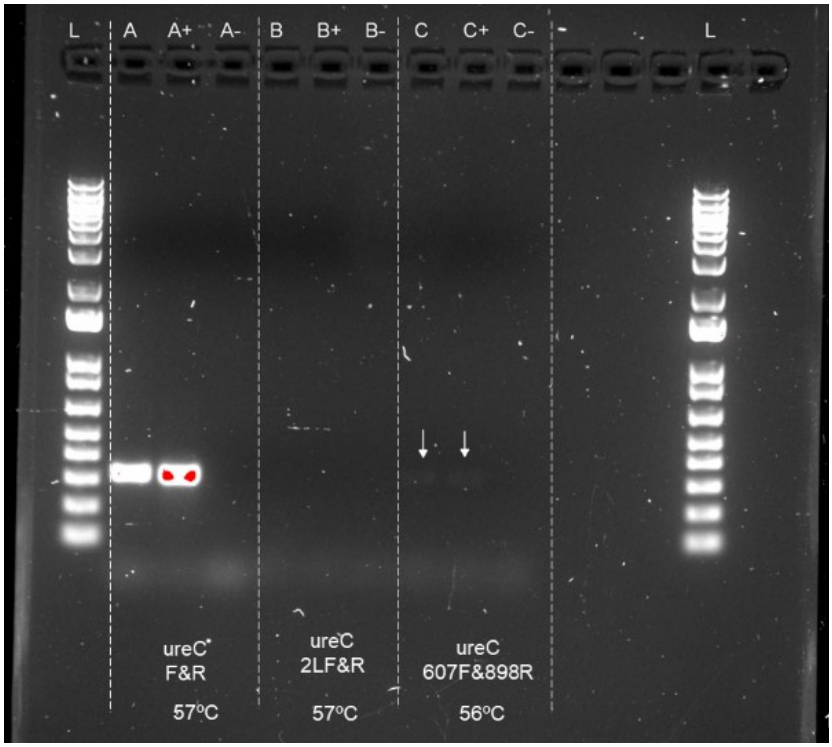

Figure S 4 PCR of ureC primers (ureC F&R, ureC 2LF&R and ureC 607F&898R) in environmental soil DNA tested at optimal annealing temperatures identified by Collier et al. (1999), Gresham et al. (2007) and

Wang et al. (2022), respectively. Column well IDs without, with plus (+) and negative (-) signs indicate environmental DNA sample, environmental DNA sample spiked with 1 µL ureC standard and control PCR water, respectively. "L" stands for ladder used to estimate the base pair (bp) length of the target gene.

