Table S1

Table S1. Oligonucleotide primers used in gap closure

Primers	Sequence (5' to 3')
contig4EF	CCAACTGGTCCCACTGATCC
contig3SR	CCCATTAAGCGCCGACGGAC
contig3EF	TCCGATTCCTGGTCCCTTTC
contig2EF	GCATCAACAAACCCAGAAGG
contig8SR	CGCCGACAACGCCGCCTACT
contig7SR	CGCAAACCCGCACAGATAAT
contig50EF	TGCGGTGGAAGTCACATTAG
contig5SR	GCTCAATCGTCACCTTCGCC
contig43EF	GCAGTATCGATGTCTTGGTG
contig18EF	CAGCGAGCAATAGCCAGGAT
contig27SR	GCTGGAATGGGCAAAGCACG
contig27EF	CGTCGTCCCGGAAGACCATA
contig47EF	CGCAGATTTTCCTCAGTACC
contig17EF	GATTGCCTTGGAGCTACCCG
contig13EF	GCTGAAAGCCTATTTTGAAG
contig26SR	CTGGAGGTATTCGGCACTAT
contig26EF	CAGATTGACAGCCATAACCT
contig24EF	TCGCTCACAACGGCAAGATT
contig42EF	TTGCCCGTAGCCGTCAGGAG
contig12EF	TTAGTGAGACATCGTCGGCG
contig34SR	GCATAGTCAGCCAACCAAGG
contig1EF	ATTCCTTTACTGAGGGCATC
contig11SR	GGTCAGGAGTTGATGCTTGC
contig23SR	CCGGCCTCGTGCGGCTCTGC
contig43SR	GAGGATGAATGACGCAACGC
contig22EF	TGCAGGGCCGTAATTTTATG
contig31EF	TCGTGGAACTCCTGGATGCG
contig22SR	ATGGATTCCTTGTCGGTCGC
contig38EF	GATTTTGACGACTTTGCCTG

contig5EF	AGATGGTCCATGAGGCGAGC
contig29EF	AACTCGCCACCGTCGTCCGC
contig44EF	GTCAACAACAACCAGCCCGT
contig18SR	CAAAGTCTCGCCGTGTTCG
contig42EF	GCTTGCCCGTAGCCGTCAGG
contig15SR	CGGACGCCCGAAGCGCTGAG
contig97EF	TTTCCAGCCATCGTTCAAGC
contig4F-sp3	GCATTTGCGGCTCCGNNNNNNNNNTAAGCC
contig4F-sp2	AATGAGGATGGAGGCAAGCT
contig4F-sp1	CAGCGACCGGATCGAAAAGG
contig30F-sp3	GCCGCTCGATCCTATNNNNNNNNNGACAGA
contig30F-sp2	CCCGGTCCTGTCGATTATGC
contig30F-sp1	TGGGGAGGGGGGAGCAAAAT
contig15EF	TGGCTACCATTTGCTGTTGC
contig15SR	CGGCTCGCCGTAGCGGTTAA
contig18SR	AGGCGACCTGGAACATCACG
contig18EF	GCAAACCACGGCAGCGAGCA
contig41SR	CTCGCAACCGTCGATATAGG
contig32SR	ACACCACGCCAAAGGTTCTC
contig21SR	GCTTCAAACCCTCGCTTCCG
contig163EF	GCCAGTCCCACCAACTTTTC
contig127EF	CCGTCCAATCTCCGCCAAGC
contig127SR	CAACCACCATTTCGCAGCAG
contig44EF	CAACAACCAGCCCGTTCCCG
contig21EF	CGGGGTTTGGTCCGGATCAC
contig41SR	TCGCAACCGTCGATATAGGC
contig35EF	ACGCGAACAGATCCGCAAAC
contig10EF	GCCCGCAAGGCGTTCACTGT
contig39SR	AGGTTCGCAGCAAAATAATG
contig10SR	GCACCCGTTTTTGAAATCCT
contig128EF	GATGCTGGAGCGGGATTACC
contig421EF	GCCAAAATCGCAGCTTCGGG
contig17SR	TGGACGACGAGTGATGCCCG
contig47EF-sp3	GTACCCAGGACGGATNNNNNNNNNCGATCA

