

Supplementary Materials

**Understanding metabolism of *E. coli* coculture for resveratrol
production with ^{13}C metabolic flux analysis**

Jaeseung Hong^{1†}, Dae-Kyun Im^{1†}, and Min-Kyu Oh^{1*}

¹Department of Chemical & Biological Engineering, Korea University, Anam-Ro 145, Seongbuk-Gu,
Seoul 02841, Republic of Korea

† Both authors contributed equally to this work

Corresponding Author:

*Telephone: +82-2-3290-3308, Fax: +82-2-926-6102, E-mail: mkoh@korea.ac.kr

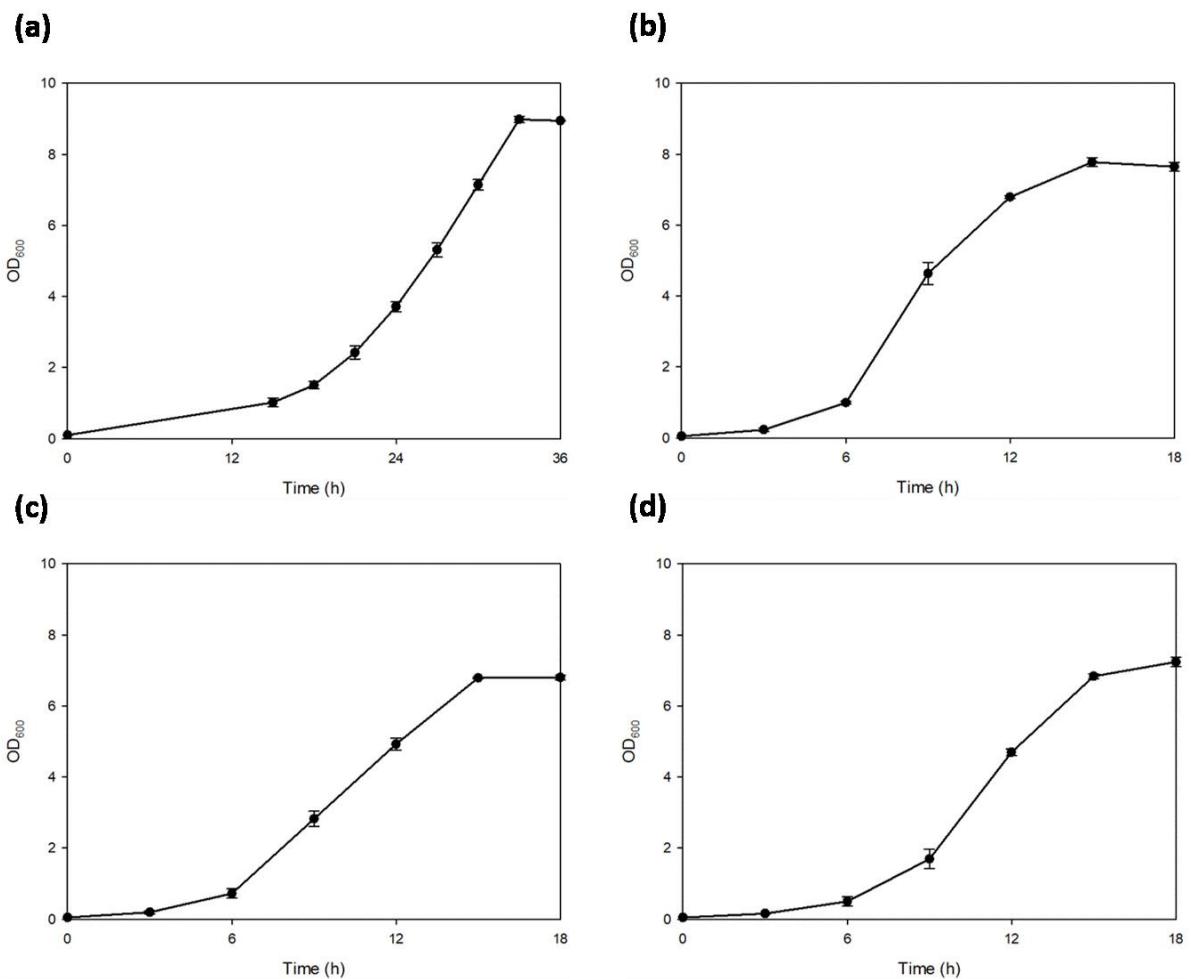


Figure S1. Growth kinetic profiles of monocultures of controls at 37°C. (a) Profile of ECH00. ($\mu = 0.15 \text{ h}^{-1}$) (b) Profile of ERH00 without p-coumaric acid. ($\mu = 0.50 \text{ h}^{-1}$) (c) Profile of ERH00 with 2 mM of p-coumaric acid. ($\mu = 0.45 \text{ h}^{-1}$) (d) Profile of ERH01 without p-coumaric acid. ($\mu = 0.39 \text{ h}^{-1}$)

