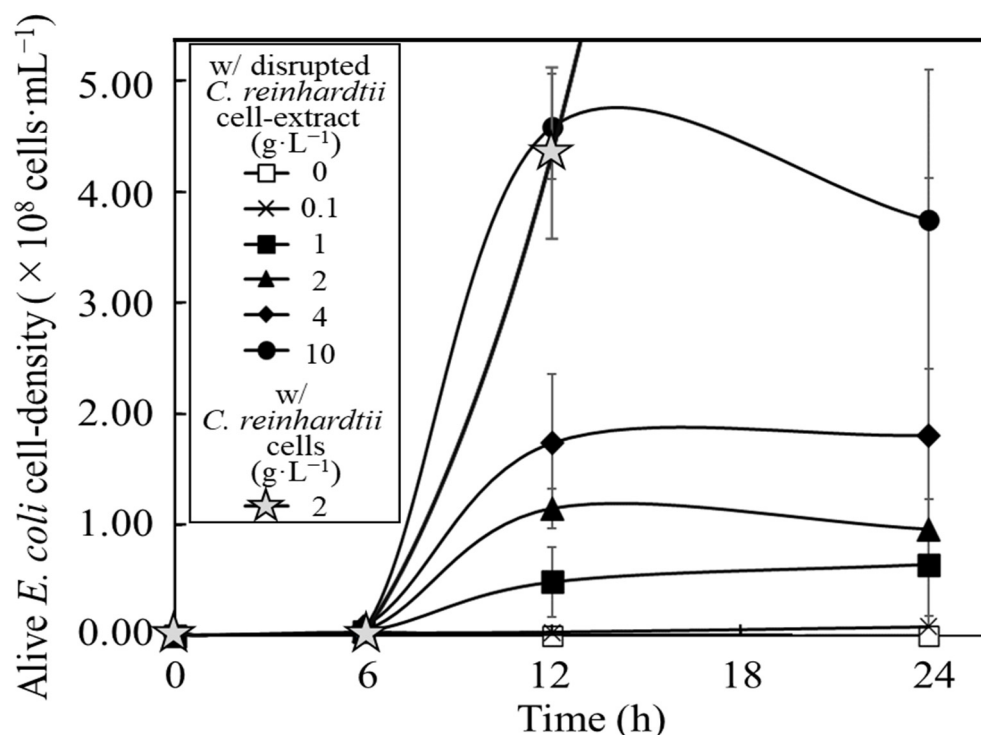


Supplemental Data
Supplemental Figure S1



Supplemental Figure S1 Complementation of growth of *E. coli* in *C. reinhardtii*-MBBM with those in disrupted cell-extract-MBBM.

Those *E. coli* growth was compared using data depending on Figure 1 (a) and Figure 2 (a).

Growth activities of *E. coli* were shown in MBBM containing 0 (□), 0.1 (×), 1 (■), 2 (▲), 4 (◆) and 10 g·L⁻¹ (●) of disrupted cell-extracts from *C. reinhardtii*, and in MBBM containing 2 g·L⁻¹ (☆) of *C. reinhardtii* cells. Error bars indicate the SD of three replicate experiments (n = 3).

Supplemental Table S1. Primer pairs used on qPCR

Category	Enzyme name [EC number]	Abbreviation	Forward/Reverse	Sequence alignment
Glycolysis	glucokinase [EC:2.7.1.2]	glk	F	agcggtcattcggttatc
			R	gtcaccggtaattgggca
	glucose-1-phosphatase [EC:3.1.3.10]	agp	F	atctgaccagcagtggaa
			R	ataactgaccagcggttc
	glucose-1-phosphatase [EC:3.1.3.10]	yihX	F	gttttcacccagcgatacg
			R	aaatagtcgggatgggtg
	phosphoglucomutase [EC:5.4.2.2]	pgm	F	gcttctattggcggtctgaa
			R	ccgttctttctcaatctgc
	glucose PTS system EIICB or EIICBA component [EC:2.7.1.199]	ptsG	F	tcttactggcggttgctg
			R	aatgccaacgcaacta