contig47EF-sp2	GATGGACCGCCCAGGATTAC
contig47EF-sp1	GGGGAGGAGGTCTTTATCTT
contig22SR-sp3	AGCGCCAGCTCAAAGNNNNNNNNCCCTGT
contig22SR-sp2	CCAGCCACTCGTTGACCCAT
contig22SR-sp1	GCTTGTCAAACAGACTCATG
contig11SR-sp3	CAGGAGTTGATGCTTNNNNNNNNNCATGCC
contig11SR-sp2	ACTGATTCCGTCGCTCCCGT
contig11SR-sp1	ATTGCTCCCCTGTCCTGTAT
contig12SR	TGGACGGCCCCATCGTTTTC
contig31SR	ACTATTTACCCGGACCACCC
contig6SR	CCAGCATCCAGAGCACCGAG
contig6EF	ACCGACCAGGAAGGGCAAGG
contig17SR-sp3	TTTCGTTCAATGGAGNNNNNNNNAAAGGG
contig17SR-sp2	GAAACCATTCGGGGTCGCAT
contig17SR-sp1	CGAAACGCAAGGTGGTGGGC
contig5SR-sp3	AATCGTCACCTTCGCNNNNNNNNNTATTGG
contig5SR-sp2	TTGGTGTGTGGTGGCTGGGC
contig5SR-sp1	GTTCCGTTTCACAACAGCCT
contig5EF-sp3	CTTTGGCCGATATTCNNNNNNNNNGAACAT
contig5EF-sp2	AGCGACTTCTGGAAACTGCC
contig5EF-sp1	ACGCGCAGGGCCTCAACATG
contig70EF	TCATCTCGTCGGTCTCCTGT
contig6EF	ACCGACCAGGAAGGGCAAGG
contig53EF	CGATGCCCGTCACCCCGAAG
contig25E-sp3	CCTGAAACAGACGGGNNNNNNNNGGCCGT
contig25E-sp2	TCGCGACCTGCGCCTGATAG
contig25E-sp1	TTGACGAGTTCGCCATAGCG
contig51SR	GACGCTCGCGACCGACCTCCT
contig7EF	CAGAGCCAGCCGCTTTCGCAC
contig29SR	ACGGACAAGCGGCACTGCAAC
contig38SR	CCGGTGACGACGATCGACTTG
contig1SR	CGACTATCAGGATGAGAACAG
contig97SR	AGGCAACAGCCCGTCACTCAG
contig2SR	CGGTACGCTGGCGGATATTCT

contig8EF	CGAACGCCTGCTCCGCCTTTG
contig128SR	TGACGGAACCACCCTTTTGT
contig14EF	GATTGATTTTGGACGGCTTG
contig44SR	TCAATCCTTATGGCCGCTTC
contig39EF	AATGCGAAGGAGTGTTGGGC
contig32EF	CCACGATGTGCGGCTGATGC
contig51EF	GGGTCACCGCCTCGCAGATG
contig20F-sp3	TCCCAGTCGAGCAAGNNNNNNNNCGGCCC
contig20F-sp2	CAGCCCCCCTAGCAGGAACG
contig20F-sp1	ATGTAGCTGTTAAATATATC
contig20R-sp3	CGACAAGCCAGCGATNNNNNNNNCCAACA
contig20R-sp2	CCCACCATACCATATCTAGT
contig20R-sp1	TTCAATCGCCGCTTCTACCC
contig18F-sp3	GTGTTCGGACAGGCGNNNNNNNNATCACG
contig18F-sp2	TGCCCACGCTTCCGCCGGTT
contig18F-sp1	AAGAATACTATCGATTGGGT
contig18R-sp3	TCGCAAACCACGGCANNNNNNNNAGCCAG
contig18R-sp2	AACGAGATTAGGGAGGGTGA
contig18R-sp1	GAGGAGGAATTGGCTTCCTC

Note："S" represents the 5' sequence of the contigs, "E" represents the 3' sequence of the contigs, "F" represents the forward primer, "R" represents the reverse primer, and "sp1-sp3" represents the SEFA-PCR primer.

