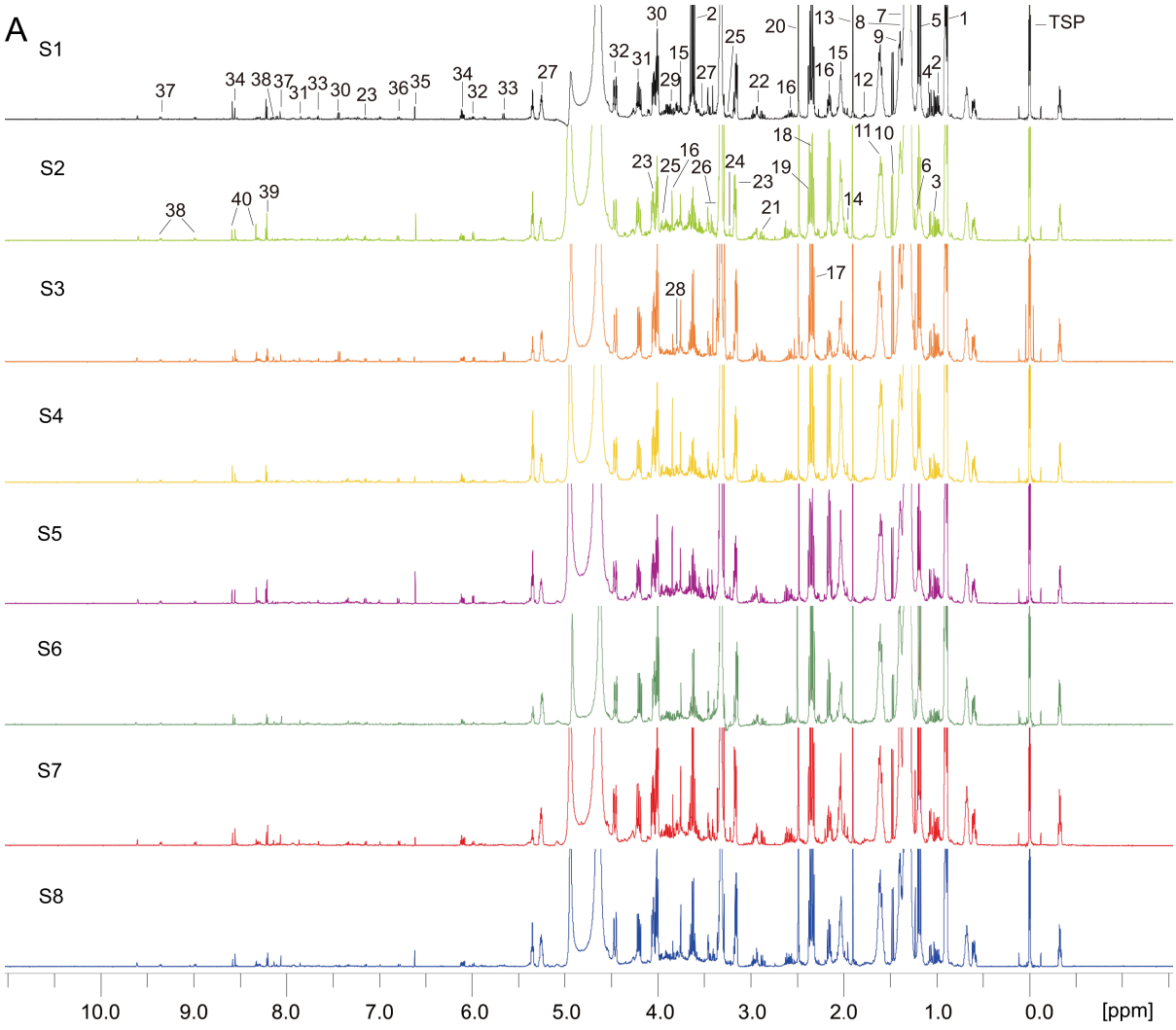
A
S1
S2
S3
S4
S5
S6
S7
S8
TSP
10.0
9.0
8.0
7.0
6.0
5.0
4.0
3.0
2.0
1.0
0.0
[ppm]

