Table 2 Continued					
Gene ID	Predicted function	Gene	Replicate 1	Replicate 2	
METTOv1_370002	NAD-linked formate dehydrogenase, subunit D	fdsD	368	312	
METTOv1_220028	NAD-linked formate dehydrogenase, subunit A	fdhA2	9	7	
C1-ASSIMILATION:SE	RINE CYCLE				
METTOv1_130002	Phosphoenolpyruvate carboxylase	ppc2	104	89	
METTOv1_400011	Glycerate kinase	gckA	229	211	
METTOv1_400012	Conserved protein of unknown function	orf1	626	708	
METTOv1_400013	Malyl-CoA lyase/beta-methylmalyl-CoA lyase	mclA	1713	1615	
METTOv1_400014	Phosphoenolpyruvate carboxylase	ppc1	141	139	
METTOv1_400015	Malate thiokinase, small subunit	mtkB	516	485	
METTOv1_400016	Malate thiokinase, large subunit	mtkA	534	455	
METTOv1_400017	Methenyltetrahydrofolate cyclohydrolase	fch	355	281	
METTOv1_400018	NADP-dependent methylenetetrahydrofolate dehydrogenase	mtdA	281	243	
METTOv1_400019	2-Hydroxyacid dehydrogenase NAD-binding	hprA	375	348	
METTOv1_400020	Serine-glyoxylate transaminase	sga	1840	1969	
METTOv1_400021	Formate-tetrahydrofolate ligase	ftfL	448	412	
METTOv1_670019	Serine hydroxymethyltransferase	glyA	1342	1197	

eno

phaA

phaB

croR

ccr

ecm

ibd

meaC

epm

ppcA

ррсВ

mcmA

mcmB

bdhA

phaC

aad

aas

phaZ

mdh

sucC

sucD

sucA

sucB

sdhB

sdhA

sdhC

fum

ofr

pps

pcx

accD

accA

mclA2

432

597

1160

235

577

187

309

341

428

137

353

472

201

144

235

30

123

116

237

539

660

1198

236

191

327

311

318

196

79

28

145

246

211

408

561

1060

275

523

162

295

317

394

135

310

455

188

144

232

30

114

114

263

473

631

1135

237

181

348

299

329

185

77

26

140

228

204

(Continued)

METTOv1_400014	Phosphoenolpyruvate carboxylase	ppc1	141
METTOv1_400015	Malate thiokinase, small subunit	mtkB	516
METTOv1_400016	Malate thiokinase, large subunit	mtkA	534
METTOv1_400017	M ethenyltetrahydrofolate cyclohydrolase	fch	355
METTOv1_400018	NADP-dependent methylenetetrahydrofolate dehydrogenase	mtdA	281
METTOv1_400019	2-Hydroxyacid dehydrogenase NAD-binding	hprA	375

Enolase

Acetyl-CoA acetyltransferase Acetoacetyl-CoA reductase

METTOv1 20135 C1-ASSIMILATION: EMP PATHWAY AND PHB CYCLE Crotonase Crotonyl-CoA reductase

METTOv1 100079 METTOv1 100080 METTOv1 50006 METTOv1 110068 METTOv1 60013 Ethvlmalonvl-CoA mutase Methylsuccinyl-CoA dehydrogenase METTOv1 510010

Mesaconyl-CoA hydratase

METTOv1 110043

Methylmalonyl-CoA epimerase

Malyl-CoA lyase/beta-Methylmalyl-CoA lyase Acetyl/propionyl-CoA carboxylase

METTOv1 30129 METTOv1 220010 Propionyl-CoA carboxylase Methylmalonyl-CoA mutase, large subunit

METTOv1 200020 METTOv1 220035

METTOv1 50067 METTOv1 10062 Methylmalonyl-CoA mutase small subunit B 3-Hydroxybutyrate dehydrogenase Poly-beta-hydroxybutyrate polymerase

METTOv1 270063 METTOv1 130047 METTOv1 200042 Acetoacetate decarboxylase METTOv1 200022 Acetoacetyl-coenzyme A synthetase Polyhydroxyalkanoate depolymerase

METTOv1 630008 C1-ASSIMILATION:TCA CYCLE METTOv1 360040 Malate dehydrogenase METTOv1 360041 Succinyl-CoA synthetase, beta subunit

Succinyl-CoA synthetase, alpha subunit

2-Oxoglutarate dehydrogenase E1

2-Oxoglutarate dehydrogenase E2

METTOv1 510003 METTOv1 510002 METTOv1 370050

Succinate:ubiquinone oxidoreductase

METTOv1 80046

METTOv1 40061

METTOv1 70038

METTOv1 120036

METTOv1_830002

METTOv1 380021

METTOv1 1080004

Fumarate hydratase

Pyruvate carboxylase

2-Oxoacid ferredoxin oxidoreductase

Acetyl-CoA carboxylase subunit alpha

Acetyl-coenzyme A carboxylase subunit beta

Phosphoenolpyruvate synthase

METTOv1 80046 Succinate: ubiquinone oxidoreductase METTOv1 80051 Succinate: ubiquinone oxidoreductase, cytochrome b556 subunit

INTERMEDIARY METABOLISM AND ANAPLEROTIC CO₂-FIXATION