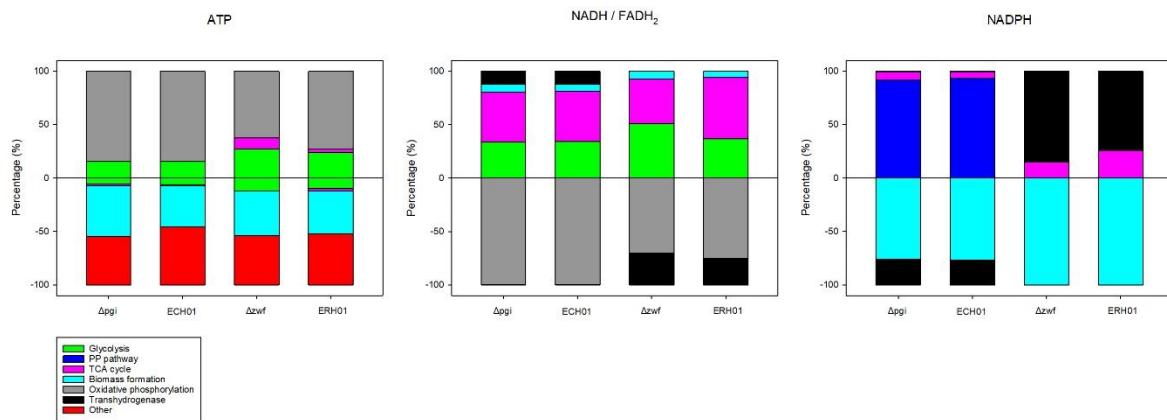


Figure S2. Cofactor balances of engineered strains. The relative production and consumption ratio of the cofactors was calculated from ¹³C-MFA results normalized with 100%. Data for $\Delta pg i$ and $\Delta zw f$ were taken from prior reported values¹

Table S1. Metabolic Network model of *E. coli* used for ^{13}C -MFA with the coculture. Network model was modified from prior reported information²

Glycolysis

- v1 Gluc_exA (abcdef) + PEPA (ghi) -> G6PA (abcdef) + PyrA (ghi)
- v2 G6PA (abcdef) <-> F6PA (abcdef)
- v3 F6PA (abcdef) + ATPA -> FBPA (abcdef)
- v4 FBPA (abcdef) <-> DHAPA (cba) + GAPA (def)
- v5 DHAPA (abc) <-> GAPA (abc)
- v6 GAPA (abc) <-> 3PGA (abc) + ATPA + NADHA
- v7 3PGA (abc) <-> PEPA (abc)
- v8 PEPA (abc) -> PyrA (abc) + ATPA

Pentose Phosphate Pathway

- v9 G6PA (abcdef) -> 6PGA (abcdef) + NADPH
- v10 6PGA (abcdef) -> Ru5PA (bcdef) + CO2A (a) + NADPH
- v11 Ru5PA (abcde) <-> X5PA (abcde)
- v12 Ru5PA (abcde) <-> R5PA (abcde)
- v13 X5PA (abcde) <-> TKC2A (ab) + GAPA (cde)
- v14 F6PA (abcdef) <-> TKC2A (ab) + E4PA (cdef)
- v15 S7PA (abcdefg) <-> TKC2A (ab) + R5PA (cdefg)
- v16 F6PA (abcdef) <-> TAC3A (abc) + GAPA (def)
- v17 S7PA (abcdefg) <-> TAC3A (abc) + E4PA (defg)

Entner-Doudoroff Pathway

- v18 6PGA (abcdef) -> KDPGA (abcdef)
- v19 KDPGA (abcdef) -> PyrA (abc) + GAPA (def)