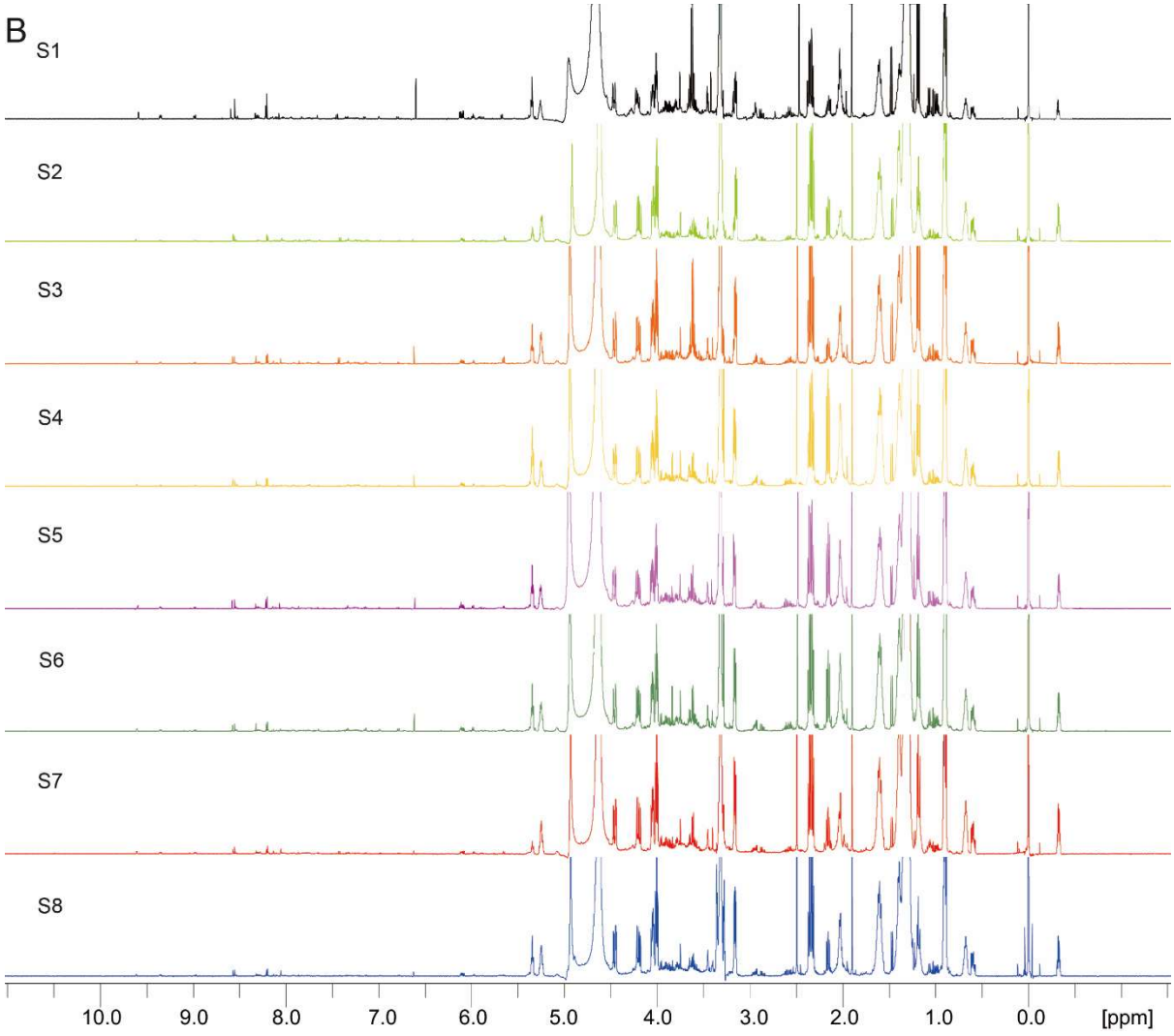

Fig. S1. Typical ^{1}H nuclear magnetic resonance (NMR) spectra of eight *E. coli* strains in pea sprouts from 10-min deionised water (DW) treatment (A) and from low concentration electrolysed water (LcEW) treatment (B). Note: S1: ATCC 25922; S2: O26:H11 (ATCC BAA-2196); S3: O45:H2 (ATCC BAA-2193); S4: O103:H11 (ATCC BAA-2215); S5: O111 (ATCC BAA-2440); S6: O121:H19 (ATCC BAA-2219); S7: O145 (ATCC BAA-2192); S8: O157:H7 (ATCC 43895).

Table S1. Metabolites identified in *E. coli* strains.