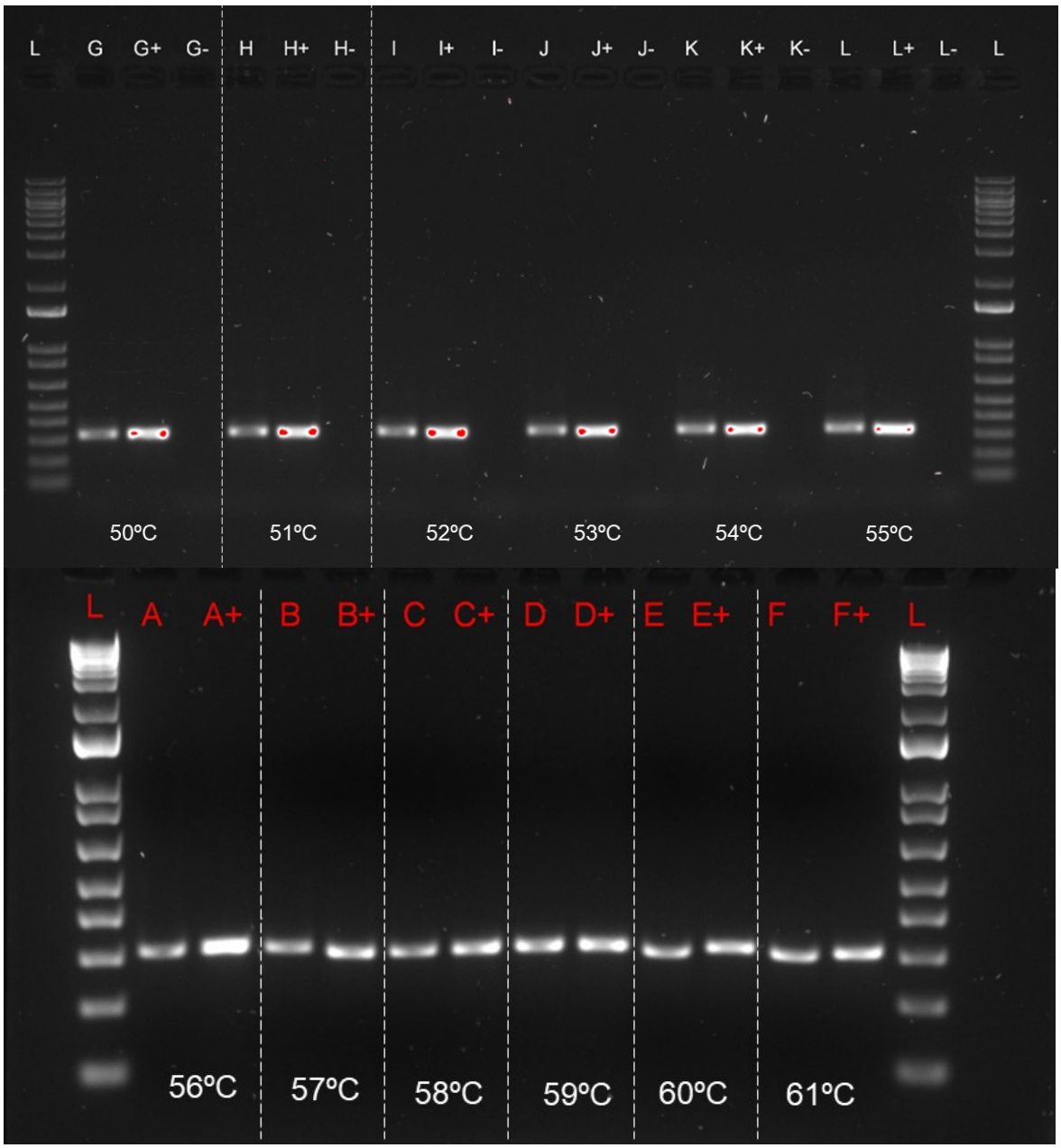

Figure S 5 Gradient PCR of ureC F&R primer (Collins et al., 1999) on environmental soil DNA sample over annealing temperature range 50-61˚C. Column well IDs without, with plus (+) and negative (-) signs indicate environmental DNA sample, environmental DNA sample spiked with 1 µL ureC standard and control PCR water, respectively. "L" stands for ladder used to estimate the base pair (bp) length of the target gene.