TCA cycle

- v20 PyrA (abc) -> AcCoAA (bc) + CO2A (a) + NADHA
- v21 OACA (abcd) + AcCoAA (ef) -> CitA (dcfea)
- v22 CitA (abcdef) <-> iCitA (abcdef)
- v23 iCitA (abcdef) <-> AKGA (abcde) + CO2A (f) + NADPH
- v24 AKGA (abcde) -> SucCoAA (bcde) + CO2A (a) + NADHA
- v25 SucCoAA (abcd) <-> SucA (0.5*abcd + 0.5*dcba) + ATPA
- v26 SucA (0.5*abcd + 0.5*dcba) -> FumA (0.5*abcd + 0.5*dcba) + FADH2A
- v27 FumA (0.5*abcd + 0.5*dcba) <-> MalA (abcd)
- v28 MalA (abcd) <-> OACA (abcd) + NADHA

Glyoxylate Shunt

v29 iCitA (abcdef) -> GlyoxA (ab) + SucA (0.5*edcf + 0.5*fcde)
v30 GlyoxA (ab) + AcCoAA (cd) -> MalA (abdc)

Amphibolic Reactions

v31 MalA (abcd) -> PyrA (abc) + CO2A (d) + NADPHA
v32 MalA (abcd) -> PyrA (abc) + CO2A (d) + NADHA
v33 PEPA (abc) + CO2A (d) -> OACA (abcd)
v34 OACA (abcd) + ATPA -> PEPA (abc) + CO2A (d)

Acetic acid formation

v35 AcCoAA (ab) <-> AcA (ab) + ATPA

Amino Acid Biosynthesis

v36 AKGA (abcde) + NADPHA + NH3 -> GluA (abcde)
v37 GluA (abcde) + ATPA + NH3 -> GlnA (abcde)
v38 GluA (abcde) + ATPA + 2*NADPHA -> ProA (abcde)
v39 GluA (abcde) + CO2A (f) + GlnA (ghijk) + AspA (lmno) + AcCoAA (pq) + 5*ATPA + NADPHA -> ArgA (abcdef) + AKGA (ghijk) + FumA (lmno) + AcA (pq)
v40 OACA (abcd) + GluA (efghi) -> AspA (abcd) + AKGA (efghi)
v41 AspA (abcd) + 2*ATPA + NH3 -> AsnA (abcd)
v42 PyrA (abc) + GluA (defgh) -> AlaA (abc) + AKGA (defgh)
v43 3PGA (abc) + GluA (defgh) -> SerA (abc) + AKGA (defgh) + NADHA
v44 SerA (abc) <-> GlyA (ab) + MEETHFA (c)
v45 GlyA (ab) <-> CO2A (a) + MEETHFA (b) + NADHA + NH3
v46 ThrA (abcd) -> GlyA (ab) + AcCoAA (cd) + NADHA
v47 SerA (abc) + AcCoAA (de) + 3*ATPA + 4*NADPHA + SO4 -> CysA (abc) + AcA (de)
v48 AspA (abcd) + PyrA (efg) + GluA (hijkl) + SucCoAA (mnop) + ATPA + 2*NADPHA -> LL_DAPA (0.5*abcdgfe + 0.5*efgdcb) + AKGA (hijkl) + SucA (0.5*mnop + 0.5*ponm)
v49 LL_DAPA (0.5*abcdefg + 0.5*gfedcba) -> LysA (abcdef) + CO2A (g)
v50 AspA (abcd) + 2*ATPA + 2*NADPHA -> ThrA (abcd)
v51 AspA (abcd) + METHFA (e) + CysA (fg) + SucCoAA (ijkl) + ATPA + 2*NADPHA -> MetA (abcde) + PyrA (fg) + SucA (0.5*ijkl + 0.5*lkji) + NH3
v52 PyrA (abc) + PyrA (def) + GluA (ghijk) + NADPHA -> ValA (abcef) + CO2A (d) + AKGA (ghijk)
v53 AcCoAA (ab) + PyrA (cde) + PyrA (fgh) + GluA (ijklm) + NADPHA -> LeuA (abdghe) + CO2A (c) + CO2A (f) + AKGA (ijklm) + NADHA
v54 ThrA (abcd) + PyrA (efg) + GluA (hijkl) + ATPA + NADPHA -> IleA (abfcgd) + CO2A (e) + AKGA (hijkl)

v55 PEPA (abc) + PEPA (def) + E4PA (ghij) + GluA (klmno) + ATPA + NADPHA -> PheA (abcefgij) + CO2A (d) + AKGA (klmno)
 v56 PEPA (abc) + PEPA (def) + E4PA (ghij) + GluA (klmno) + ATPA + NADPHA -> TyrA (abcefgij) + CO2A (d) + AKGA (klmno) + NADHA
 SerA (abc) + R5PA (defgh) + PEPA (ijk) + E4PA (lmno) + PEPA (pqr) + GlnA (stuvw) +
 v57 3*ATPA + NADPHA -> TrpA (abcdklmnoj) + CO2A (i) + GAPA (fgh) + PyrA (pqr) + GluA (stuvw)
 v58 R5PA (abcde) + FTHFA (f) + GlnA (ghijk) + AspA (lmno) + 5*ATPA -> HisA (edcbaf) +
 AKGA (hgijk) + FumA (lmno) + 2*NADHA