	Metabolites	Assignments	^{1}H chemical shifts (ppm)	^{13}C chemical shifts (ppm)
1	Leucine	αCH; βCH_2; γCH; δCH_3; $\delta' CH_3$	**3.74 (m); 1.70(m); 0.96 (d); 0.87 (d)**	**56.2; 42.6; 24.4; 22.12**
2	Valine	αCH; βCH; γCH_3; $\gamma' CH_3$	**3.60 (d); 2.26 (m); 0.98 (d); 1.03 (d)**	**63.3; 31.9; 19.4; 20.8**
3	Isoleucine	αCH; βCH; γCH_2; $\gamma' CH_3$; δCH_3	**3.71 (d);** 2.01 (m); **1.63 (m), 1.03 (d); 1.00 (t)**	**61.88;** 39.0; **24.6; 18.1; 14.8**
4	1,2-propanediol	C_1H_2; C_2H; C_3H_3	**3.45 (dd); 3.87 (m); 1.08 (d)**	**69.9; 71.0; 18.9**
5	Ethanol	αCH_2; βCH_3	**3.64 (m); 1.17 (t)**	**60.3; 19.6**
6	3-hydroxybutyric acid	αCH_2; βCH_2; γCH_3	2.35 (dd); **4.15 (m); 1.20 (d)**	49.1; **68.4; 24.4**
7	Threonine	αCH; βCH; γCH_3	**3.54 (d); 4.23 (m); 1.30 (d)**	**63.4; 68.3; 20.3**
8	Lactic acid	αCH; βCH_3	**4.10 (q); 1.31 (d)**	**71.4; 22.9**
9	Lysine	αCH; βCH_2; γCH_2; δCH_2; εCH_2	**3.75 (t); 1.88 (m); 1.46 (m); 1.72 (m); 3.02 (t)**	**57.5; 32.7; 24.0; 29.1; 42.1**
10	Alanine	αCH; βCH_3	**3.77 (q); 1.47 (d)**	**53.1; 18.9**
11	Arginine	αCH; βCH_2; γCH_2; δCH_2	**3.76 (t); 1.91 (dd); 1.68 (m);** 3.24 (t)	**57.3; 30.5; 26.5;** 43.3
12	Putrescine	αCH_2; βCH_2	**3.02 (t); 1.73 (m)**	**38.6; 26.4**
13	Acetic acid	CH_3	**1.91 (s)**	**26.1**
14	Proline	C_1H_2; C_2H_2; C_3H_2; C_4H	**3.33 (d); 1.99 (m); 2.20 (m); 4.13 (dd)**	**49.0; 26.5; 31.8; 64.0**
15	Glutamic acid	αCH; βCH_2; γCH_2	**3.74 (m); 2.09 (m); 2.34 (m)**	**57.6; 29.8; 36.4**
16	Methionine	αCH; βCH_2; γCH_2; SCH_3	**3.85 (dd); 2.18 (m); 2.63 (t); 2.10 (m)**	**56.8; 32.7; 31.6; 16.6**
17	Pyroglutamic acid	αCH; βCH_2; γCH_2	**4.16 (dd); 2.25 (m); 2.38 (m)**	**61.0; 28.0; 32.3**
18	Pyruvic acid	CH_3	**2.36 (s)**	**29.2**
19	Succinic acid	CH_2	**2.39 (s)**	**36.8**
20	α-ketoglutaric acid	αCH_2; βCH_2	**3.01 (t); 2.44 (t)**	**38.8; 33.4**
21	Aspartic acid	αCH; βCH_2	**3.91 (dd); 2.73 (dd)**	**55.1; 39.4**
22	γ-aminobutyric acid	αCH_2; βCH_2; γCH_2	**2.28 (t); 1.89 (m); 3.01 (t)**	**37.0; 26.4; 42.2**
23	Histidine	αCH; βCH_2; NCHC; NCHN	**4.00 (dd); 3.26 (dd); 7.14 (d);** 8.03 (d)	**57.3; 30.16; 120.0;** 138.4
24	Phosphorylcholine	αCH2; βCH2; NCHN	**4.15 (d); 3.57 (d); 3.20(s)**	**60.6; 68.9; 56.5**
25	Betaine	CH_3; CH_2	**3.25 (s); 3.89 (s)**	**55.9; 68.6**

