

Table S1. Oligonucleotides used in this study.

Primer name	Sequence (5'-3')	References
PE-RT-amoC-F	TATTGGGTAAAGCCGTGGAAGAGTT	This study
PE-RT-amoC-R	ATGTTGGATACTGCTTCCCCTTGAT	This study
PE-RT-EaCoMT-F	ACGACGAAGCCAATTAATAATCCAGT	This study
PE-RT-EaCoMT-R	ATAGGACTCAACTTTCCGCGAACTC	This study
PE-RT-2KPCC-F	CAGCAGAACTGATGTTGAATCGAGA	This study
PE-RT-2KPCC-R	AACTGCAGTATCACCAGGCTCGTAG	This study
PE-RT-RHPCDH-F	ATCAGTCCGCTATGGAATTACACATT	This study
PE-RT-RHPCDH-R	CTGTGCCCGCTACATCGTCGACACT	This study
PE-RT-SHPCDH-F	GTCAGCAAAGCACTTTCGAATAG	This study
PE-RT-SHPCDH-R	TATTTTCAGAAACGCTGGCAAATCTCC	This study
9F	GAGTTTGATCCTGGCTCAG	Brosius 1981 (7)
1510R	GGTTACCTTGTTACGACTT	Weisburg 1991 (41)
degenerate-amoC-F3	TGGGARGARTGGGTIGTIGAYGAYTTYGTI	This study
degenerate-amoC-R4	ICKDATRTRCRTC DATIGTCCA	This study
degenerate-amoA-F2	TGGCCIBTIMRITTYGAYRAYGGI	This study
PE-amoCR1	TGGATACTGCTTCCCCTTGATGTCTATTAATCGAAATTCATTAATG	This study
PE-amoD-F1	AARTAYGGITGYAARCAYGGIGGITGY	This study
PE-ctnD-R5	IGGIGCIADICCGAICCCIGCDAT	This study
PE-seq-F1	CTTCAAACGACTGGGCTGAGATTGTTCTAG	This study
PED-2R4	CAAGGATTTACGCGTAGGAGATAAGTTAGTAGTACATGGC	This study
PE-CoM-Nde	CTATTAATCATATGTCACAAGCTACCCCGCTCATCC	This study
PE-CoM-Bam	TAAGATCTGGATCCTTAAGCTAGCTCCGCTCGAACAAT	This study

Table S2 Putative gene products and database similarities of PE-TB08W

ORF No.	Predictive gene products	AA	Protein name and Organism (accession number)	Identity (%)
ORF1	DNA binding protein containing Methanogen/methylotroph, DcmR Sensory domain (MEDS)	243	DNA binding domain-containing protein, Xaut_4864: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409311)	31
			DNA-binding protein, excisionase family: <i>Methylomicrobium album</i> BG8 (ZP_09865456)	37
ORF2	Epoxyalkane:coenzyme M transferase (EaCoMT)	369	2-hydroxypropyl-CoM lyase, Xaut_4865: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409312)	66
			Epoxyalkane:coenzyme M transferase: <i>Haliea</i> sp. ETY-M	63
			Epoxyalkane:coenzyme M transferase: <i>Haliea</i> sp. ETY-NAG	62
			Epoxyalkane:coenzyme M transferase: <i>Rhodococcus rhodochrous</i> B-276 (AF426826)	46
			Epoxyalkane:coenzyme M transferase: <i>Mycobacterium chubuense</i> NBB4 (ACZ56343)	45
ORF3	Hypothetical protein	64	Fumarate lyase, Xaut_4866: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409313)	43
ORF4	(S)-2-Hydroxypropyl-CoM dehydrogenase (S-HPCDH)	259	S-HPCDH, Xaut_4869: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409316)	49
			S-HPCDH, Xaut_5050: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409484)	49
			S-HPCDH, Xaut_5073: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409507)	48
ORF5	Hypothetical protein	312	Hypothetical protein, Xaut_5051: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409485)	59
			Hypothetical protein, Xaut_5070: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409504)	57
			Hypothetical protein: <i>Nocardioides</i> sp. JS614 (YP_919264)	44
ORF6	Phosphosulfolactate synthase (ComA)	294	Phosphosulfolactate synthase, Xaut_4872: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409317)	54
			Phosphosulfolactate synthase, Xaut_5052: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409486)	54
			Phosphosulfolactate synthase, Xaut_5069: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409503)	54
ORF7	Fumarate lyase	510	Argininosuccinate lyase, Xaut_4873: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409318)	43
			Fumarate lyase, Xaut_5053: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409487)	44
			Argininosuccinate lyase: <i>Nocardioides</i> sp. JS614 (YP_919267.1)	35
ORF8	Fumarate lyase	451	Fumarate lyase, Xaut_4874: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409319)	47
			Fumarate lyase, Xaut_5054: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409488)	45
			Fumarate lyase: <i>Nocardioides</i> sp. JS614 (YP_919284.1)	43
ORF9	1-Aminocyclopropane-1-carboxylate deaminase (ACC)	337	ACC deaminase, Xaut_4875: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409320)	49
			ACC deaminase, Xaut_5055: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409489)	49
			ACC deaminase: <i>Mycobacterium rhodesiae</i> NBB3 (YP_005000702)	41
ORF10	2-Ketopropyl-CoM oxidoreductase/carboxylase (2-KPCC)	525	2-KPCC, Xaut_4867: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409314)	67
			2-KPCC, Xaut_5048: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409482)	67
			Putative 2-ketopropyl-CoM carboxylase: <i>Mycobacterium chubuense</i> NBB4 (ACZ56354)	53