One Carbon Metabolism

v59 MEETHFA (a) + NADHA -> METHFA (a)
 v60 MEETHFA (a) -> FTHFA (a) + NADPHA

Oxidative Phosphorylation

v61 NADHA + 0.5*O2A -> 2*ATPA
 v62 FADH2A + 0.5*O2A -> ATPA

Transhydrogenation

v63 NADHA <-> NADPHA

ATP Hydrolysis

v64 ATPA -> ATP_exA

Transport

v65 AcA (ab) -> Ac_exA (ab)
 v66 CO2A (a) -> CO2_exA (a)

Biomass Formation

0.488*AlaA + 0.281*ArgA + 0.229*AsnA + 0.229*AspA + 0.087*CysA + 0.25*GluA +
 0.25*GlnA + 0.582*GlyA + 0.09*HisA + 0.276*IleA + 0.428*LeuA + 0.3265*LysA +
 v67 0.146*MetA + 0.176*PheA + 0.21*ProA + 0.205*SerA + 0.241*ThrA + 0.054*TrpA +
 0.131*TyrA + 0.402*ValA + 0.205*G6PA + 0.071*F6PA + 0.754*R5PA + 0.129*GAPA +
 0.619*3PGA + 0.051*PEPA + 0.083*PyrA + 2.51*AcCoAA + 0.087*AKGA + 0.34*OACA +
 0.443*MEETHFA + 33.25*ATPA + 5.363*NADPHA -> 39.68*BiomassA + 1.455*NADHA

CO2 exchange

v68 CO2_unlabeledA (a) + CO2A (b) -> CO2A (a) + CO2_outA (b)

Resveratrol synthesis 1

v69 TyrA -> CouAc

Glycolysis

v70 Gluc_exB (abcdef) + PEPB (ghi) -> G6PB (abcdef) + PyrB (ghi)

v71 G6PB (abcdef) <-> F6PB (abcdef)
 v72 F6PB (abcdef) + ATPB -> FBPB (abcdef)
 v73 FBPB (abcdef) <-> DHAPB (cba) + GAPB (def)
 v74 DHAPB (abc) <-> GAPB (abc)
 v75 GAPB (abc) <-> 3PGB (abc) + ATPB + NADHB
 v76 3PGB (abc) <-> PEPB (abc)
 v77 PEPB (abc) -> PyrB (abc) + ATPB

Pentose Phosphate Pathway

v78 G6PB (abcdef) -> 6PGB (abcdef) + NADPHB
 v79 6PGB (abcdef) -> Ru5PB (bcdef) + CO2B (a) + NADPHB
 v80 Ru5PB (abcde) <-> X5PB (abcde)
 v81 Ru5PB (abcde) <-> R5PB (abcde)
 v82 X5PB (abcde) <-> TKC2B (ab) + GAPB (cde)
 v83 F6PB (abcdef) <-> TKC2B (ab) + E4PB (cdef)
 v84 S7PB (abcdefg) <-> TKC2B (ab) + R5PB (cdefg)
 v85 F6PB (abcdef) <-> TAC3B (abc) + GAPB (def)
 v86 S7PB (abcdefg) <-> TAC3B (abc) + E4PB (defg)

Entner-Doudoroff Pathway

v87 6PGB (abcdef) -> KDPGB (abcdef)
 v88 KDPGB (abcdef) -> PyrB (abc) + GAPB (def)

TCA cycle

v89 PyrB (abc) -> AcCoAB (bc) + CO2B (a) + NADHB
 v90 OACB (abcd) + AcCoAB (ef) -> CitB (dcfea)
 v91 CitB (abcdef) <-> iCitB (abcdef)
 v92 iCitB (abcdef) <-> AKGB (abcde) + CO2B (f) + NADPHB
 v93 AKGB (abcde) -> SucCoAB (bcde) + CO2B (a) + NADHB
 v94 SucCoAB (abcd) <-> SucB (0.5*abcd + 0.5*dcba) + ATPB
 v95 SucB (0.5*abcd + 0.5*dcba) -> FumB (0.5*abcd + 0.5*dcba) + FADH2B
 v96 FumB (0.5*abcd + 0.5*dcba) <-> MalB (abcd)
 v97 MalB (abcd) <-> OACB (abcd) + NADHB