26	β-D-glucose	C_1H_2; C_2H; C_3H; C_4H; C_5H; C_6H	**3.89 (m); 3.47 (dd); 3.46 (dd); 3.40 (m); 3.23 (dd);** 4.69 (d)	**63.4; 79.6; 79.5; 72.5; 77.0;** 97.5
27	α-D-glucose	C_1H_2; C_2H; C_3H; C_4H; C_5H; C_6H	**3.82 (m); 3.81 (m); 3.52 (m); 3.70 (m); 3.72 (m); 5.22 (d)**	**63.3; 74.3; 74.9; 75.6; 63.5; 94.9**
28	Glucose-1-phosphate	C_1H; C_2H; C_3H; C_4H; C_5H; C_6H_2	5.44 (dd); **3.47 (d); 3.77 (m); 3.38 (t); 3.91 (m); 3.80 (m)**	96.5; **75.1; 75.9; 72.5; 74.8; 63.5**
29	Ribose-5-phosphate	C_1H_2; C_2H; C_3H; C_4H; C_5H	**3.88 (m); 4.07 (m); 4.23 (t); 4.05 (m);** 5.40 (m)	**67.5; 84.4; 77.2; 78.0;** 98.9
30	Phenylalanine	C_1H; C_2H_2; C_4H; C_5H; C_6H	**3.98 (dd);** 3.19 (dd); **7.37 (m); 7.42 (m);** 7.32 (m)	**58.9;** 39.2; **130.4; 131.8;** 132.1
31	Uridine	C_1H; C_2H; C_3H; C_4H; C_5H_2; ^1C_1H; ^1C_2H	**5.90 (d); 4.35 (dd); 4.23 (dd); 4.12 (dd); 3.86 (dd); 7.86 (d); 5.89 (d)**	**92.1; 76.5; 72.1; 87.1; 63.6; 144.6; 105.1**
32	Adenosine	C_1H; C_2H; C_3H; C_4H; C_5H_2; N^1CHN; N^2CHN	**6.03 (d);** 4.74 (s); **4.43 (dd); 4.29 (dd); 3.91 (dd); 8.30 (s);** 8.18 (s)	**91.1;** 76.7; **73.5; 88.6; 64.4; 143.3;** 155.3
33	Uracil	αCH; βCH	**5.76 (d); 7.52 (d)**	**101.2; 146.3**
34	ATP	C_1H; C_2H; C_3H; C_4H; C_5H_2; N^1CHN; N^2CHN	**6.15 (d);** 4.82 (d); 4.64 (t); **4.42 (m); 4.28 (m); 8.55 (s);** 8.24 (s)	**89.3;** 77.0; 73.0; **86.6; 67.7;** 142.5; 155.4
35	Fumaric acid	αCH	**6.51 (s)**	**138.0**
36	Tyrosine	C_1H; C_2H_2; C_4H; C_5H	**3.93 (dd); 3.17 (dd);** 7.19 (d); **6.85 (m)**	**59.0; 38.3;** 133.5; **115.9**
37	NADP	C_1H; C_2H; C_3H; C_5H; N^1CHN; N^2CHN	**9.10 (d);** 8.17 (s); 8.80 (d); **9.28 (s); 8.10 (d);** 8.40 (s)	**144.9;** 131.3; 148.3; **142.5; 155.2;** 142.9
38	NAD	C_1H; C_2H; C_3H; C_5H; N^1CHN; N^2CHN	**9.16 (d);** 8.19 (s); **8.82 (d); 9.33 (s); 8.12 (d);** 8.41 (s)	145.1; 131.1; **148.4; 142.5; 155.4;** 142.4
39	Cyclic AMP	C_1H; C_2H; C_3H; C_4H; C_5H_2; N^1CHN; N^2CHN	**6.13 (d); 4.34 (d); 4.73 (d); 4.75 (d); 4.47 (m); 8.17 (s); 8.19 (s)**	**94.3; 72.2; 75.0; 79.9; 69.9; 155.4; 142.4**
40	ADP	C_1H; C_2H; C_3H; C_4H; C_5H_2; N^1CHN; N^2CHN	**5.94 (m); 4.58 (d);** 4.22 (d); **4.11 (d); 4.12 (m); 8.54 (s); 8.30 (s)**	**87.1; 73.7;** 70.1; **65.4; 83.3; 140.4; 148.4**

Note: **Bold** chemical shifts indicate identified peaks in the spectra. Multiplicity: s: singlet; d: doublet; t: triplet; q: quartet; m: multiplet.