Table S2

Table S2. Results of the peptide mass of fingerprint analysis.

| Spot no.	Homologous protein	% Identity	Source (GenBank accession no.)	Position	Peptide	Molecular weight
A	3-hydroxy-2-methylbutyryl-CoA dehydrogenase	100	*Sphingomonas* sp. DC-6 (WP_030092748)	pMEA02 9382-10158	R.IAAFDLSAER.L	1091.56
					K.IAIVTGAGSGLGR.S	1170.67
					K.AGVMGLTLPVAR.D	1183.67
B	acyl-CoA dehydrogenase	99	*Sphingomonas* sp. DC-6 (WP_030092751)	pMEA02 12713-13861	R.VPVENVVGAVGCGYR.D	1574.78
					R.EAYGKPIIELQGVAFK.L	1761.96
					R.VCSEALQVHGGAGYTR.D	1703.80
C	pigment production hydroxylase	39	*Rhodococcus opacus* (WP_012691790)	pMEA02 45926-47104	R.VHGSLDLETGSQALGR.V	1638.83
					R.VAAITDFCANGVNEMK.G	1837.87
	hypothetical protein (HP1)	99	*Sphingomonas* sp. DC-6 (WP_030092907)		K.ALTDSALADDMLR.N	1390.67
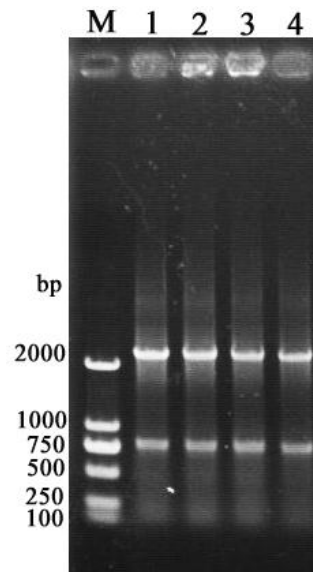
Fig.   S1

Fig. S1 Agarose gel electrophoresis of the ERIC-PCR patterns of strains MEA3-1 and

MEA3-1Mut. M, DL2000 marker; lanes 1 and 2. ERIC-PCR of strain MEA3-1; lane 3

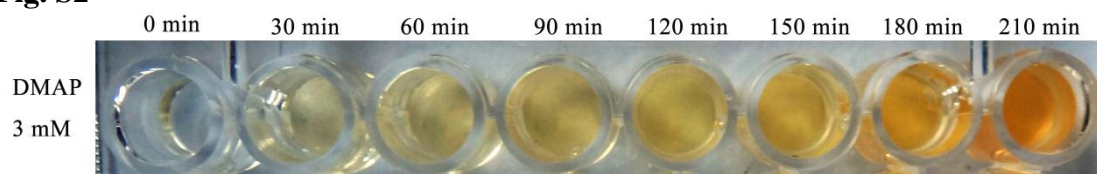and 4. ERIC-PCR of strain MEA3-1Mut.

