

Supplementary files of

The initial inoculation ratio regulates bacterial coculture interactions and metabolic capacity

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The authors declare no competing financial interests.

Table S1 List of 71 carbon sources

Id	Name	Usage¹	Prefer²
2	Dextrin	U1	EC
3	D-Maltose	U2	EC
4	D-Trehalose	U2	EC
5	D-Cellobiose	U1	None
6	Gentiobiosse	U1	EC
7	Sucrose	U1	None
8	D-Turanose	U1	None
9	Stachyose	U1	None
10	D-Raffinose	U1	None
11	α -D-Lactose	U1	None
12	D-Melibiose	U1	EC
13	β -Methyl-D-Glucoside	U1	None
14	D-Salicin	U1	None
15	N-Acetyl-D-Glucosamine	U2	None
16	N-Acetyl- β -Dmannosamine	U1	None
17	N-Acetyl-D-Galactosamine	U1	None
18	N-AcetylNeuraminic Acid	U2	EC
19	α -D-Glucose	U3	PP
20	D-Mannose	U2	PP
21	D-Fructose	U2	EC
22	D-Galactose	U1	EC
23	3-MethylGlucose	U1	None
24	D-Fucose	U1	PP
25	L-Fucose	U2	EC

26	L-Rhamnose	U1	EC
27	Inosine	U2	None
28	D-Sorbitol	U1	EC
29	D-Mannitol	U2	EC
30	D-Arabitol	U1	None
31	myo-Inositol	U1	None
32	Glycerol	U1	None
33	D-Glucose-6-PO4	U2	EC
34	D-Fructose-6-PO4	U2	EC
35	D-Aspartic Acid	U1	None
36	D-Serine	U2	EC
37	Gelatin	U1	None
38	Glycyl-L-Prolin	U1	EC
39	L-Alanine	U3	PP
40	L-Arginine	U3	PP
41	L-Aspartic Acid	U3	PP
42	L-Glutamic	U3	PP
43	L-Histidine	U3	PP
44	L-Pyroglutamic	U3	PP
45	L-Serine	U1	None
46	Pectin	U1	EC
47	D-Galacturonic Acid	U3	PP
48	L-Galactonic Acid Lactone	U2	EC
49	D-Gluconic	U2	PP
50	D-Glucuronic	U3	PP
51	Glucuronamid	U1	PP
52	Mucic Acid	U3	PP

53	Quinic Acid	U3	PP
54	D-Saccharic	U3	PP
55	p-Hydroxy-Phenylacetic Acid	U1	PP
56	Methyl Pyruvate	U1	PP
57	D-Lactic Acid Methyl Ester	U1	None
58	L-Lactic Acid	U3	PP
59	Citric Acid	U3	PP
60	α -Keto-Glutaric Acid	U1	PP
61	D-Malic Acid	U1	None
62	L-Malic Acid	U3	PP
63	Bromo-Succinic	U1	PP
64	Tween 40	U1	None
65	γ -Amino-Butyric Acid	U3	PP
66	α -Hydroxy-Butyric Acid	U1	None
67	β -Hydroxy-D,L-Butyric Acid	U1	PP
68	α -Keto-Butyric Acid	U1	None
69	Acetoacetic Acid	U1	PP
70	Propionic Acid	U1	PP
71	Acetic Acid	U1	None
72	Formic Acid	U1	None

Note: ¹ Carbon usage groups were determined by hierarchical clustering of CUE profiles of all cultures (see Figure 4 for more information). ² Carbon preferences were determined by comparing the CUE of monocultures as follows (see also Figure 3). EC, *Escherichia coli* K-12 preferred carbon source; PP, *Pseudomonas putida* KT2440 preferred carbon source; None: no preference.

Figure S1

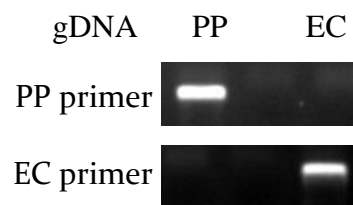


Figure S1. Specificity of species-specific primers. The PCR experiments were performed with *E. coli* and *P. putida* specific primers (left) and their genomic DNA (top), respectively. EC, *Escherichia coli* K-12; PP, *Pseudomonas putida* KT2440.