Table S2. Summary of fit of orthogonal projection to latent structures-discriminant analysis (OPLS-DA) models.

Strain	Principle component 1		Principle component 2	
	R^2X	Q^2	R^2X	Q^2
S1	0.96	0.81	1.00	0.93
S2	0.99	0.96	1.00	0.98
S3	0.96	0.78	0.99	0.95
S4	0.89	0.70	0.99	0.95
S5	0.99	0.91	0.99	0.97
S6	0.98	0.83	1.00	0.96
S7	0.98	0.87	1.00	0.97
S8	0.99	0.93	1.00	0.97

Note: S1: ATCC 25922; S2: O26:H11 (ATCC BAA-2196); S3: O45:H2 (ATCC BAA 2193); S4: O103:H11 (ATCC BAA-2215); S5: O111 (ATCC BAA-2440); S6: O121:H19 (ATCC BAA-2219); S7: O145 (ATCC BAA-2192); S8: O157:H7 (ATCC 43895).

Table S3. Contents of metabolites significantly varied in each *E. coli* strain.

Strain	Metabolite	Content (mM)		*P* value
		LcEW	DW	
S1	Leucine	0.85±0.01	0.95±0.01	0.000
	Glutamic acid	1.58±0.02	1.11±0.03	0.003
	Methionine	0.87±0.02	0.62±0.03	0.009
	Proline	0.25±0.01	0.17±0.01	0.014
	Acetic acid	0.24±0.00	0.32±0.01	0.008
	α-ketoglutaric acid	0.15±0.01	0.92±0.02	0.000
	Ethanol	1.03±0.19	2.64±0.33	0.024
S2	Leucine	1.14±0.01	1.27±0.01	0.002
	Isoleucine	0.04±0.00	0.10±0.00	0.000
	α-ketoglutaric acid	0.74±0.02	0.26±0.00	0.000
	Tyrosine	0.02±0.00	0.05±0.00	0.003
	Glutamic acid	0.90±0.07	1.94±0.01	0.001
	Proline	0.19±0.01	0.28±0.00	0.006
	Methionine	0.47±0.00	1.09±0.01	0.000
	Acetic acid	0.16±0.01	0.26±0.00	0.002
	Fumaric acid	0.02±0.01	0.08±0.01	0.003
	β-D-glucose	0.20±0.04	0.51±0.01	0.005
	ATP	0.06±0.01	0.13±0.00	0.000
	NADP	0.01±0.00	0.02±0.00	0.000
	Phosphorylcholine	0.26±0.00	0.47±0.00	0.000
	Isoleucine	0.07±0.00	0.12±0.00	0.001
S3	Valine	1.18±0.03	1.02±0.06	0.046
	Tyrosine	0.02±0.01	0.04±0.00	0.014
	Acetic acid	0.18±0.01	0.32±0.00	0.005
	Fumaric acid	0.05±0.01	0.03±0.00	0.019
	3-hydroxybutyric acid	0.12±0.06	0.24±0.08	0.045
	α-ketoglutaric acid	0.65±0.03	1.59±0.01	0.000
	1,2-propanediol	0.07±0.01	0.10±0.00	0.010
	β-D-glucose	0.29±0.04	0.41±0.06	0.025
	NAD	0.06±0.01	0.07±0.00	0.010
S4	Isoleucine	0.05±0.00	0.09±0.01	0.010
	Methionine	0.65±0.03	0.85±0.04	0.026
	α-ketoglutaric acid	0.57±0.02	0.80±0.03	0.018
	Betaine	0.13±0.02	0.23±0.01	0.031
	Phosphorylcholine	0.33±0.00	0.38±0.01	0.022
S5	Valine	0.79±0.02	0.95±0.01	0.005
	Isoleucine	0.06±0.00	0.12±0.00	0.000
	Proline	0.25±0.00	0.31±0.00	0.003
	Methionine	0.81±0.00	1.04±0.01	0.001
	Aspartic acid	0.09±0.01	0.13±0.00	0.004
	Acetic acid	0.18±0.00	0.26±0.01	0.002
	Fumaric acid	0.05±0.00	0.08±0.01	0.012
	γ-aminobutyric acid	0.14±0.00	0.20±0.00	0.000
	1,2-propanediol	0.07±0.00	0.12±0.00	0.000
	Cyclic AMP	0.12±0.00	0.15±0.00	0.005
	Putrescine	0.03±0.00	0.05±0.00	0.008