maltose/glucose PTS system EIICB component [EC:2.7.1.199; 2.7.1.208]	malX	F	attaccgctctgcgtttgtc
		R	actgaacttgaggcccgat a
sugar PTS system EIIA component [EC:2.7.1.-]	crr	F	agacggcaccattggtaa aa
		R	cgataccgaagtggacga ac
galactose-1-epimerase aldose 1-epimerase [EC:5.1.3.3]	galM	F	gccctgagttcagatgatg g
		R	ggcgcgataagtaatgga ga
putative sulfoquinovose mutarotase YihR aldose 1-epimerase [EC:5.1.3.3]	yihR	F	acggctatccgtttatgctg
		R	agtgcgcatattctggcttg
putative aldose 1-epimerase YeaD glucose-6-phosphate 1-epimerase [EC:5.1.3.15]	yeaD	F	tcgaacaaatctccctgtc
		R	gaggctttacctggggat g
glucose-6-phosphate isomerase [EC:5.3.1.9]	pgi	F	caatacccgatttggttg
		R	tcaccggaataatcgctt c
fructose 1,6-bisphosphatase YggF fructose-1,6-bisphosphatase II [EC:3.1.3.11]	yggF	F	tatcggcgaaggagaaat tg
		R	gtgccttcaatgggatcaa c
fructose-1,6-bisphosphatase 2 fructose-1,6-bisphosphatase II [EC:3.1.3.11]	glpX	F	tcgtcattggtgaaggtga a
		R	gtgccttcaatcggatcaa c
fructose-1,6-bisphosphatase 1 fructose-1,6-bisphosphatase I [EC:3.1.3.11]	fbp	F	tctggatatcatcccgga a
		R	agcggttcgacatcttcaac
6-phosphofructokinase 2 [EC:2.7.1.11]	pfkB	F	aactcagtgcgctggtga at
		R	tgccgctattaacgatttc
6-phosphofructokinase 1 [EC:2.7.1.11]	pfkA	F	aattcagccgtgaagacct g
		R	tttcacgaccggtttcttc
fructose-bisphosphate aldolase, class I [EC:4.1.2.13]	fbaB	F	ttgctgctaaccgctctac
		R	cgtaagttgacgccacaca g
fructose-bisphosphate aldolase, class II [EC:4.1.2.13]	fbaA	F	aatcgcatgactctggaa a
		R	gtacagtgacagaagcgtc ca
triose-phosphate isomerase triosephosphate isomerase (TIM) [EC:5.3.1.1]	tpiA	F	tgacgctaacatcgctgaa c
		R	atatccggctgagcaaac ag
glyceraldehyde-3-phosphate dehydrogenase A glyceraldehyde 3-phosphate	gapA	F	agttgacctgaccgttcgtc
		R	acgtcatcttcggtgtagcc

dehydrogenase (phosphorylating)
[EC:1.2.1.12]

phosphoglycerate kinase [EC:2.7.2.3]	pgk	F	acgaagctgacctgggtg
		R	ac ttgctacgcgaacatcaga c
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.11]	gpmA	F	aaaagtatggcgacgagc
		R	ag gtcagcggcagttcttctc
putative phosphatase 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.11]	ytjC	F	cggctgtgacatcatcttg
		R	cgacgccagttcttcttc
2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.12]	gpmM	F	ttgggatcgcgtagaaaa
		R	ag ataagcagcctgcaaacc ag
enolase [EC:4.2.1.11]	eno	F	gcgaaactgaagacgcta
		R	cc acggtcagaacggctcat ag
phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	pck	F	caaacgtctgttcgtgtcg
		R	aacctgccagttcttcatcg
pyruvate kinase I [EC:2.7.1.40]	pykF	F	caccgtactgggtgacgat
		R	g ggcaggttcacaccttgtt
pyruvate kinase II [EC:2.7.1.40]	pykA	F	acatcatcctgcctctgac
		R	tgattaccgctcggtttagc
pyruvate-ferredoxin/flavodoxin oxidoreductase [EC:1.2.7.1; 1.2.7.-]	ydbK	F	gtggtacgcacagggcta
		R	tt caaaatcagcctgggaaa tg
phosphoenolpyruvate synthetase pyruvate, water dikinase [EC:2.7.9.2]	ppsA	F	aacggatgaaagacggt
		R	gag attccagcaactccgcata g
acetyl-CoA synthetase (AMP-forming) [EC:6.2.1.1]	acs	F	ggcgcatattgattccaac
		R	gtgacgttcgggttttcag
pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	aceF	F	tgctgaaaacgacgcttat
		R	g cgcaggatacgcacctttac g
pyruvate dehydrogenase E1 component [EC:1.2.4.1]	aceE	F	actgggtactgatggcttc
		R	g atcgatttcgccagtttag
lipoamide dehydrogenase dihydrolipoamide dehydrogenase [EC:1.8.1.4]	lpd	F	tcaccaagcgtatcagcaa
		R	g tgccttccatcgtcacataa
aldehyde dehydrogenase B [EC:1.2.1.-]	aldB	F	taccccgcttctgtactgc
		R	ttcgaggctgccagatatt c
	adhE	F	cctgactctgggtgtggtt

acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10; 1.1.1.1]		R	ctcgcttagcaacggttttc
ethanol dehydrogenase/alcohol dehydrogenase [EC:1.1.1.1]	adhP	F	ggatatccacgtcttgctg
		R	ttcggcaccactttaccttc
		F	ttttaccgagcaggaagtg
malate dehydrogenase [EC:1.1.1.37]	mdh	R	g
		R	tgcacgaaccagagacag
			ac
quinone oxidoreductase		F	agtgtctggggttgaactac
malate dehydrogenase (quinone) [EC:1.1.5.4]	mgo	R	g
		R	tccgccacttcttttgaac
citrate synthase [EC:2.3.3.1]	gltA	F	atgattctttccgcctgatg
		R	cccagctctttcagcacttc
		F	aagtgcgtaaccacgaaa
aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]	acnB	R	cc
		R	cagcacgcacttcatcaat
			c
putative hydratase YbhJ		F	aaaatggctgcctgaaag
aconitate hydratase [EC:4.2.1.3]	ybhJ	R	tg
		R	gtaaactgccagcgagaa
			gg
		F	tatctcggcaaagcagtg
aconitate hydratase 1 [EC:4.2.1.3]	acnA	R	g
		R	tgcgagtcagtagcaacg
			ag
		F	cccgtggctgaaagttaa
isocitrate dehydrogenase [EC:1.1.1.42]	icd	R	a
		R	aggatctgttcaggaat
			gc
2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]	sucA	F	cttacctctctggcgcaaac
		R	accaggtactgtctggaa
			cg
dihydrolipoyltranssuccinylase		F	tggctgctgactcgtgaa
2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61]	sucB	R	g
		R	gtcatcgggacacgttttc
succinyl-CoA synthetase beta subunit [EC:6.2.1.5]	sucC	F	ggtccgtgggtagtgaag
		R	tg
		R	gcacggatgtcttctttgct
		F	tgctgaccgtgaaagtga
succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]	sucD	R	ag
		R	cggttgtgaatgtgacca
			g
succinate:quinone oxidoreductase, membrane protein SdhC		F	cgggtgtgatcaccttgttg
succinate dehydrogenase / fumarate reductase, cytochrome b subunit [EC:1.3.5.1]	sdhC	R	aagcttgctcgaaaccttc
			a
succinate:quinone oxidoreductase, membrane protein SdhD	sdhD	F	cgtctgacgctctacatca
succinate dehydrogenase / fumarate		R	atagaaaacagcgccagc
			ag

reductase, membrane anchor subunit [EC:1.3.5.1]				
Pentose phosphate pathway	succinate:quinone oxidoreductase, FAD binding protein		F	ggtcttcgtaaggtgat g
	succinate dehydrogenase / fumarate reductase, flavoprotein subunit [EC:1.3.5.1; 1.3.5.4]	sdhA	R	tgttgaaactcgctggaagt g
	succinate:quinone oxidoreductase, iron- sulfur cluster binding protein		F	aaaactcgacgggctgtat g
	succinate dehydrogenase / fumarate reductase, iron-sulfur subunit [EC:1.3.5.1; 1.3.5.4]	sdhB	R	acgatatgccgctaaca gc
	fumarate reductase membrane protein FrdD	frdD	F	cttcattggtcgctattcc
	fumarate reductase subunit D		R	agcagccagaccgtagaa aa
	fumarate reductase membrane protein FrdC	frdC	F	gtttgaactggcaccgaaa g
	fumarate reductase subunit C		R	gggcaacaacaggatta cg
	fumarate reductase iron-sulfur protein		F	gtatggcgatttgtggtcc
	fumarate reductase iron-sulfur subunit [EC:1.3.5.4]	frdB	R	acgcttaacctcataccg
	fumarate reductase flavoprotein subunit [EC:1.3.5.4]	frdA	F	cgaatgaccaactgga ac
			R	tatggaagccggtcttatc g
	fumarase C		F	cattacctgtgcaccgtttg
	fumarate hydratase, class II [EC:4.2.1.2]	fumC	R	ggacatcattggcgatttc
	fumarase A		F	ggggatctggatcgaaaa ac
	fumarate hydratase, class I [EC:4.2.1.2]	fumA	R	aaacgggatactgcgaca ac
	fumarase D		F	tgggaaatcgacaaaag ag
	fumarate hydratase D [EC:4.2.1.2]	fumD	R	cgctgcgataacaatatg c
	fumarase E		F	tgtgcttgagcaactggat g
	fumarate hydratase E [EC:4.2.1.2]	fumE	R	acggcttcactgcatttcc
	fumarase B		F	ccggtatccactcgttgtc
	fumarate hydratase, class I [EC:4.2.1.2]	fumB	R	gaagttcttaccggcgctc a
Pentose phosphate pathway	quinoprotein glucose dehydrogenase [EC:1.1.5.2]	gcd	F	actgtggcagggctgttta c
	glyoxylate reductase		R	tagtcgcccatcttcgtacc
	glyoxylate/hydroxypyruvate/2- ketogluconate reductase [EC:1.1.1.79; 1.1.1.81; 1.1.1.215]	ghrB	F	atttcgttgcctgatcctg
			R	cagtgcattttcgtcaacca
	D-gluconate kinase, thermostable gluconokinase [EC:2.7.1.12]	gntK	F	ttcttgatggcgatttctc
			R	tagtgcgctgcatagcaaa c