Figure S2

Preference █ None █ *E. coli* █ *P. putida*

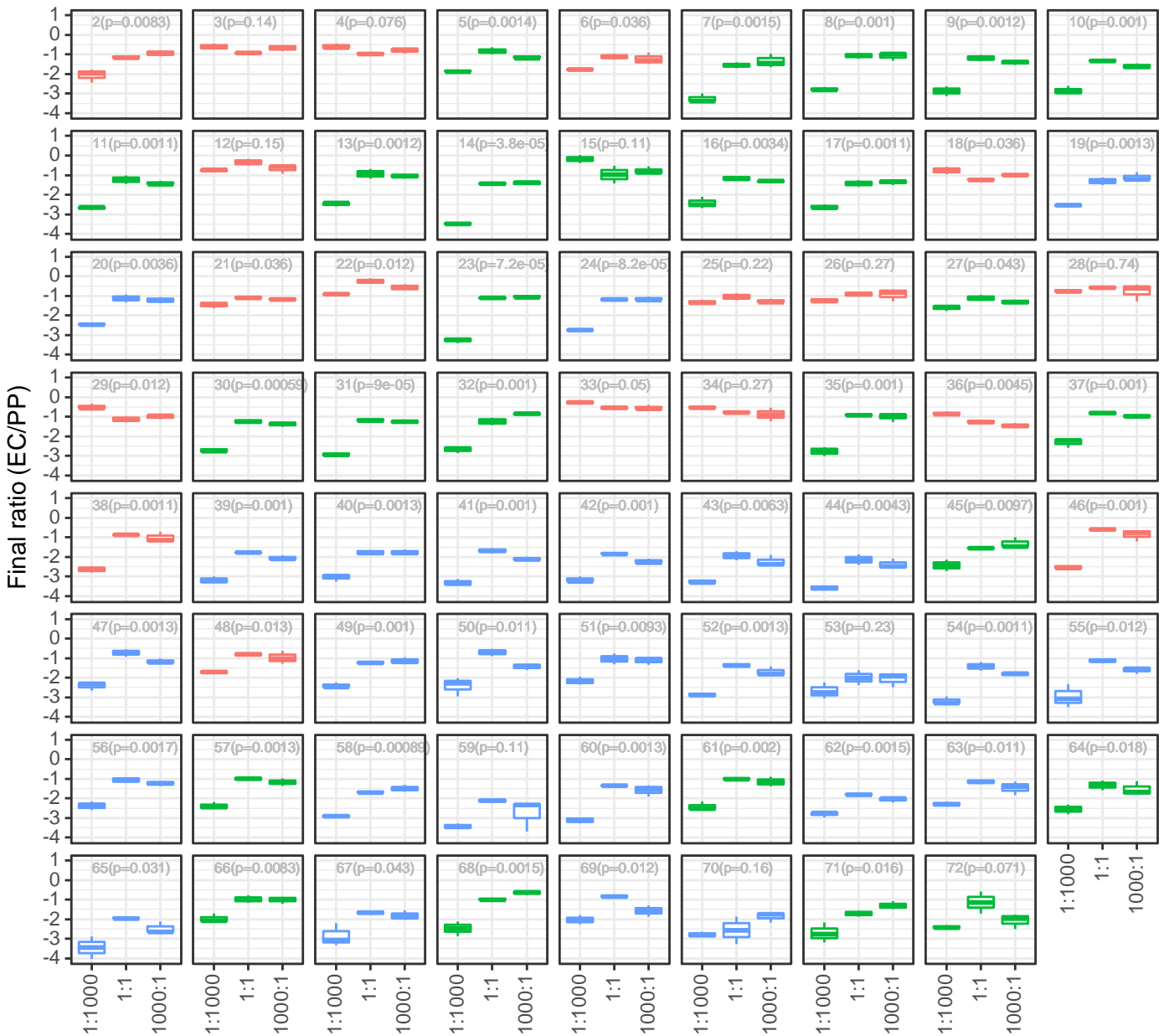


Figure S2. Final ratio of all cocultures in 71 carbon sources (left to right, top to down, carbon id from 2 to 72). The adjusted p-value (ANOVA) were showed on the top of each subplot. The x-axis indicates coculture initial ratios (*E. coli*/*P. putida*), and the y-axis is the final ratio (log₁₀-transformed). Green, none preferred carbon sources; Red, *E. coli* preferred carbon sources; Blue, *P. putida* preferred carbon sources.