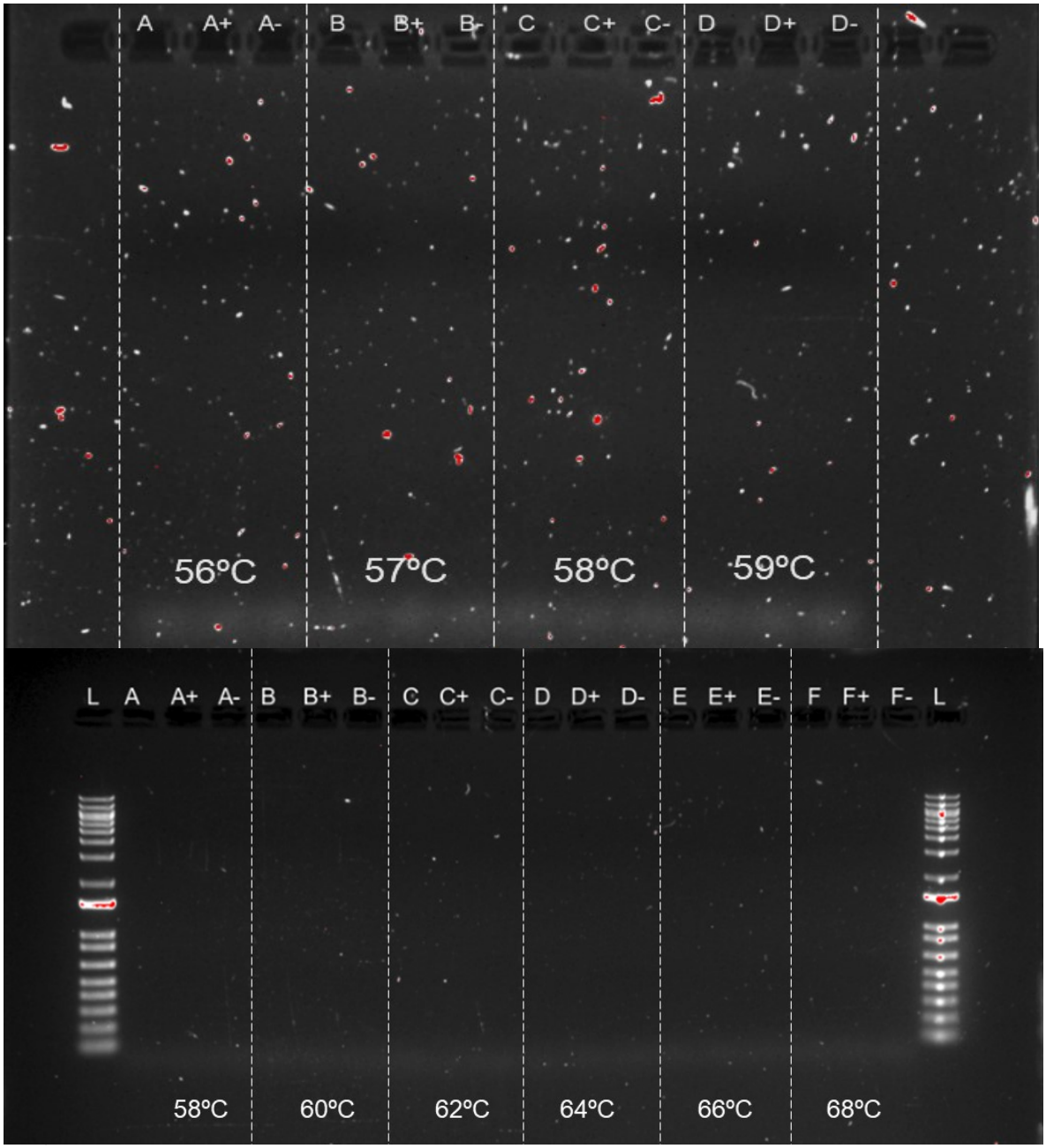

Figure S 6 Gradient PCR of ureC 2LF&R primer (Gresham et al., 2007) on environmental soil DNA sample over annealing temperature range 58-68˚C. Column well IDs without, with plus (+) and negative (-) signs indicate environmental DNA sample, environmental DNA sample spiked with 1 µL ureC standard and control PCR water, respectively. "L" stands for ladder used to estimate the base pair (bp) length of the target gene.