Fig. S2

Fig. S2 Spontaneous ammonia release of the 4-OH-DMA in the water measured using the Nessler's reagent colorimetric method.
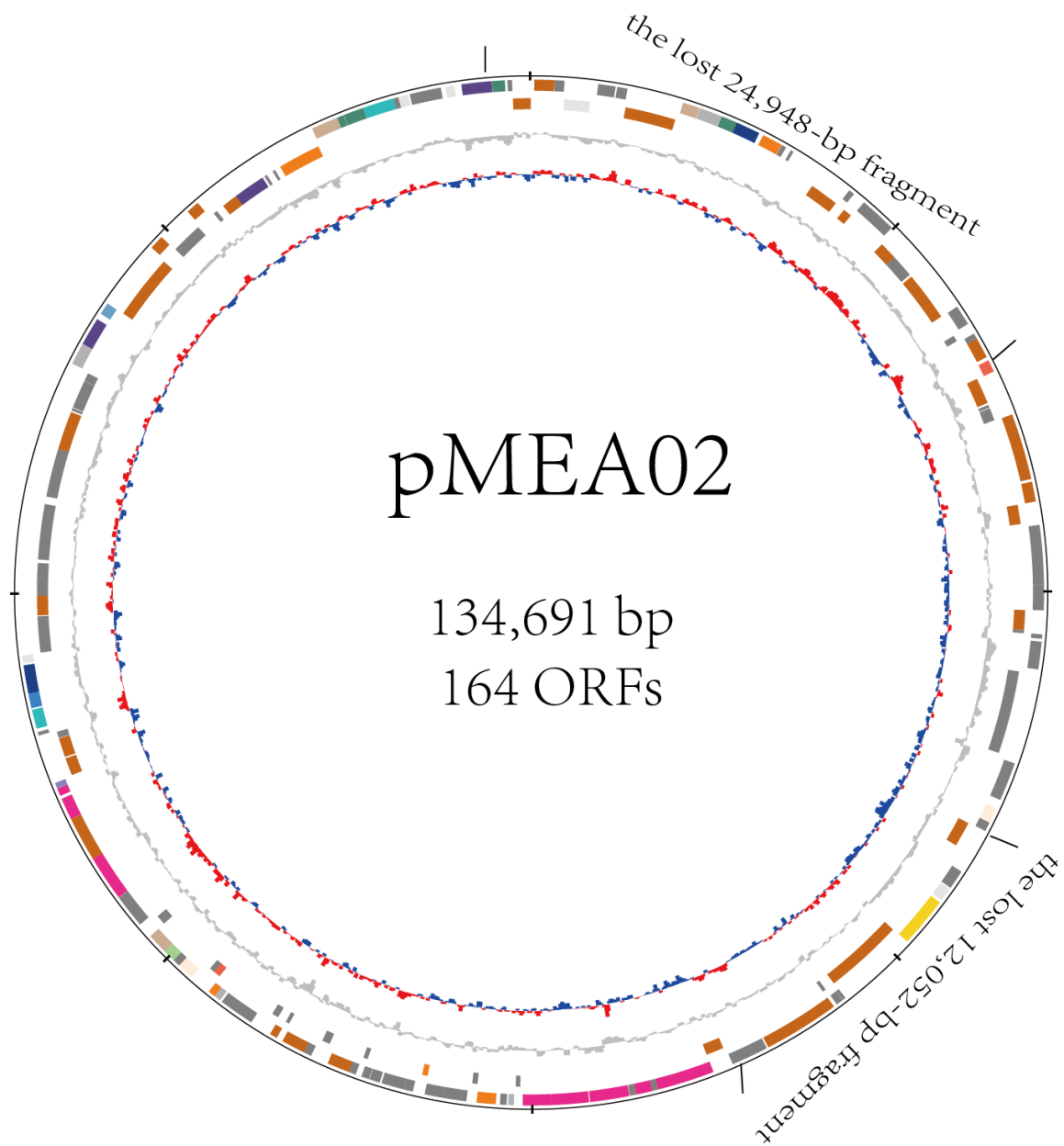
Fig. S3

Fig. S3 Physical map of the circular plasmid pMEA02 from strain MEA3-1. The two lost fragments are indicated in the map. The CDSs outside of the first circle are transcribed in the clockwise direction and those inside of the first circle in the counterclockwise direction, The coding regions on the plus strand are colored by functional category as follows: DNA replication, recombination and repair (dark orange3); transcription (dark orange1); cell division and chromosome partitioning

