

Supporting information

High-fidelity *de novo* synthesis of pathways using microchip-synthesized oligonucleotides and general molecular biology equipment

Wan Wen², Lu Min¹, Wang Dongmei¹, Gao Xiaolian^{1,3}, Hong Jiong^{1*}

¹School of Life Sciences, University of Science and Technology of China, Hefei, Anhui 230027, China

²The Key Laboratory of Biotechnology for Medicinal Plant of Jiangsu Province, Jiangsu Normal University, Xuzhou, Jiangsu, 221116, China

³Department of Biology and Biochemistry, University of Houston, Houston, TX77004-5001, USA

Correspondence: hjiong@ustc.edu.cn

	Name	Page
Supplementary Table S1	Primers and RBS sequences used in this study	3-5
Supplementary Table S2	Primers used in lycopene gene synthesis	6
Supplementary Table S3	Summary of oligonucleotides design of lycopene biosynthesis genes	7
Supplementary Table S4	Primers used in the construction of strain WW1	8
Supplementary Figure S1	Design of oligonucleotides of lycopene pathway genes for synthesis on microchips (<i>mvaS</i> oligonucleotides are described as an example).	9
Supplementary Figure S2	Schematic representation of the construction of the WW1 strain harboring the genes of the lycopene biosynthetic pathway	10
Supplementary Figure S3	Production of lycopene via the engineered lycopene biosynthesis pathway	11
Supplementary Methods	Construction of <i>dxr</i> -deleted <i>Escherichia coli</i> WW1 and expression of the synthetic lycopene pathway	12
Supplementary Methods	PCR amplification of oligos	13
Supplementary Methods	PCR amplification of error-depleted fragments	13
Supplementary Methods	Gibson assemble of operons	14
Supplementary Methods	PCR amplification of full-length operons	14
Supplementary data		15-48
Supplementary Reference		49

Supplementary Tables:

Supplementary Table S1 Primers and RBS sequences used in this study.

Primers ID	Sequence ^a
MlyI_1F	CACAGGAGTCCTCAC
MlyI_2F	CCAAGGAGTCGCTAG
MlyI-3F	CAGAGGAGTCCTGAG
MlyI-4F	CCTACGAGTCGCAAC
MlyI-5F	CATTGAGTCGTCTG
MlyI-6F	CGTACGAGTCCTTC
MlyI-7F	CTGTCGAGTCGTAT
MlyI-8F	GGTACGAGTCCGATC
MlyI-9F	CTTACGAGTCGTCTC
MlyI-10F	GGATCGAGTCTCTAC
MlyI-11F	GTGTGGAGTCATATG
MlyI-12F	GGATCGAGTCAATTC
MlyI-13F	CGTTCGAGTCATCCA
MlyI-14F	GCATGGAGTCGGATG
xMlyI_1F	GTATAGAGTCAGTCG
xMlyI-2F	GTCACGAGTCATGGC
xMlyI-3F	GATAAGAGTCTCAGC
xMlyI-4F	GAGTGGAGTCTACCG
Fra-F	ACGCTCTGAAGACCC
Fra-R	CGAGATAGAAGACAG
mvaE-F	ATGAAAACCGTTGTTATCATCGACG
mvaE-2-R	TTGAAAACCGTTTTTCAGGGT
mvaE-3-F	GGGCACCCTGAAAACCGTTT
mvaE-4-R	CAGATAGTCGGTTTCGTCA
mvaE-5-F	GACCGTTGACGAAACCGAC
mvaE-5-R	ACAACGCCTTCCAGCATCG
mvaE-6-F	GCGATGCTGGAAGGCGTTG
mvaE-6-R	GTTCGCCGTCCAGGGTCC
mvaE-7-F	TGGACCCTGGACGGCGAAC
mvaE-R	TTACTGTTTACGCAGGTCGTTT
mvaS-F	ATGACCATTGGCATTGATAAAATCTCT
mvaS-2-R	ACGGGTGGCCGGTCGGA
mvaS-3-R	GCAGAGAAATCAGGCCAG
mvaS-R	TTAGTTACGGTAAGAACGAACGGTGT
MvaK1-F	ATGAATATCAAGAAGCAAGGTCTGG
MvaK1-2-R	TAGTCTCCGCGATGGCGGT
MvaK1-3-F	ACCGCCATCGCGGAGACTAT
MvaK1-R	TTACTTCTTAACCTCCAGGGACT
MvaK2-F	ATGATCGAAGTTACCAACCCCG
MvaK2-2-F	GCAAATACGGTCTGGGTTC
MvaK2-2-R	TTTTTCTTCTTAGACTGGTG
MvaK2-R	TTAGCATTCTTCTGGCCGTAGG