Glyoxylate Shunt

v98 iCitB (abcdef) -> GlyoxB (ab) + SucB (0.5*edcf + 0.5*fcde)
 v99 GlyoxB (ab) + AcCoAB (cd) -> MalB (abdc)

Amphibolic Reactions

v100 MalB (abcd) -> PyrB (abc) + CO2B (d) + NADPHB

- v101 MalB (abcd) -> PyrB (abc) + CO2B (d) + NADHB
v102 PEPB (abc) + CO2B (d) -> OACB (abcd)
v103 OACB (abcd) + ATPB -> PEPB (abc) + CO2B (d)

Acetic acid formation

- v104 AcCoAB (ab) <-> AcB (ab) + ATPB

Amino Acid Biosynthesis

- v105 AKGB (abcde) + NADPHB + NH3 -> GluB (abcde)
v106 GluB (abcde) + ATPB + NH3 -> GlnB (abcde)
v107 GluB (abcde) + ATPB + 2*NADPHB -> ProB (abcde)
v108 GluB (abcde) + CO2B (f) + GlnB (ghijk) + AspB (lmno) + AcCoAB (pq) + 5*ATPB + NADPHB -> ArgB (abcdef) + AKGB (ghijk) + FumB (lmno) + AcB (pq)
v109 OACB (abcd) + GluB (efghi) -> AspB (abcd) + AKGB (efghi)
v110 AspB (abcd) + 2*ATPB + NH3 -> AsnB (abcd)
v111 PyrB (abc) + GluB (defgh) -> AlaB (abc) + AKGB (defgh)
v112 3PGB (abc) + GluB (defgh) -> SerB (abc) + AKGB (defgh) + NADHB
v113 SerB (abc) <-> GlyB (ab) + MEETHFB (c)
v114 GlyB (ab) <-> CO2B (a) + MEETHFB (b) + NADHB + NH3
v115 ThrB (abcd) -> GlyB (ab) + AcCoAB (cd) + NADHB
v116 SerB (abc) + AcCoAB (de) + 3*ATPB + 4*NADPHB + SO4 -> CysB (abc) + AcB (de)
v117 AspB (abcd) + PyrB (efg) + GluB (hijkl) + SucCoAB (mnop) + ATPB + 2*NADPHB -> LL_DAPB (0.5*abcdgfe + 0.5*efgdcb) + AKGB (hijkl) + SucB (0.5*mnop + 0.5*ponm)
v118 LL_DAPB (0.5*abcdefg + 0.5*gfedcba) -> LysB (abcdef) + CO2B (g)
v119 AspB (abcd) + 2*ATPB + 2*NADPHB -> ThrB (abcd)
v120 AspB (abcd) + METHFB (e) + CysB (fgh) + SucCoAB (ijkl) + ATPB + 2*NADPHB -> MetB (abcde) + PyrB (fgh) + SucB (0.5*ijkl + 0.5*lkji) + NH3
v121 PyrB (abc) + PyrB (def) + GluB (ghijk) + NADPHB -> ValB (abcef) + CO2B (d) + AKGB (ghijk)
v122 AcCoAB (ab) + PyrB (cde) + PyrB (fg) + GluB (ijklm) + NADPHB -> LeuB (abdgh) + CO2B (c) + CO2B (f) + AKGB (ijklm) + NADHB
v123 ThrB (abcd) + PyrB (efg) + GluB (hijkl) + ATPB + NADPHB -> IleB (abfcg) + CO2B (e) + AKGB (hijkl)
v124 PEPB (abc) + PEPB (def) + E4PB (ghij) + GluB (klmno) + ATPB + NADPHB -> PheB (abcefhij) + CO2B (d) + AKGB (klmno)
v125 PEPB (abc) + PEPB (def) + E4PB (ghij) + GluB (klmno) + ATPB + NADPHB -> TyrB (abcefgij) + CO2B (d) + AKGB (klmno) + NADHB

SerB (abc) + R5PB (defgh) + PEPB (ijk) + E4PB (lmno) + PEPB (pqr) + GlnB (stuvw) +
v126 3*ATPB + NADPHB -> TrpB (abcdklmnoj) + CO2B (i) + GAPB (fg) + PyrB (pqr) + GluB
(stuvw)

v127 R5PB (abcde) + FTHFB (f) + GlnB (ghijk) + AspB (lmno) + 5*ATPB -> HisB (edcbaf) +
AKGB (hgijk) + FumB (lmno) + 2*NADHB