	Betaine	0.08±0.01	0.22±0.01	0.002
	Phosphorylcholine	0.36±0.01	0.51±0.01	0.001
S6	Leucine	1.46±0.02	1.23±0.01	0.003
	Isoleucine	0.08±0.00	0.06±0.00	0.001
	Glutamic acid	1.94±0.01	1.10±0.04	0.000
	Proline	0.29±0.00	0.22±0.02	0.014
	Histidine	2.39±0.09	1.82±0.26	0.032
	Acetic acid	0.19±0.00	0.22±0.01	0.014
	Fumaric acid	0.06±0.01	0.02±0.01	0.024
	α-ketoglutaric acid	0.64±0.00	1.15±0.02	0.000
	1,2-propanediol	0.09±0.00	0.04±0.02	0.030
S7	Isoleucine	0.05±0.00	0.12±0.00	0.000
	Alanine	0.09±0.02	0.23±0.03	0.004
	Glutamic acid	1.33±0.03	1.69±0.05	0.018
	Proline	0.28±0.01	0.34±0.01	0.049
	Methionine	0.70±0.03	0.94±0.03	0.019
	Acetic acid	0.20±0.01	0.38±0.02	0.006
	α-ketoglutaric acid	0.70±0.02	2.01±0.04	0.001
	γ-aminobutyric acid	0.11±0.02	0.26±0.02	0.013
	Ethanol	1.11±0.10	2.06±0.17	0.021
	1,2-propanediol	0.08±0.01	0.16±0.00	0.003
	β-D-glucose	0.34±0.03	0.42±0.00	0.038
	ADP	0.09±0.01	0.14±0.00	0.009
	ATP	0.07±0.01	0.13±0.01	0.017
	Betaine	0.08±0.02	0.15±0.01	0.040
	Phosphorylcholine	0.37±0.01	0.85±0.04	0.002
S8	Isoleucine	0.05±0.00	0.08±0.00	0.005
	Arginine	3.43±0.01	3.14±0.01	0.001
	Tyrosine	0.02±0.00	0.03±0.00	0.002
	Methionine	0.68±0.00	0.70±0.00	0.010
	Aspartic acid	0.08±0.00	0.12±0.00	0.009
	Acetic acid	0.22±0.00	0.25±0.00	0.001
	Fumaric acid	0.03±0.00	0.05±0.00	0.002
	α-ketoglutaric acid	0.87±0.00	1.31±0.00	0.000
	γ-aminobutyric acid	0.09±0.00	0.17±0.00	0.002
	1,2-propanediol	0.06±0.00	0.08±0.00	0.002
	ADP	0.07±0.00	0.10±0.00	0.014
	ATP	0.08±0.00	0.10±0.00	0.011
	NAD	0.06±0.00	0.08±0.00	0.016
	Putrescine	0.03±0.00	0.04±0.00	0.016
	Betaine	0.12±0.01	0.08±0.01	0.037
	Phosphorylcholine	0.29±0.00	0.48±0.01	0.002

Note: Content is expressed as mean ± standard deviation (n = 3); S1: ATCC 25922; S2: O26:H11 (ATCC BAA-2196); S3: O45:H2 (ATCC BAA 2193); S4: O103:H11 (ATCC BAA-2215); S5: O111 (ATCC BAA-2440); S6: O121:H19 (ATCC BAA-2219); S7: O145 (ATCC BAA-2192); S8: O157:H7 (ATCC 43895); LcEW: Low concentration electrolysed water; DW: Deionised water.

Table S4. Metabolic pathway analysis for the screened metabolites in each *E. coli* strain.

