

Supporting Information

Table S1. Metabolism pathways of carbon degradation annotated by KEGG.

KO	KEGG Name	KO Description	Pathway ID
Starch			
		4-alpha-	
K00705	malQ	glucanotransferase [EC:2.4.1.25]	ko00500, ko01100, ko01110
K01187	malZ	alpha-glucosidase [EC:3.2.1.20]	ko00500, ko00052, ko01110, ko01100
K01214	ISA, treX	isoamylase [EC:3.2.1.68]	ko00500, ko01100, ko01110
Pectin			
K01728	pel	pectate lyase [EC:4.2.2.2]	ko00040, ko02024, ko01100
K01184	E3.2.1.15	polygalacturonase [EC:3.2.1.15]	ko01100, ko00040
Cellulose			
K19668	CBH2, cbhA	cellulose 1,4-beta- cellobiosidase [EC:3.2.1.91]	ko01100, ko00500, ko02020
K01179	E3.2.1.4	endoglucanase [EC:3.2.1.4]	ko01100, ko00500, ko02020
Chitin			

K01183	E3.2.1.14	chitinase [EC:3.2.1.14]	ko01100, ko00520
Hemicellulose			
K01710	rfbB, rmlB, rffG	dTDP-glucose 4,6-dehydratase [EC:4.2.1.46]	ko01055, ko00523, ko01110, ko01100, ko00541, ko00521, ko00525
K01805	xylA	xylose isomerase [EC:5.3.1.5]	ko00051, ko01100, ko00040

Table S2. Metabolism pathways of carbon fixation annotated by KEGG.

KEGG			
KO	Name	KO Description	Pathway ID
Multiple systems			
K01962	accA	acetyl-CoA carboxylase	ko01212, ko01100, ko00620,
		carboxyl transferase subunit	ko00640, ko01200, ko00061,
		alpha [EC:6.4.1.2 2.1.3.15]	ko01110, ko01120, ko00720
K01895	ACSS1_2, acs	acetyl-CoA synthetase	ko01100, ko00010, ko01120,
		[EC:6.2.1.1]	ko00720, ko01110, ko00680,
			ko01200, ko00630, ko00640,
K11263	bccA, pccA	acetyl-CoA/propionyl-CoA carboxylase, biotin	ko00620
		carboxylase, biotin carboxyl	ko00280, ko00630, ko00640,
		carrier protein [EC:6.4.1.2 6.4.1.3 6.3.4.14]	ko00620, ko01120, ko01110,
Reductive tricarboxylic acid cycle (rTCA cycle)			
K00031	IDH1, IDH2, icd	isocitrate dehydrogenase	ko01200, ko00061, ko01212,
		[EC:1.1.1.42]	ko01100
			ko01120, ko05230, ko01110,
			ko00720, ko00020, ko04146,
			ko01200, ko01230, ko01210,
			ko00480, ko01100

K00174		2-oxoglutarate/2-oxoacid	ko01200, ko00650, ko01120,
	korA, oorA,	ferredoxin oxidoreductase	ko00720, ko01110, ko00020,
	oforA	subunit alpha [EC:1.2.7.3 1.2.7.11]	ko00620, ko00010, ko01100
K00175		2-oxoglutarate/2-oxoacid	ko00020, ko01120, ko00720,
	korB, oorB,	ferredoxin oxidoreductase	ko01110, ko00650, ko01200,
	oforB	subunit beta [EC:1.2.7.3 1.2.7.11]	ko00620, ko01100, ko00010
Reductive acetyl-CoA pathway			
K01938	fhs	formate--tetrahydrofolate	ko00720, ko01120, ko01100,
		ligase [EC:6.3.4.3]	ko01240, ko00670, ko01200
Calvin cycle			
K01601	rbcL, cbbL	ribulose-bisphosphate	ko00630, ko01200, ko01120,
		carboxylase large chain [EC:4.1.1.39]	ko00710, ko01110, ko01100
K01602	rbcS, cbbS	ribulose-bisphosphate	ko00630, ko01200, ko00710,
		carboxylase small chain [EC:4.1.1.39]	ko01120, ko01110, ko01100

Table S3. Metabolism pathways of methane metabolism annotated by KEGG.

KO	KEGG Name	KO Description	Pathway ID
Methane oxidation			
K10944	pmoA-	methane/ammonia	ko00910, ko01100,
		monooxygenase subunit A	
	amoA	[EC:1.14.18.3 1.14.99.39]	ko00680, ko01120, ko01200
K10945	pmoB-	methane/ammonia	ko00910, ko01200,
	amoB	monooxygenase subunit B	ko00680, ko01120, ko01100
K10946	pmoC-	methane/ammonia	ko00680, ko01120,
	amoC	monooxygenase subunit C	ko01100, ko01200, ko00910
Methanogenesis			
K00577	mtrA	tetrahydromethanopterin S-	
		methyltransferase subunit A	ko01100, ko00680,
		[EC:2.1.1.86]	ko01120, ko01200
K14083	mttB	trimethylamine---corrino protein	
		Co-methyltransferase	ko01100, ko01120,
		[EC:2.1.1.250]	ko00680, ko01200

Table S4. Metabolism pathways of amino acids metabolism annotated by KEGG.

KO	KO Description	KO	KO Description
ko01230	Biosynthesis of amino acids	ko00300	Lysine biosynthesis
ko00220	Arginine biosynthesis	ko00310	Lysine degradation
ko00250	Alanine, aspartate and glutamate metabolism	ko00330	Arginine and proline metabolism
ko00260	Glycine, serine and threonine metabolism	ko00340	Histidine metabolism
ko00270	Cysteine and methionine metabolism	ko00350	Tyrosine metabolism
ko00280	Valine, leucine and isoleucine degradation	ko00360	Phenylalanine metabolism
ko00290	Valine, leucine and isoleucine biosynthesis	ko00380	Tryptophan metabolism
		ko00400	Phenylalanine, tyrosine and tryptophan biosynthesis

Table S5. Metabolism pathways of other amino acids metabolism annotated by KEGG.

KO	KO Description	KO	KO Description
ko00410	beta-Alanine metabolism	ko00450	Selenocompound metabolism
ko00430	Taurine and hypotaurine metabolism	ko00460	Cyanoamino acid metabolism
ko00440	Phosphonate and phosphinate metabolism	ko00480	Glutathione metabolism