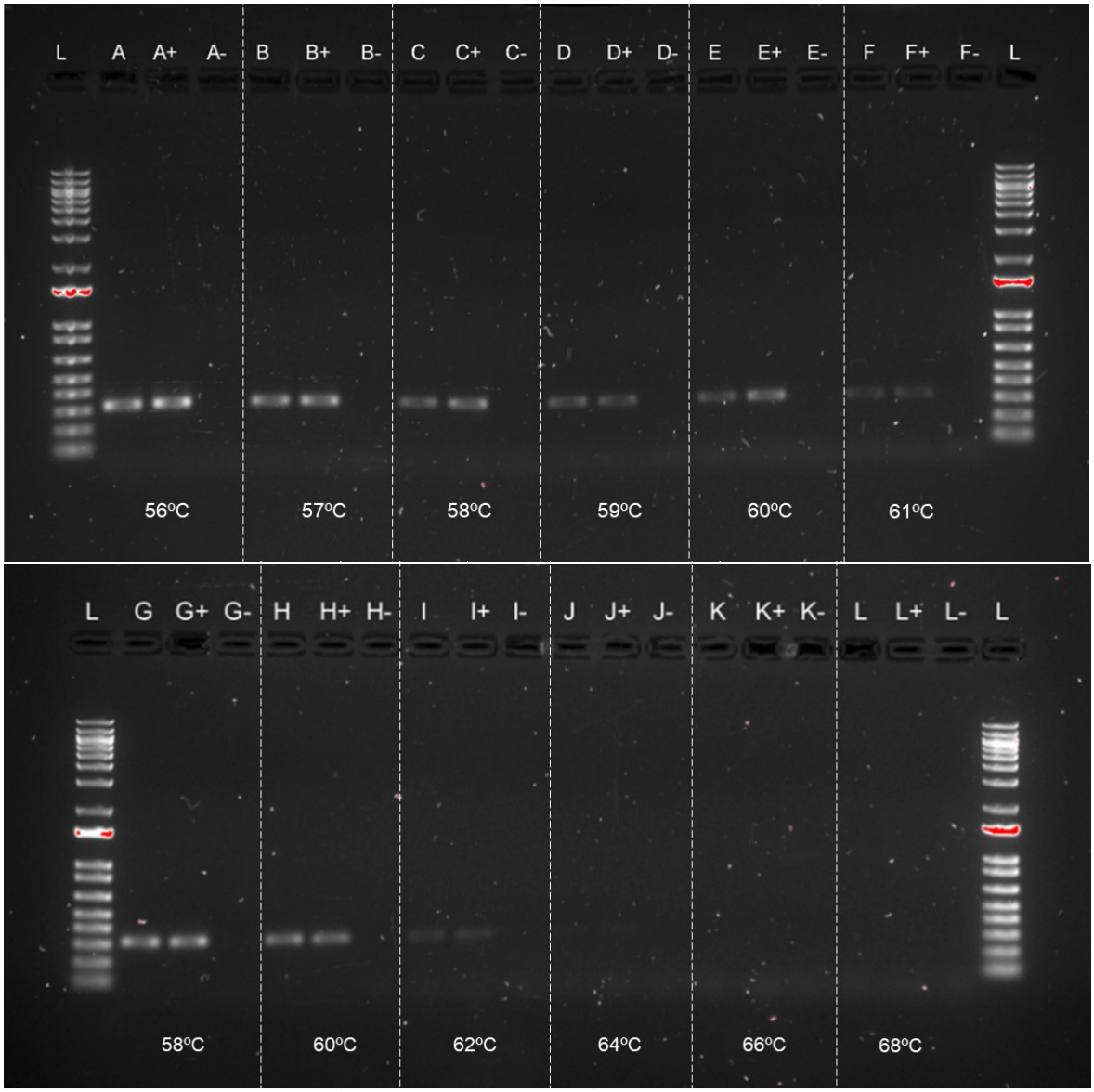

Figure S 7 Gradient PCR of ureC 607F&898R primer (Wang et al., 2022) on environmental soil DNA sample over annealing temperature range 58-68˚C. Column well IDs without, with plus (+) and negative (-) signs indicate environmental DNA sample, environmental DNA sample spiked with 1 µL ureC standard and control PCR water, respectively. "L" stands for ladder used to estimate the base pair (bp) length of the target gene

3. Urease activity assay

3.1. Linear regression model EC v time

Table S 3 Glycine max linear regression model of EC vs time.

ID	Urease	Urea	HC	Dil	r	intercept	slope	std.err	r.sqr	p.value	QCcor	sig	UAmean	UAsd
0 0 0	0	0	0	0	0.39	3.7	0.27	0.14	0.15	7.03E-02	low		5.99	3.13
0 666 0	0	666	0	0	0.48	6.3	0.43	0.40	0.23	3.40E-01	low		9.53	8.81
0 666 10	0	666	10	0.1	0.31	108.1	0.38	0.27	0.10	1.77E-01	low		8.46	6.02
0 666 100	0	666	100	0.01	0.06	15.5	0.04	0.15	0.00	7.92E-01	low		0.90	3.37
0 666 1000	0	666	1000	0.001	0.65	7.2	0.15	0.09	0.42	1.63E-01	low		3.39	1.98
0 666 2.5	0	666	2.5	1	-0.11	773.0	-0.47	2.04	0.01	8.30E-01	low		-10.36	45.18
0 666 5	0	666	5	0.2	0.16	164.5	0.03	0.08	0.02	7.68E-01	low		0.59	1.87
1 0 0	1	0	0	0	0.02	37.5	0.01	0.13	0.00	9.46E-01	low		0.19	2.79
1 666 0	1	666	0	0	0.92	47.3	5.16	0.33	0.85	3.72E-19	high	sign	114.47	7.30
1 666 10	1	666	10	0.1	0.85	145.5	3.71	0.34	0.73	6.17E-14	med	sign	82.44	7.64
1 666 100	1	666	100	0.01	0.86	58.4	4.58	0.42	0.75	8.65E-14	med	sign	101.61	9.25
1 666 1000	1	666	1000	0.001	0.92	50.6	4.71	0.29	0.85	5.57E-20	high	sign	104.58	6.53
1 666 2.5	1	666	2.5	1	0.82	786.9	2.00	0.20	0.68	7.91E-13	med	sign	44.47	4.54
1 666 5	1	666	5	0.2	0.98	203.4	2.32	0.07	0.96	8.98E-33	high	sign	51.49	1.55
100 0 0	100	0	0	0	0.11	2303.1	0.87	1.91	0.01	6.53E-01	low		19.40	42.39
100 666 0	100	666	0	0	0.91	3124.9	203.63	13.71	0.84	1.56E-18	high	sign	4520.56	304.44
100 666 10	100	666	10	0.1	0.90	3122.6	215.73	15.66	0.81	1.45E-17	high	sign	4789.11	347.63
100 666 100	100	666	100	0.01	0.91	3097.8	212.35	14.92	0.82	7.18E-18	high	sign	4714.23	331.29
100 666 1000	100	666	1000	0.001	0.90	3145.4	214.55	15.32	0.82	7.99E-18	high	sign	4762.94	340.03
100 666 2.5	100	666	2.5	1	1.00	3690.0	196.70	1.16	1.00	6.27E-66	high	sign	4366.65	25.82
100 666 5	100	666	5	0.2	1.00	3027.9	203.49	2.92	0.99	1.85E-47	high	sign	4517.48	64.92