(antique white); intracellular trafficking and secretion (deep pink); energy production and conversion (royal blue); amino acid transport and metabolism (Dodger blue); lipid metabolism (cyan); inorganic ion transport and metabolism (medium purple); secondary metabolite biosynthesis, transport and catabolism (aquamarine); general function prediction (dark gray); function unknown (middle gray); and no COG (light gray). Moving toward the center, the second circle shows G+C content. The points on the outside indicate that the average GC contents of these regions are higher than that of pMEA02. The third circle shows G+C skew(G-C/G+C) in red (G+C skew > 0) and blue (G+C skew < 0).
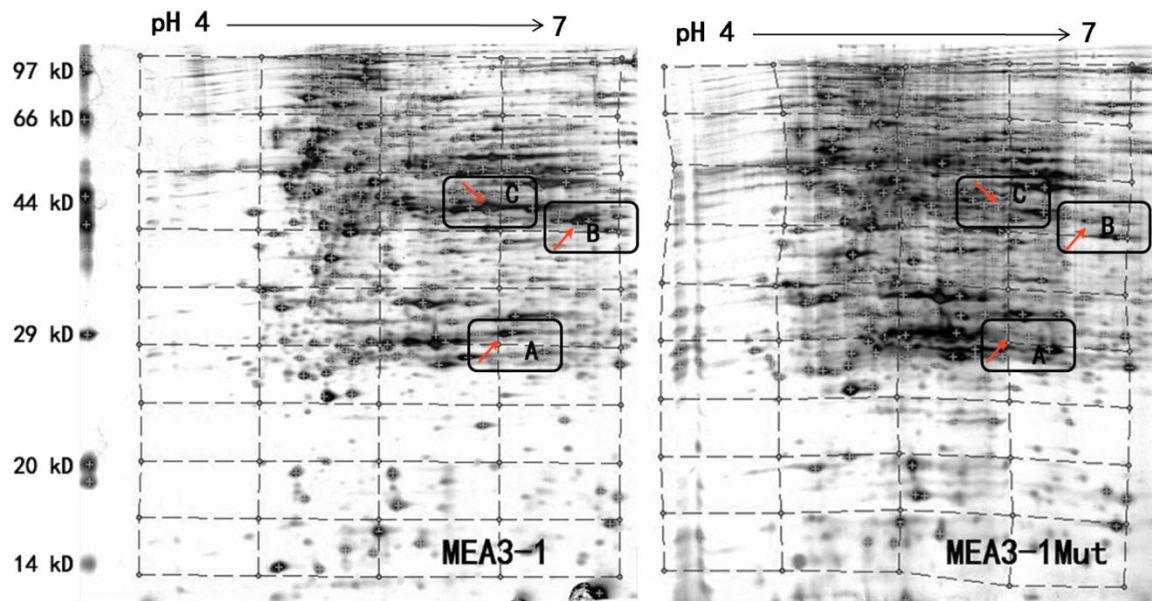
Fig. S4

Fig. S4 Representative 2-DE protein maps of strains MEA3-1 and MEA3-1Mut. The total protein of MEA3-1 is located on the left; the total protein of MEA3-1Mut is located on the right. Points A, B, and C were significantly different proteins between strains MEA3-1 and MEA3-1Mut.

Fig. S5

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HsaA      LQPEQWGGYQADPVLFYSAVRKIASACGSTGWVSSIIGVHNWHLALFSQQAQEDVWGNDTDVRISSSYAPMGAGQVVDGG    120
C2-hpah   FQPKVYGGLEMSLPDFANCIVTLAGACAGTAWAFSLLCTHSHQIAMFSKQLQDEIWLKDPDATASSSIAPFGKVEEVEGG    160
MeaA      FVPKIYGGYEMAPDVMAEVVKEISPYSTSAAWVLAFYIGHNFLHALFPKQSQDEVFAPRGFSLTPGTSAPGYKLTPVEGG    134
NcnH      FVPVRWGGADGTFADLLAAVARVGEGCTSAAWVAALAATVPRMAAHLPRQGQAEVWSDGPDTLLVGALMPLGRAERAAGG    154
                *    **            :  :    : : *  :          *         ::              *        **