Strain	Pathway name	Matching	*P* value	FDR
S1	Aminoacyl-tRNA biosynthesis	4/45	0.000	0.001
	Arginine biosynthesis	2/16	0.004	0.180
	Alanine, aspartate and glutamate metabolism	2/22	0.008	0.227
	Glycolysis / Gluconeogenesis	2/29	0.014	0.234
	Arginine and proline metabolism	2/29	0.014	0.234
	Carbapenem biosynthesis	1/3	0.019	0.268
	Glyoxylate and dicarboxylate metabolism	2/37	0.022	0.268
	D-Glutamine and D-glutamate metabolism	1/7	0.045	0.483
S2	Aminoacyl-tRNA biosynthesis	6/45	0.000	0.000
	Arginine biosynthesis	3/16	0.001	0.031
	Alanine, aspartate and glutamate metabolism	3/22	0.002	0.054
	Butanoate metabolism	2/17	0.017	0.292
	Citrate cycle (TCA cycle)	2/20	0.023	0.292
	Valine, leucine and isoleucine biosynthesis	2/22	0.027	0.292
	Glutathione metabolism	2/22	0.027	0.292
	Valine, leucine and isoleucine degradation	2/23	0.030	0.292
	Carbapenem biosynthesis	1/3	0.036	0.292
	Novobiocin biosynthesis	1/3	0.036	0.292
	Pyruvate metabolism	2/26	0.038	0.292
	Glycolysis / Gluconeogenesis	2/29	0.046	0.303
	Arginine and proline metabolism	2/29	0.046	0.303
S3	Arginine biosynthesis	2/16	0.007	0.358
	Citrate cycle (TCA cycle)	2/20	0.011	0.358
	Alanine, aspartate and glutamate metabolism	2/22	0.013	0.358
	Pyruvate metabolism	2/26	0.018	0.358
	Glycolysis / Gluconeogenesis	2/29	0.023	0.358
	Novobiocin biosynthesis	1/3	0.025	0.358
S4	Aminoacyl-tRNA biosynthesis	2/45	0.016	1.000
S5	Aminoacyl-tRNA biosynthesis	5/45	0.000	0.009
	Alanine, aspartate and glutamate metabolism	3/22	0.002	0.081
	Arginine and proline metabolism	3/29	0.004	0.121
	beta-Alanine metabolism	2/13	0.010	0.211
	Arginine biosynthesis	2/16	0.015	0.239
	Butanoate metabolism	2/17	0.017	0.239
	Valine, leucine and isoleucine biosynthesis	2/22	0.027	0.308
	Valine, leucine and isoleucine degradation	2/23	0.030	0.308
	Pantothenate and CoA biosynthesis	2/24	0.032	0.308
	Pyruvate metabolism	2/26	0.037	0.322
S6	Aminoacyl-tRNA biosynthesis	5/45	0.000	0.001
	Arginine biosynthesis	3/16	0.000	0.009
	Alanine, aspartate and glutamate metabolism	3/22	0.001	0.017
	Butanoate metabolism	2/17	0.008	0.171
	Citrate cycle (TCA cycle)	2/20	0.011	0.177
	Valine, leucine and isoleucine biosynthesis	2/22	0.013	0.177
	Valine, leucine and isoleucine degradation	2/23	0.014	0.177
	Pyruvate metabolism	2/26	0.018	0.197

	Arginine and proline metabolism	2/29	0.023	0.215
	Carbapenem biosynthesis	1/3	0.025	0.215
	Glyoxylate and dicarboxylate metabolism	2/37	0.036	0.280
S7	Alanine, aspartate and glutamate metabolism	4/22	0.000	0.010
	Aminoacyl-tRNA biosynthesis	5/45	0.000	0.010
	Glycolysis / Gluconeogenesis	3/29	0.006	0.140
	Arginine and proline metabolism	3/29	0.006	0.140
	Arginine biosynthesis	2/16	0.020	0.315
	Butanoate metabolism	2/17	0.022	0.315
	Carbapenem biosynthesis	1/3	0.041	0.445
	D-Alanine metabolism	1/3	0.041	0.445
S8	Arginine biosynthesis	4/16	0.000	0.005
	Alanine, aspartate and glutamate metabolism	4/22	0.000	0.009
	Aminoacyl-tRNA biosynthesis	5/45	0.000	0.009
	Arginine and proline metabolism	3/29	0.008	0.169
	beta-Alanine metabolism	2/13	0.015	0.254
	Nicotinate and nicotinamide metabolism	2/15	0.020	0.280
	Butanoate metabolism	2/17	0.025	0.306
	Citrate cycle (TCA cycle)	2/20	0.034	0.364
	Novobiocin biosynthesis	1/3	0.044	0.422

Note: S1: ATCC 25922; S2: O26:H11 (ATCC BAA-2196); S3: O45:H2 (ATCC BAA 2193); S5: O111 (ATCC BAA-2440); S6: O121:H19 (ATCC BAA-2219); S7: O145 (ATCC BAA-2192); S8: O157:H7 (ATCC 43895).