D-gluconate kinase, thermosensitive gluconokinase [EC:2.7.1.12]	idnK	F	ctggctggaacgcttaaat g
		R	cgccatctaaccagagga aa
2-dehydro-3-deoxygluconokinase [EC:2.7.1.45]	kdgK	F	tactactggcggaacgaa gc
		R	taatcgaaattcgccagct c
NADP(+)-dependent glucose-6-phosphate dehydrogenase	zwf	F	cgctgtaaatgctgccttc
glucose-6-phosphate 1-dehydrogenase [EC:1.1.1.49; 1.1.1.363]		R	tatgccgctttatcccagtc
6-phosphogluconolactonase [EC:3.1.1.31]	pgl	F	atccgcacggtaatatcga a
		R	cgtataaatggcgaccatc c
phosphogluconate dehydratase [EC:4.2.1.12]	edd	F	cgattgtgtcgttgtgtcc ggagagtcgtccatcggt aa
KHG/KDPG aldolase	eda	F	agaagtgcctgaagcgat tg
2-dehydro-3-deoxyphosphogluconate aldolase / (4S)-4-hydroxy-2-oxoglutarate aldolase [EC:4.1.2.14; 4.1.3.42]		R	ccttcggtagcagctttcag
6-phosphogluconate dehydrogenase, decarboxylating	gnd	F	agatcggcgtagtcggtat g
6-phosphogluconate dehydrogenase [EC:1.1.1.44 1.1.1.343]		R	tttcggcaatcacttcttc
transketolase 2	tktB	F	tacgccggatcaggttaaa g
transketolase [EC:2.2.1.1]		R	gctaatttctctgccgcttg
transketolase 1	tktA	F	acggctccatgctgatcta c
transketolase [EC:2.2.1.1]		R	gcagctgacggaagtttt c
ribulose-phosphate 3-epimerase [EC:5.1.3.1]	rpe	F	aagtacgtcgccgtatcga c
		R	gtctggctgggtgaagatt g
ribose 5-phosphate isomerase A [EC:5.3.1.6]	rpiA	F	ctgtattgcagacgcttcca ctacgtgcatcgggataa c
allose-6-phosphate isomerase/ribose-5- phosphate isomerase B	rpiB	F	gtactggcgtcggtatttc g
ribose 5-phosphate isomerase B [EC:5.3.1.6]		R	accactcgtgaacaaaa gc
transaldolase B	talB	F	gggcgtggtttctgtatctg agaatttcgccgatgttac g
transaldolase [EC:2.2.1.2]		R	
transaldolase A [EC:2.2.1.2]	talA	F	agttgatgcacgcctctctt atttctcaacgccttgttgc
		R	