mvaD-F	ATGCTGTCTGGTAAAGCGCGT
MvaD-2-R	GCTTCGTGAACCTGAGAC
MvaD-2-F	CTCTGCGTCTGGCCTGGCTG
MvaD-R	TTATTTGTCCATACCTTTGGTTTCGA
idi-F	ATGAACCGCAAAGATGAACACCTG
idi-1-R	CGAAGATCAGACCGTCCG
idi-2-F	AAACCCGGACGGTCTGATC
idi-2-R	GGCCCCAGTCGTCCAGG
idi-3-F	TTTCCTGGACGACTGGGGCCA
idi-R	TTAGCGTTTCGCGAAAACGGTAG
lspA-F	ATGGATTTCCCGCAGCAGCTG
lspA-2-R	CTTTGTCGCCCCGACAGACAG
lspA-R	TTATTTGTTACGCTGAATGATATAATCC
crtE-F	ATGACCGTTTGTGCGAAAAAACAC
crtE-2-F	GATATGCCGTGCATGGACG
crtE-2-R	TAGACGCCATCTGCATAGACG
crtE-R	TTAAGAAACCGCCGCCAGTTTTTTAT
crtB-F	ATGGAAGTCGGTTCCAAGTCC
crtB-2-F	CCGGCCTACGCATTTGACC
crtB-R	TTAAACCGGACGCTGCCACAG
crtI-F	ATGAACCGTACGACCGTAATTGG
crtI-2-F	GTGATGTAGAGGGCTATCGC
crtI-2-R	GGCGAGCTACAGACGCGTTC
crtI-3-F	TGAACGCGTCTGTAGCTCG
crtI-3-R	AGCTGCCGACGCCCTCAG
crtI-R	TTAGGCCAGGTCTCCAGCAT
T7F-H-F	ACCCAAGCTTGATCTCGATCCCGCGAAATTA
mS-X-R	ACTGTTCTCGAGTTAGTTACGGTAAGAACGAACGGTGT
mk1-N-F	CTAGCTAGCATGAATATCAAGAAGCAAGGTCTGG
ii-H-R	ACTGTTAAGCTTTTAGCGTTTCGCGAAAACGGTAG
iA-N-F	CTAGCTAGCATGGATTTCCCGCAGCAGCTG
T7T-H-R	ACCCAAGCTTGCGGCCGCACTCGAGCACCACCACCACCAC
RBS1 ^b	ACGACCTGCGTAAACAGTAAGGAGGATATTTAGATGACCATTGGCATTGATAAAA (5'-3') TGCTGGACGCATTTGTCATTCTCTATAAATCTACTGGTAACCGTAACCTATTTT (3'-5')
RBS2 ^b	CCCTGGAGGTTAAGAAGTAAAAAGAGGAGAGAAATACTAGATGCTGTCTGGTAAAGCG (5'-3') GGGACCTCCAATTCTTCATTTTTCTCTCTTTATGATCTACGACAGACCATTTCGC (3'-5')
RBS3 ^b	AACCAAAGGTATGGACAAATAAGGAGAAGCATGATCGAAGTTACCACCC (5'-3') TTGGTTTCCATACCTGTTTATTCCTCTTCGTACTAGCTTCAATGGTGGG (3'-5')
RBS4 ^b	ACGGCCAGAAAGAATGCTAAGGAGAAGCATGAACCGCAAAGATGAACAC (5'-3') TGCCGGTCTTTCTTACGATTCTCTTCGTACTTGGCGTTTCTACTTGTG (3'-5')
RBS5 ^b	TATATCATTCAGCGTAACAAATAAGGAGGATATTTAGATGACCGTTTGTGCGAAAAA (5'-3') ATATAGTAAGTCGCATTGTTTATTCCTCTATAAATCTACTGGCAAACACGCTTTTT (3'-5')

RBS6 ^b	CTGGAGGACCTGGCCTAAGGAGGATATTTAGATGGAAGTCGGTTCCAAGTC (5'-3') GACCTCCTGGACCGGATTCTCCTATAAATCTACCTTCAGCCAAGGTTTCTAG (3'-5')
RBS7 ^b	CTGGCGGCGGTTTCTTAAGGAGGATATTTAGATGAACCGTACGACCGTAAT (5'-3') GACCGCCGCCAAAGAATTCCTCCTATAAATCTACTTGGCATGCTGGCATTG (3'-5')

^a Underline: the restriction enzyme site

^b These RBS sequences were dsDNA, and prepared by annealing of the two complementary single strand oligos.