Figure S3

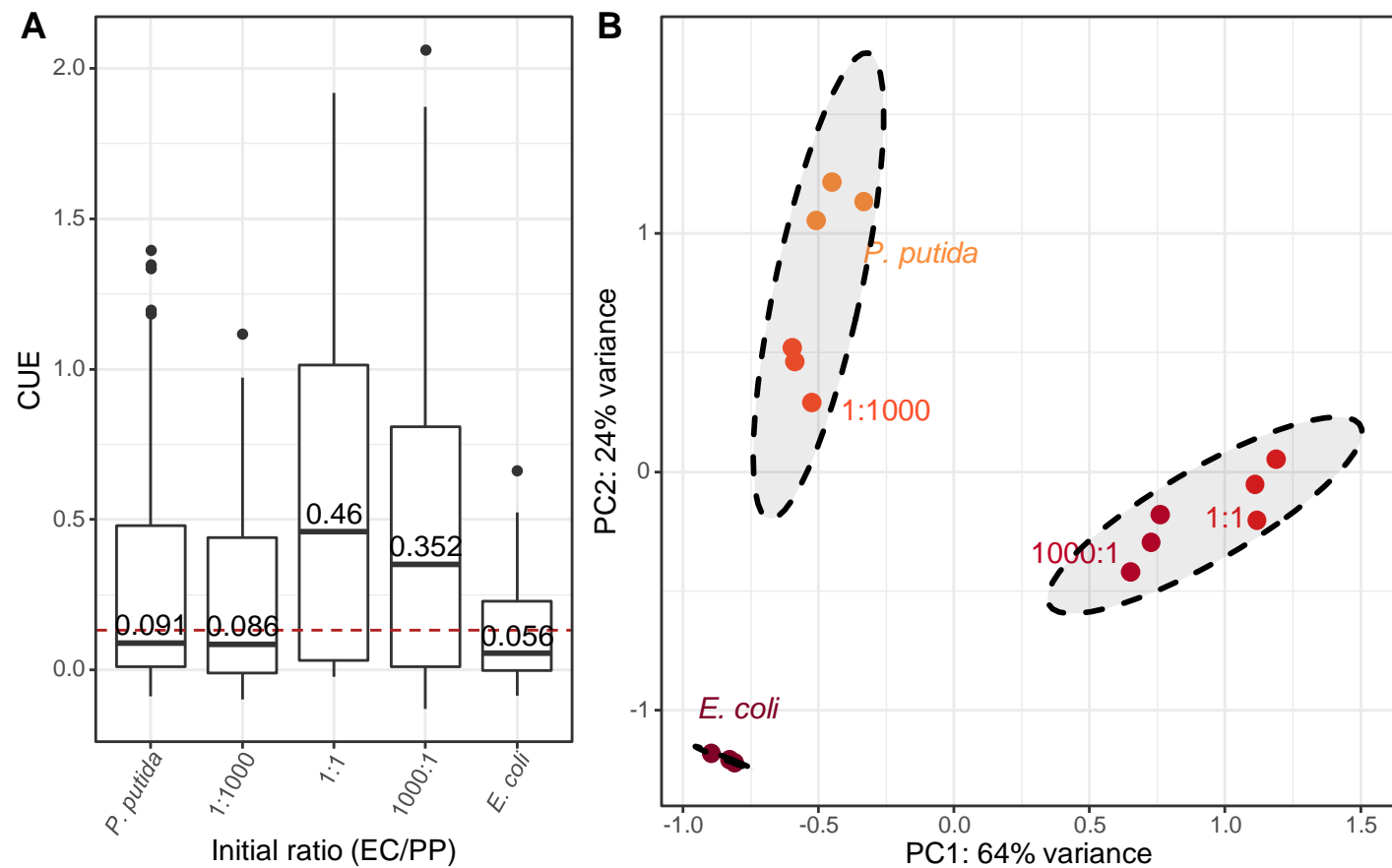


Figure S3. The carbon usage profiles of two monocultures (*E.coli* and *P. putida*) and three cocultures (1:1000, 1:1, and 1000:1). (A) boxplot. Number shows the median of each culture, and horizontal line shows the mean of all cultures. (B) PCA analysis of carbon usage profiles. Ellipses represent the 95% confidence interval of clustering.