Fatty acid biosyntheses	ribokinase [EC:2.7.1.15]	rbsK	F	aaagctcaccggtattcgtg
			R	ccattcacgctagcccatac
	putative mutase YhfW phosphopentomutase [EC:5.4.2.7]	yhfW	F	cgcgatttggtgtagtg
			R	aactggctcaggatgtgacc
	phosphopentomutase [EC:5.4.2.7]	deoB	F	attgctgccatgaagaaac
			R	tggagttaccggctttgtc
	ribose-phosphate pyrophosphokinase [EC:2.7.6.1]	prs	F	ttgtggtttctccgacatc
			R	catcacctgtgaaacgttcg
	ribose 1,5-bisphosphokinase [EC:2.7.4.23]	phnN	F	aggattgccatacgtcaac
			R	caggcatggtgtttctcctt
	deoxyribose-phosphate aldolase [EC:4.1.2.4]	deoC	F	cggtaaccaacttcccacac
			R	caggtaaaaaccaacctgct
	acetyl-CoA carboxyltransferase subunit alpha		F	ccgtcaggatgagaaactgg
	acetyl-CoA carboxylase carboxyl transferase subunit alpha [EC:6.4.1.2; 2.1.3.15]	accA	R	atcggcgaagattttacgtg
	acetyl-CoA carboxyltransferase subunit beta		F	aagcactgatgtcgctgatg
	acetyl-CoA carboxylase carboxyl transferase subunit beta [EC:6.4.1.2; 2.1.3.15]	accD	R	atggcgaaactgcagaaac
	biotin carboxyl carrier protein		F	aaagtcaacgtgggcgat
	acetyl-CoA carboxylase biotin carboxyl carrier protein	accB	R	ctttcacgggtaccggatttg
	biotin carboxylase		F	tatctgaacatcccggaat
	acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2; 6.3.4.14]	accC	R	tcgggccaatgaagataaag
	[acyl-carrier-protein] S-malonyltransferase [EC:2.3.1.39]	fabD	F	tattgcgaaagcgtgtgaa
			R	cgctcaaccgcttctttatg
	3-oxoacyl-[acyl-carrier-protein] synthase III [EC:2.3.1.180]	fabH	F	cgcagctgtcagattcaaa
			R	aaccgacgaccagagcat
	3-oxoacyl-[acyl-carrier-protein] synthase I [EC:2.3.1.41]	fabB	F	ctctgatggtgcagacatg
			R	cgtagggagttcaggaatcg
		fabF	F	aactcgtcggctttggtatg

Fatty acid degradation	3-oxoacyl-[acyl-carrier-protein] synthase II [EC:2.3.1.179]		R	cgcgtaacgtagccaatc t
	3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]	fabG	F	ccgtctgtcaaagcggtg a
			R	ttcccatggtaccaaccac
	beta-hydroxyacyl-acyl carrier protein dehydratase/isomerase		F	cgaacatgctgatgatgg ac
	3-hydroxyacyl-[acyl-carrier protein] dehydratase / trans-2-decenoyl-[acyl- carrier protein] isomerase [EC:4.2.1.59; 5.3.3.14]	fabA	R	cataaccggatcgccaata a
	3-hydroxyacyl-[acyl-carrier-protein] dehydratase [EC:4.2.1.59]	fabZ	F	ccgttctactggtggatcg
			R	ccattgcttcagaatcagc
			F	gtgcgatgttgcagaaga tg
	enoyl-[acyl-carrier protein] reductase I [EC:1.3.1.9; 1.3.1.10]	fabI	R	gccagggtgcaaaaccaat ag
			F	aggcacggtagtcaatttc g
	long-chain-fatty-acid--CoA ligase long-chain acyl-CoA synthetase [EC:6.2.1.3]	fadD	R	gggtttgacgtactgcatc c
			F	cgctgattacctacggcatt
	acyl-CoA dehydrogenase [EC:1.3.99.-]	fadE	R	ccggtaatatccatcgcat c
			F	atcgtagccagcaaaatg g
	putative 2,3-dehydroadipyl-CoA hydratase enoyl-CoA hydratase [EC:4.2.1.17]	paaF	R	tgccagctgtaaggcgatat t
	3-hydroxyacyl-CoA dehydrogenase FadJ 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl- CoA epimerase [EC:1.1.1.35; 4.2.1.17; 5.1.2.3]	fadJ	F	tctgataggcgtagcacac g
			R	agaatggagtgccgaac aac
	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase /		F	tctggaggaaggcattatc g
	3-hydroxybutyryl-CoA epimerase / enoyl- CoA isomerase [EC:1.1.1.35; 4.2.1.17; 5.1.2.3; 5.3.3.8]	fadB	R	tcgaggatatttgcgctacc
	3-ketoacyl-CoA thiolase FadI acetyl-CoA acyltransferase [EC:2.3.1.16]	fadI	F	cttaatgccgtaccacctg
			R	taggttttcgccatttgctc
	3-ketoacyl-CoA thiolase acetyl-CoA acyltransferase [EC:2.3.1.16]	fadA	F	gtcattgtcgatgcaattcg
			R	cgcattaaatgagcggag ag
			F	atcgcttggagacggac ag
	acetyl-CoA acetyltransferase acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	atoB	R	aatgtagcgccagttcatc c
	putative acyltransferase acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	yqeF	F	tcagttgcaggatgcttac g
			R	aacgtctgcccgttactttg
	fused 2-acylglycerophospho-ethanolamine acyltransferase/acyl-acyl carrier protein	aas	F	aaaacgattgccgacttca c