Supplementary Table S2 Primers used in lycopene gene synthesis.

Subpool (pool) Name	Oligos primer (5'→3')		Fragments primer_1 ^a (5'→3')		Fragments primer_2 ^b (5'→3')	
	forward	reverse	forward	reverse	forward	reverse
mvaE-1	Mlyl_1F	Mlyl-3F	mvaE-F	Fra-R		
mvaE-2	Mlyl_1F	Mlyl-4F	Fra-F	mvaE-2-R		
mvaE-3	Mlyl_1F	Mlyl-5F	mvaE-3-F	Fra-R		
mvaE-4	Mlyl_1F	Mlyl-6F	Fra-F	mvaE-4-R		
mvaE-5	Mlyl_1F	Mlyl-7F	mvaE-5-F	Fra-R	mvaE-5-F	mvaE-5-R
mvaE-6	Mlyl_1F	Mlyl-8F	Fra-F	mvaE-6-R	mvaE-6-F	mvaE-6-R
mvaE-7	Mlyl_1F	Mlyl-9F	Fra-F	mvaE-R	MvaE-7-F	mvaE-R
mvaS-1	XMlyl_1F	Mlyl-3F	mvaS-F	Fra-R		
mvaS-2	XMlyl_1F	Mlyl-4F	Fra-F	mvaS-2-R		
mvaS-3	XMlyl_1F	Mlyl-5F	Fra-F	mvaS-3-R		
mvaS-4	XMlyl_1F	Mlyl-6F	Fra-F	mvaS-R		
mvaK1-1	Mlyl_2F	Mlyl-3F	MvaK1-F	Fra-R		
mvaK1-2	Mlyl_2F	Mlyl-4F	Fra-F	MvaK1-2-R		
mvaK1-3	Mlyl_2F	Mlyl-5F	Fra-F	MvaK1-R	MvaK1-3-F	MvaK1-R
mvaK2-1	XMlyl_2F	Mlyl-10F	MvaK2-F	Fra-R		
mvaK2-2	XMlyl_2F	Mlyl-11F	MvaK2-2-F	Fra-R	MvaK2-2-F	MvaK2-2-R
mvaK2-3	XMlyl_2F	Mlyl-12F	Fra-F	MvaK2-R		
mvaD-1	XMlyl-3F	Mlyl-10F	mvaD-F	Fra-R		
mvaD-2	XMlyl-3F	Mlyl-11F	Fra-F	MvaD-2-R	MvaD-2-F	MvaD-2-R
mvaD-3	XMlyl-3F	Mlyl-12F	Fra-F	MvaD-R		
idi-1	XMlyl-4F	Mlyl-12F	idi-F	Fra-R	idi-F	idi-1-R
idi-2	XMlyl-4F	Mlyl-13F	idi-2-F	Fra-R	idi-2-F	idi-2-R
idi-3	XMlyl-4F	Mlyl-14F	Fra-F	idi-R	idi-3-F	idi-R
ispA-1	XMlyl_1F	Mlyl-10F	IspA-F	Fra-R		
ispA-2	XMlyl_1F	Mlyl-11F	Fra-F	IspA-2-R		
ispA-3	XMlyl_1F	Mlyl-12F	Fra-F	IspA-R		
crtE-1	Mlyl_1F	Mlyl-10F	crtE-F	Fra-R		
crtE-2	Mlyl_1F	Mlyl-11F	Fra-F	CrtE-2-R	CrtE-2-F	CrtE-2-R
crtE-3	Mlyl_1F	Mlyl-12F	Fra-F	CrtE-R		
crtB-1	XMlyl_1F	Mlyl-7F	crtB-F	Fra-R		
crtB-2	XMlyl_1F	Mlyl-9F	crtB-2-F	Fra-R		
crtB-3	XMlyl_1F	Mlyl-8F	Fra-F	crtB-R		
crtl-1	Mlyl_2F	Mlyl-6F	crtl-F	Fra-R		
crtl-2	Mlyl_2F	Mlyl-7F	Fra-F	crtl-2-R	crtl-2-F	crtl-2-R
crtl-3	Mlyl_2F	Mlyl-8F	Fra-F	crtl-3-R	crtl-3-F	crtl-3-R
crtl-4	Mlyl_2F	Mlyl-10F	Fra-F	crtl-R		

The sequences of primers were listed in Supplementary Table S1.