HsaA      YTVNGAWAWSSGCDHASWAVLGGPVIKDGRPVDFVSFLIPREDYRIDDVWNVVGLRGTGSNTVVVEDVFVPTHRVLSFKA    200
C2-hpah   IILNGDYGWSSGCDHAEYAIVGFNRFDADGNKIYSFGVIPRSDYEIVDNWYAQAIKSSGSKMLKLVNVFIPEYRISKAKD    240
MeaA      YIVKGKSSWNSGSSRAEWYMNGG.MVENAEKPELILFMAPASDVQVIGNWDVAGMRATSSCDIAIDGAFVPHHQCVPAVD    213
NcnH      WRLTGTWSYVSGVDFSDWALVCARTAEDG.VEVPRYFALPREAYAIRDTWFTVGMRGTGSNTLSVDDVYVPDHRVCTRAA    233
                *   : :  **                              :    *      ::   *   : :     ::*  ::

HsaA      MSNLTAPGLERN.TAPVYKMPWGTIHPTTISAPIVGMAYGAYDAHVEHQGKRVRAAFAGEKAKDDPFAKVRIAEASSDID    279
C2-hpah   MMEGKSAGFGLYPDSKIFYTPYRPYFASGFSAVSLGIAERMIEAFKEKQRNRVR.AYTGANVGLATPALMRIAESTHQVA    319
MeaA      MLEGRSPGAKLH.ANPIYSLPMVPLLQCEVLPCVVGAFQGAVREFQKLTQQRVQ.SHTSEKAAEKQSAQIRLGKALTDSA    291
NcnH      VLDGDCPDAPAD....CTRVPLKAVNGLSFAAPVLGAAKGLLAEWTRWAAPRIT....GTGDGDPRLAENALRHGVLARA    305
            :                     *              :*             *:                :          :

HsaA      AAWRQLSGNVADEYALLVAGEEVPFELRLRARRDQVRATGRAISSIDKLFESSGATALANGTPLQRFWRDAHAGRVHAAN    359
C2-hpah   AARALLEKTWEDHRIHGLNHQYPNKETLAFWRTNQAYAVKMCIEAVDRLMAAAGATSFMDNSELQRLFRDAHMTGAHAYT    399
MeaA      LADDMLR.NYLDLVLNMDREEIKTVEARAAIRARVAAITDFCANGVNEVMKGSSASVFRNDSPLQRIFRDINMLRVHGSL    370
NcnH      AGEVDGAELLLDRTARAADTGALDPLLTARGGRDCALAAELLLTAADRLFRAAGTSAQVEGSPFERGWRDVSAAVSHLVL    385
            ::                      : :            : ::       ::     : ::* ** *    *
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Fig. S5 Multiple sequence alignment of the MeaA amino acid sequence and related protein sequences.
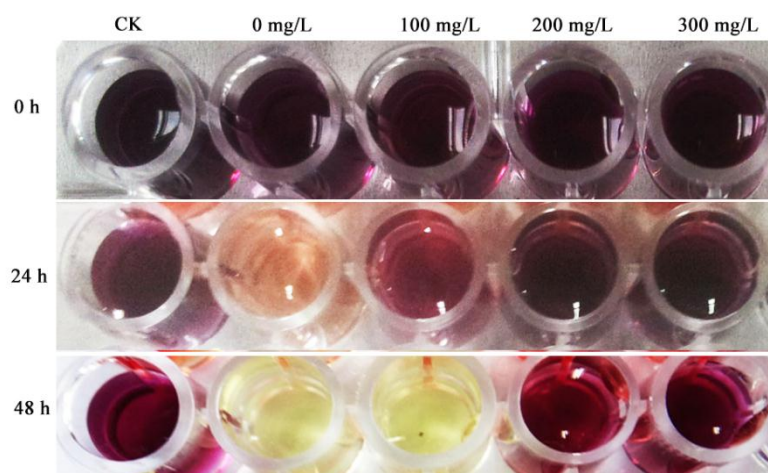
Fig. S6

Fig. S6 Effect of different concentrations of the cytochrome P450 inhibitor metapyrone on the degradation of MEA.