One Carbon Metabolism

v128 MEETHFB (a) + NADHB -> METHFB (a)

v129 MEETHFB (a) -> FTHFB (a) + NADPHB

Oxidative Phosphorylation

v130 NADHB + 0.5*O2B -> 2*ATPB

v131 FADH2B + 0.5*O2B -> ATPB

Transhydrogenation

v132 NADHB <-> NADPHB

ATP Hydrolysis

v133 ATPB -> ATP_exB

Transport

v134 AcB (ab) -> Ac_exB (ab)

v135 CO2B (a) -> CO2_exB (a)

Biomass Formation

0.488*AlaB + 0.281*ArgB + 0.229*AsnB + 0.229*AspB + 0.087*CysB + 0.25*GluB +
0.25*GlnB + 0.582*GlyB + 0.09*HisB + 0.276*IleB + 0.428*LeuB + 0.3265*LysB +
0.146*MetB + 0.176*PheB + 0.21*ProB + 0.205*SerB + 0.241*ThrB + 0.054*TrpB +
0.131*TyrB + 0.402*ValB + 0.205*G6PB + 0.071*F6PB + 0.754*R5PB + 0.129*GAPB +
0.619*3PGB + 0.051*PEPB + 0.083*PyrB + 2.51*AcCoAB + 0.087*AKGB + 0.34*OACB +
0.443*MEETHFB + 33.25*ATPB + 5.363*NADPHB -> 39.68*BiomassB + 1.455*NADHB

CO2 exchange

v137 CO2_unlabeledB (a) + CO2B (b) -> CO2B (a) + CO2_outB (b)

Resveratrol synthesis 2

v138 AcCoAB -> MalCoA

v139 CouAc -> CouAc_ex

v140 CouAc -> CouCoA

v141 CouCoA + 3*MalCoA -> RESV

Table S2. Growth and production parameters of ECH01 and ERH01 in culture media, at each temperature

Strain	μ (h^{-1})	X_{\max} (g/L)	$Y_{P/S}$ (mg _P /g _S)	Q_P (mg _P /L·h)	p-CA (mg/L)	Resv (mg/L)
ECH01 - 30°C	0.06±0.00	3.06±0.04	2.56±0.13	0.50±0.02	36.2±0.8	nd
ECH01 - 37°C	0.11±0.00	3.22±0.04	2.83±0.05	1.52±0.01	54.2±0.8	nd
^a ERH01 - 30°C	0.20±0.01	1.22±0.01	15.2±0.5	2.42±0.06	105±37 ^b	54.8±1.60
^a ERH01 - 37°C	0.34±0.00	1.89±0.02	12.1±0.5	5.27±0.06	87.1±23.0 ^b	79.9±1.23
Coculture - 37°C	0.15±0.00	2.91±0.02	5.13±0.19	2.92±0.03	13.8±0.2	55.7±2.70

^a Resveratrol production was performed with addition of 2 mM (328 mg/L) of p-coumaric acid

^b The amount of p-coumaric acid consumed

Table S3. Measured isotope distributions of proteogenic amino acids

		OD ₆₀₀ = 1.00	OD ₆₀₀ = 0.82	OD ₆₀₀ = 1.34
Ala123	m0	0.4227	0.4281	0.4056
260m/z	m1	0.1928	0.1993	0.1801
	m2	0.2896	0.2807	0.3071
	m3	0.0670	0.0651	0.0755
	m4	0.0237	0.0225	0.0266
	m5	0.0033	0.0031	0.0040
Ala23	m0	0.4313	0.4374	0.4164
232m/z	m1	0.3285	0.3463	0.2997
	m2	0.1801	0.1616	0.2137
	m3	0.0461	0.0427	0.0523
	m4	0.0119	0.0101	0.0150
Ser123	m0	0.3662	0.3889	0.3298
390m/z	m1	0.2785	0.2772	0.2727
	m2	0.2368	0.2238	0.2605
	m3	0.0814	0.0761	0.0930
	m4	0.0290	0.0266	0.0342
	m5	0.0064	0.0056	0.0077
Ser23	m0	0.4008	0.4208	0.3639
362m/z	m1	0.3286	0.3286	0.3188
	m2	0.1840	0.1715	0.2134
	m3	0.0628	0.0582	0.0736
	m4	0.0184	0.0163	0.0236
Gly2	m0	0.6636	0.5766	0.6303
218m/z	m1	0.2382	0.3104	0.2647
	m2	0.0786	0.0896	0.0824
	m3	0.0162	0.0231	0.0188
Gly12	m0	0.5446	0.3122	0.5145
246m/z	m1	0.3252	0.4513	0.3483
	m2	0.0983	0.1712	0.1025
	m3	0.0268	0.0519	0.0291
	m4	0.0041	0.0111	0.0046
Val2345	m0	0.2455	0.2679	0.2273
260m/z	m1	0.3101	0.3205	0.2865