^a half-specific primer pair with one specific fragment primer and one F-primer.

^b full-specific primer pair with two specific fragment primers.

Supplementary table S3 Summary of oligonucleotides design of lycopene biosynthesis genes.

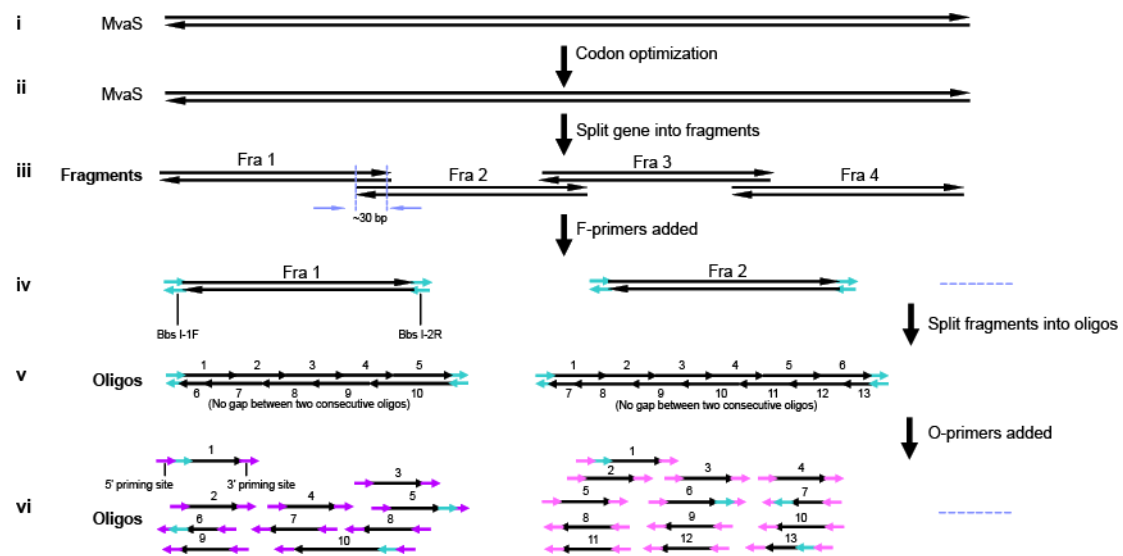
Gene (length: bp)	Fragments (length: bp)	Oligos subpool (length: nt; oligos)
crtB (891)	crtB-F1 (328)	crtB_1 (71-101; 13)
	crtB-F2 (349)	crtB_2 (71-100; 13)
	crtB-F3 (348)	crtB_3 (70-93; 15)
crtE (909)	crtE-F1 (334)	crtE_1 (72-102; 13)
	crtE-F2 (355)	crtE_2 (69-101; 14)
	crtE-F3 (355)	crtE_3 (73-103; 13)
crtI (1479)	crtI-F1 (400)	crtI_1 (72-102; 14)
	crtI-F2 (423)	crtI_2 (72-106; 15)
	crtI-F3 (420)	crtI_3 (65-102; 15)
	crtI-F4 (419)	crtI_4 (70-100; 15)
idi (1044)	idi-F1 (279)	idi_1 (76-113; 13)
	idi-F2 (401)	idi_2 (71-103; 14)
	idi-F3 (397)	idi_3 (72-107; 13)
ispA (900)	ispA-F1 (331)	ispA_1 (65-96; 13)
	ispA-F2 (348)	ispA_2 (66-99; 13)
	ispA-F3 (349)	ispA_3 (69-113; 12)
mvaD (996)	mvaD-F1 (363)	mvaD_1 (66-99; 13)
	mvaD-F2 (381)	mvaD_2 (68-115; 13)
	mvaD-F3 (389)	mvaD_3 (75-115; 13)
mvaE (2412)	mvaE-F1 (375)	mvaE_1 (76-103; 13)
	mvaE-F2 (399)	mvaE_2 (80-119; 13)
	mvaE-F3 (398)	mvaE_3 (72-104; 14)
	mvaE-F4 (397)	mvaE_4 (72-108; 13)
	mvaE-F5 (399)	mvaE_5 (71-104; 14)
	mvaE-F6 (394)	mvaE_6 (71-113; 13)
	mvaE-F7 (396)	mvaE_7 (67-98; 16)
mvaK1 (945)	mvaK1-F1 (346)	mvaK1_1 (71-109; 12)
	mvaK1-F2 (368)	mvaK1_2 (68-105; 13)
	mvaK1-F3 (363)	mvaK1_3 (71-101; 14)
mvaK2 (1083)	mvaK2-F1 (392)	mvaK2_1 (73-116; 13)
	mvaK2-F2 (416)	mvaK2_2 (73-106; 16)
	mvaK2-F3 (419)	mvaK2_3 (77-111; 14)
mvaS (1152)	mvaS-F1 (319)	mvaS_1 (71-113; 10)
	mvaS-F2 (341)	mvaS_2 (64-99; 13)
	mvaS-F3 (334)	mvaS_3 (68-109; 11)
	mvaS-F4 (340)	mvaS_4 (77-124; 11)