ORF11	(R)-2-Hydroxypropyl-CoM dehydrogenase (R-HPCDH)	250	<i>R</i> -HPCDH, Xaut_4868: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409483) <i>R</i> -HPCDH, Xaut_5049: <i>Xanthobacter autotrophicus</i> Py2 (YP_001409508) Short-chain dehydrogenase/reductase SDR: <i>Nocardioides</i> sp. JS614 (YP_919273)	64 64 45
ORF12	Hypothetical protein	62	No similarity	—
ORF13	Antibiotic biosynthesis monooxygenase	116	Antibiotic biosynthesis monooxygenase: <i>Bacillus cellulosilyticus</i> DSM 2522 (YP_004095752) Antibiotic biosynthesis monooxygenase: <i>Cyanothece</i> sp. PCC 7425 (YP_002484368)	29 35
ORF14	Hypothetical protein (truncated)	49	No similarity	—
ORF15	Hypothetical protein (truncated)	44	No similarity	—
ORF16	Hypothetical protein (truncated)	53	No similarity	—
ORF17	Hypothetical protein (truncated)	47	No similarity	—
ORF18	Hypothetical protein (truncated)	66	No similarity	—
ORF19	Alkene monooxygenase β -subunit (AmoA)	342	AmoA: <i>Rhodococcus rhodochrous</i> B-276 (BAA07112) Putative propene monooxygenase beta subunit: <i>Mycobacterium chubuense</i> NBB4 (ACZ56350) PmoA: <i>Mycobacterium</i> sp. M156 (AAS19482)	43 41 41
ORF20	Alkene monooxygenase coupling/effector protein (AmoB)	100	AmoB: <i>Rhodococcus rhodochrous</i> B-276 (BAA07113) Putative propene monooxygenase coupling protein: <i>Mycobacterium chubuense</i> NBB4 (ACZ56351) PmoB: <i>Mycobacterium</i> sp. M156 (AAS19483)	60 58 60
ORF21	Alkene monooxygenase α -subunit (AmoC)	505	AmoC: <i>Rhodococcus rhodochrous</i> B-276 (BAA07114) Putative propene monooxygenase alpha subunit: <i>Mycobacterium chubuense</i> NBB4 (ACZ56352) PmoC: <i>Mycobacterium</i> sp. M156 (AAS19484)	68 67 66
ORF22	Alkene monooxygenase reductase (AmoD)	344	AmoD: <i>Rhodococcus rhodochrous</i> B-276 (BAA07115) Putative propene monooxygenase reductase: <i>Mycobacterium chubuense</i> NBB4 (ACZ56353) PmoD: <i>Mycobacterium</i> sp. M156 (AAS19485)	56 50 51
ORF23	Outer membrane protein W	253	OmpW family protein: <i>Hahella chejuensis</i> KCTC 2396 (YP_434757) OmpW family protein: <i>Vibrio splendidus</i> LGP32 (YP_002395839)	48 46
ORF24	iSSod13, transposase integrase catalytic subunit	273	iSSod13, transposase: <i>Pseudoalteromonas haloplanktis</i> ANT/505 (ZP_08411520) integrase catalytic subunit: <i>Shewanella</i> sp. MR-7 (YP_737813)	85 83