	m2	0.2723	0.2555	0.2884
	m3	0.0853	0.0785	0.0876
	m4	0.0669	0.0598	0.0843
	m5	0.0145	0.0129	0.0185
	m6	0.0043	0.0039	0.0058
Val12345	m0	0.2410	0.2572	0.2192
288m/z	m1	0.2319	0.2420	0.2180
	m2	0.2813	0.2646	0.2855
	m3	0.1346	0.1365	0.1432
	m4	0.0833	0.0745	0.0982
	m5	0.0209	0.0190	0.0267
	m6	0.0057	0.0050	0.0077
	m7	0.0008	0.0006	0.0010
Asp12	m0	0.4082	0.4178	0.3641
302m/z	m1	0.3423	0.3493	0.3619
	m2	0.1819	0.1729	0.1986
	m3	0.0515	0.0491	0.0573
	m4	0.0131	0.0120	0.0146
Asp234	m0	0.2635	0.2728	0.2088
390m/z	m1	0.3110	0.3196	0.3210
	m2	0.2496	0.2388	0.2698
	m3	0.1195	0.1153	0.1354
	m4	0.0414	0.0392	0.0475
	m5	0.0115	0.0109	0.0136
Asp1234	m0	0.2258	0.2338	0.1687
418m/z	m1	0.2758	0.2873	0.2759
	m2	0.2631	0.2585	0.2852
	m3	0.1443	0.1356	0.1598
	m4	0.0639	0.0597	0.0769
	m5	0.0200	0.0185	0.0246
	m6	0.0054	0.0048	0.0068
Leu23456	m0	0.1640	0.1742	0.1369
274m/z	m1	0.2830	0.2962	0.2704
	m2	0.2753	0.2752	0.2677
	m3	0.1572	0.1489	0.1756

	m4	0.0694	0.0634	0.0837
	m5	0.0386	0.0319	0.0493
	m6	0.0092	0.0075	0.0123
	m7	0.0024	0.0019	0.0032
Ile23456	m0	0.1765	0.2279	0.1329
274m/z	m1	0.2709	0.2743	0.2629
	m2	0.2800	0.2634	0.2919
	m3	0.1567	0.1413	0.1754
	m4	0.0782	0.0623	0.0939
	m5	0.0285	0.0236	0.0398
	m6	0.0072	0.0055	0.0100
	m7	0.0016	0.0012	0.0021
Tyr12	m0	0.5250	0.5391	0.4914
302m/z	m1	0.3277	0.3202	0.3519
	m2	0.1103	0.1060	0.1163
	m3	0.0302	0.0287	0.0333
	m4	0.0052	0.0049	0.0060
Thr1234	m0	0.2272	0.2306	0.1716
404m/z	m1	0.2763	0.2875	0.2742
	m2	0.2639	0.2579	0.2936
	m3	0.1430	0.1386	0.1591
	m4	0.0631	0.0602	0.0716
	m5	0.0197	0.0186	0.0222
	m6	0.0052	0.0047	0.0058
Lys23456	m0	0.1737	0.1829	0.1270
329m/z	m1	0.2713	0.2813	0.2538
	m2	0.2761	0.2774	0.2897
	m3	0.1565	0.1540	0.1767
	m4	0.0803	0.0696	0.0963
	m5	0.0312	0.0262	0.0417
	m6	0.0083	0.0067	0.0113
	m7	0.0016	0.0013	0.0024
Lys123456	m0	0.1446	0.1450	0.1001
431m/z	m1	0.2168	0.2181	0.1977
	m2	0.2583	0.2588	0.2664