Glycerolipid metabolism	synthetase acyl-[acyl-carrier-protein]-phospholipid O-acyltransferase / long-chain-fatty-acid-- [acyl-carrier-protein] ligase [EC:2.3.1.40 6.2.1.20]		R	tctgcacctgtaagcagtg g
	putative 3-phenylpropionate/cinnamate dioxygenase ferredoxin reductase subunit 3-phenylpropionate/trans-cinnamate dioxygenase ferredoxin reductase component [EC:1.18.1.3]	hcaD	F	atgaacgacctccactctc g
			R	ttacaccggaatgcagatg a
	glycerate 2-kinase 2 glycerate 2-kinase [EC:2.7.1.165]	glxK	F	ggcgaattgccatattgaa g
			R	taattttgcagccctgttc .
	glycerate 2-kinase 1 glycerate 2-kinase [EC:2.7.1.165]	garK	F	gaagggtaccgattgggtgc g
			R	tgctggtaataacgctgaa g
	aldehyde reductase, NADPH-dependent alcohol dehydrogenase (NADP+) [EC:1.1.1.2]	yahK	F	agccgttggtgatcaggta g
			R	accggtcttcacactcttcg .
	dihydroxyacetone kinase subunit M phosphoenolpyruvate---glycerone phosphotransferase subunit DhaM [EC:2.7.1.121]	dhaM	F	cggtagcaggcaaatcaaa cc
			R	ggcttctgctttcgctgtta .
	L-1,2-propanediol dehydrogenase/glycerol dehydrogenase glycerol dehydrogenase [EC:1.1.1.6]	gldA	F	aaatgagatcgaccgtctg c
			R	taccggaacacccatgaa at
	glycerol kinase [EC:2.7.1.30]	glpK	F	ttgctgtttggtacggttga .
			R	agcattttgtcgtcccagtc .
	putative phosphate acyltransferase phosphate acyltransferase [EC:2.3.1.274]	plsX	F	tttgccattatgggctcagt .
			R	tccgaatactgtcgagac c
	putative glycerol-3-phosphate acyltransferase acyl phosphate:glycerol-3-phosphate acyltransferase [EC:2.3.1.275]	plsY	F	gttacgtatcggtggcaag g
			R	cagaaggggctgacacct aa
	glycerol-3-phosphate 1-O-acyltransferase glycerol-3-phosphate O-acyltransferase [EC:2.3.1.15]	plsB	F	tactgcgctactggcatca c
			R	tggtgaaggaacggtag ag
	1-acylglycerol-3-phosphate O- acyltransferase PlsC 1-acyl-sn-glycerol-3-phosphate acyltransferase [EC:2.3.1.51]	plsC	F	tggtgacagcatcgaacat c
			R	accagtacaactgcccga ag
	diacylglycerol kinase (ATP) [EC:2.7.1.107]	dgkA	F	tcaaagctgctggctattcc .
			R	atgaccaccgccaacaata c
	alpha-galactosidase [EC:3.2.1.22]	melA	F	cgcatatttggtgctgtaa g
			R	tcaccgtgcaagggtcata a

Housekeeping gene	16S ribosomal RNA	rrsA	F	attgacgttaccgcagaa g
			R	attccgattaacgcttgac
	integration host factor subunit beta	ihfB	F	tttcggcagtttctcttgc
			R	atcgcgagttctttaccag
	uroporphyrin-III C-methyltransferase	cysG	F	gtttatTTTTggccgtggtg
			R	gatgcgtgagtggaatac cc
	MFS transporter	hcaT	F	ctgatgctggtgatgattg g
			R	agtcgcactttgccgtaatc
	L-idonate/5-ketogluconate/gluconate transporter	idnT	F	aagtgggttttgcctgctg
			R	acagagagcgctgctacc at
	outer membrane protein A	ompA	F	tgagtacgcgatcactcct g
			R	ctgaccgaaacggtagga aa
	RNA polymerase, sigma 70 (sigma D) factor	rpoD	F	ttcgtacgcaagaacgtct g
			R	aggtatcgctggtttcgttg