Table S 4 Sporosarcina Pasteurii linear regression model of EC vs time.

ID	OD600	Urea	HC	Dil	r	intercept	slope	std.err	r.sqr	p.value	QCcor	sig	UAmean	UAsd
0 666 10	0	666	10	0.1	-0.69	3000	-1.848	0.180	0.478	6.47E-18	low	sign	-41.01	4.00
0 666 100	0	666	100	0.01	0.94	2881	2.205	0.158	0.891	5.05E-13	high	sign	48.96	3.50
0 666 2.5	0	666	2.5	1	0.75	3578	1.884	0.157	0.558	4.30E-22	med	sign	41.82	3.47
0 666 5	0	666	5	0.2	0.57	3044	1.250	0.170	0.320	3.07E-11	low	sign	27.74	3.77
0.01 0 0	0.01	0	0	0	-0.11	2888	-0.202	0.167	0.013	2.28E-01	low		-4.48	3.70
0.01 666 0	0.01	666	0	0	0.29	2438	1.379	0.431	0.086	1.80E-03	low	sign	30.62	9.57
0.01 666 10	0.01	666	10	0.1	0.96	2764	1.587	0.480	0.916	1.87E-01	high		35.22	10.65
0.01 666 100	0.01	666	100	0.01	0.98	2398	1.084	0.025	0.962	1.70E-53	high	sign	24.05	0.56
0.01 666 2.5	0.01	666	2.5	1	0.31	3672	0.623	0.548	0.097	2.78E-01	low		13.83	12.17
0.01 666 5	0.01	666	5	0.2	0.80	2711	2.108	0.342	0.633	3.31E-06	med	sign	46.80	7.59
1 0 0	1	0	0	0	-0.76	3387	-1.763	0.416	0.580	9.72E-04	low	sign	-39.15	9.24
1 666 0	1	666	0	0	0.99	3536	94.685	1.161	0.989	3.23E-74	high	sign	2102.02	25.78
1 666 10	1	666	10	0.1	1.00	2998	86.606	0.370	0.999	5.66E-108	high	sign	1922.65	8.21
1 666 100	1	666	100	0.01	1.00	3292	80.459	0.650	0.993	8.96E-121	high	sign	1786.20	14.43
1 666 2.5	1	666	2.5	1	0.99	3799	65.155	0.625	0.990	2.47E-113	high	sign	1446.45	13.88
1 666 5	1	666	5	0.2	1.00	3173	78.921	0.136	1.000	2.79E-201	high	sign	1752.04	3.01

3.2. Statistical analysis

Table S 5 Glycine max ANOVA and multiple pairwise-comparisons between the means of groups. Results of LSD (Least Significant Difference) test on ANOVA.

ENZYME CONCENTRATION = 1 g/L		
ANOVA p = 4.24e-05 ***		
$groups		
HC	slope	groups
0	5.00039	a
1000	4.86739	a
100	4.58799	a
10	3.58599	b
5	2.29679	c
2.5	2.00294	c
ENZYME CONCENTRATION = 100 g/L		
ANOVA p = 0.881		
$groups		
HC	slope	groups
100	212.9493	a
1000	212.231	a
10	211.9708	a
0	208.4268	a
5	203.3631	a
2.5	196.6961	a

Table S 6 Sporosarcina Pasteurii ANOVA and multiple pairwise-comparisons between the means of groups. Results of LSD (Least Significant Difference) test on ANOVA.

CELL CONCENTRATION = 0.01		
ANOVA p = 0.131		
$groups		
	slope	groups
5	2.197416	a
10	1.586502	ab
0	1.426494	ab
100	1.081262	b
2.5	1.007535	b
CELL CONCENTRATION = 1		
ANOVA p = 5.01e-05 ***		
$groups		
	slope	groups

0	94.68267	a
10	86.52793	b
100	80.52324	bc
5	78.92065	c
2.5	65.19964	d