	m3	0.1875	0.1867	0.2021
	m4	0.1156	0.1138	0.1323
	m5	0.0511	0.0512	0.0644
	m6	0.0190	0.0192	0.0263
	m7	0.0054	0.0055	0.0081
	m8	0.0012	0.0014	0.0021
Phe12	m0	0.5211	0.5287	0.4900
302m/z	m1	0.3315	0.3283	0.3515
	m2	0.1103	0.1073	0.1176
	m3	0.0303	0.0294	0.0336
Phe23456789	m0	0.2338	0.2376	0.2061
308m/z	m1	0.2878	0.3080	0.2604
	m2	0.2525	0.2520	0.2723
	m3	0.1071	0.1032	0.1117
	m4	0.0783	0.0686	0.1007
	m5	0.0246	0.0197	0.0296
	m6	0.0113	0.0084	0.0143
	m7	0.0035	0.0018	0.0032
	m8	0.0009	0.0004	0.0008
Phe123456789	m0	0.2268	0.2292	0.2001
336m/z	m1	0.2294	0.2410	0.2082
	m2	0.2620	0.2544	0.2782
	m3	0.1383	0.1397	0.1377
	m4	0.0921	0.0891	0.1133
	m5	0.0323	0.0311	0.0388
	m6	0.0135	0.0120	0.0173
	m7	0.0042	0.0028	0.0041
	m8	0.0011	0.0007	0.0010
	m9	0.0002	0.0001	0.0002

Table S4. Results of ^{13}C -MFA with coculture (unit: mmol / 100 mmol glucose uptake rate of the two strains)

Flux No.	Best Fit	Flux No.	Best Fit
v1	72.85	v70	27.15
v2	0.00	v71	26.63
v3	38.47	v72	24.61
v4	38.47	v73	24.61
v5	38.47	v74	24.61
v6	98.70	v75	47.66
v7	87.53	v76	43.28
v8	2.90	v77	11.90
v9	71.54	v78	0.00
v10	66.45	v79	0.00
v11	38.92	v80	-1.83
v12	27.53	v81	1.83
v13	38.92	v82	-1.83
v14	-17.16	v83	1.37
v15	-21.76	v84	0.46
v16	-21.76	v85	0.46
v17	21.76	v86	-0.46
v18	5.09	v87	0.00
v19	5.09	v88	0.00
v20	67.26	v89	32.34
v21	28.96	v90	16.45
v22	28.96	v91	16.45
v23	9.50	v92	11.32
v24	2.59	v93	8.58
v25	-0.44	v94	7.38
v26	22.04	v95	13.70
v27	24.42	v96	14.65
v28	40.56	v97	19.77
v29	19.45	v98	5.12
v30	19.45	v99	5.12
v31	0.01	v100	0.00
v32	3.30	v101	0.00

v33	5.92	v102	6.60
v34	3.68	v103	4.34
v35	-3.30	v104	-1.31
v36	44.18	v105	16.67
v37	4.33	v106	1.72
v38	1.35	v107	0.53
v39	1.80	v108	0.72
v40	11.66	v109	4.72
v41	1.47	v110	0.58
v42	3.13	v111	1.24
v43	7.20	v112	2.81
v44	4.04	v113	1.56
v45	0.31	v114	0.17
v46	0.00	v115	0.10
v47	1.49	v116	0.59
v48	2.09	v117	0.83
v49	2.09	v118	0.83
v50	3.32	v119	1.41
v51	0.94	v120	0.37
v52	2.58	v121	1.02
v53	2.75	v122	1.09
v54	1.77	v123	0.70
v55	1.13	v124	0.45
v56	3.13	v125	0.33
v57	0.35	v126	0.14
v58	0.58	v127	0.23
v59	0.94	v128	0.37
v60	0.58	v129	0.23
v61	265.68	v130	83.97
v62	22.04	v131	13.70
v63	-34.62	v132	31.89
v64	355.86	v133	118.54
v65	0.00	v134	0.00
v66	161.91	v135	55.09
v67	6.42	v136	2.55

v68	0.00	v137	247.88
v69	2.29	v138	3.39
		v139	1.16
		v140	1.13
		v141	1.13

The proportion of the first species

f-value 0.72

The proportion of labeled amino acids (G-value)

AlaA	1.00
SerA	0.89
GlyA	0.83
ValA	1.00
AspA	0.92
LeuA	0.97
IleA	0.94
TyrA	0.93
ThrA	0.96
LysA	0.97
PheA	0.95
AlaB	0.84
SerB	1.00
GlyB	0.86
ValB	0.99
AspB	0.78
LeuB	0.83
IleB	0.99
TyrB	0.84
ThrB	1.00
LysB	0.95
PheB	1.00

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