Figure S4

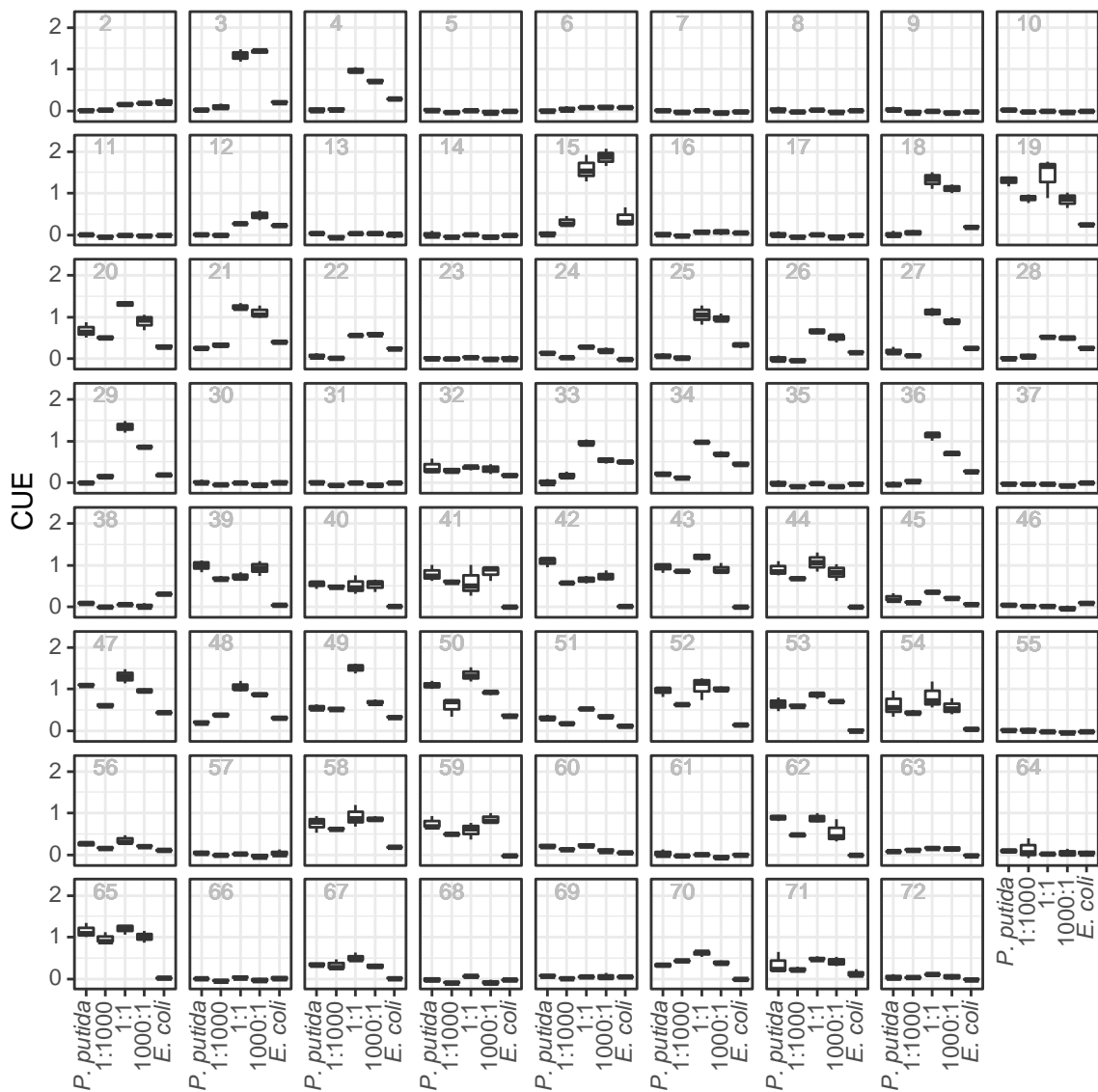


Figure S4. The CUE of mono- and cocultures in 71 carbon sources (left to right, top to down, carbon id from 2 to 72). The x-axis indicates culture conditions (there are a total of 5 culture conditions: *P. putida*, the “1:1000” coculture ; the “1:1” coculture; the “1000:1” coculture and *E. coli*), and the y-axis indicates CUE.