Supplementary Table S4 Primers used in the strain WW1 construction.

Primers ID	Sequence ^a
dxr-N-F	CTAGCTAGCATGAAGCAACTCACCATTCTGG
dxr-X-R	CCGCTCGAGTCAGCTTGCAGACGCATCAC
Tc-A-F	ACTTGGCGCGCCCGATATAAGTTGTAATTCTC
Tc-S-R	TTGGACTAGTTCAGGTCGAGGTGGCC
Pet21c-A-F	CACTTGGCGCGCCACATTTCCCGAAAAGTGCCAC
Pet21c-S-R	TTGGACTAGTCTGTCAGACCAAGTTTACTC

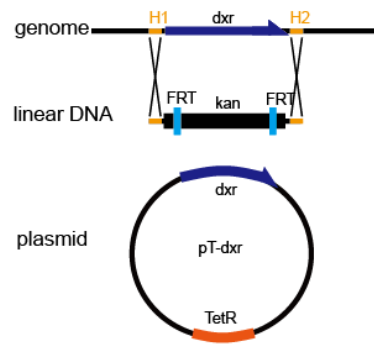
^a Underline: the restriction enzyme site

Supplementary Figures:

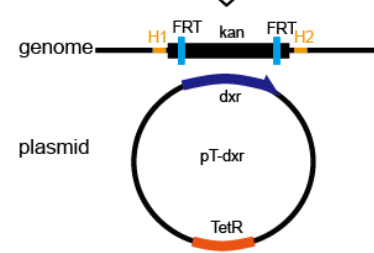


Supplementary Figure S1. Design of oligonucleotides of lycopene biosynthetic pathway genes for synthesis on microchips (*mvaS* oligonucleotides are described as an example).

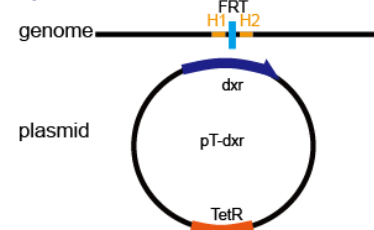
a. Homologous recombination using Red system



b. Select kan-resistant transformants



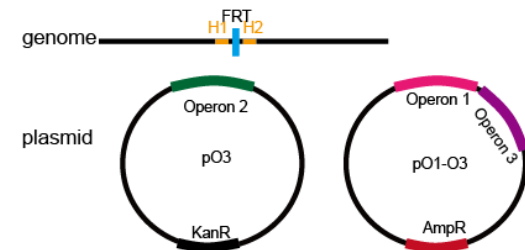
c. Eliminate kan-resistant cassette using a FLP expression plasmids



d. Transform plasmids of the lycopene pathway



e. Eliminate Tet-resistant plasmid on plates without Tet



Strain WW1 containing constructed lycopene pathway

Supplementary Figure S2. Schematic representation of the construction of the WW1 strain harboring the genes of the lycopene biosynthetic pathway.

1**2**

Supplementary Figure S3. Production of lycopene via the synthesized lycopene biosynthetic pathway. 1: JM109 (DE3) harboring pET-21c and pET-28a; 2: strain WW1 harboring pET-O1-O3 and pET-O2.

Supplementary Methods

Construction of *dxr*-deleted *Escherichia coli* WW1 and expression of the synthetic lycopene pathway

The strategy to construct the WW1 strain is illustrated in Supplementary Figure S6. Because *Dxr*-disrupted *E. coli* cannot grow without 2-C-methyl-D-erythritol (1), a copy of *dxr* in the pT-*dxr* plasmid was used to complement the deletion during the deficient strain construction. In brief, the Tc^R gene sequence was PCR-amplified from pACYC184 with Tc-A-F and Tc-S-R primers (Supplementary Table S4) and the pET21c DNA fragment without the *bla* coding sequence was obtained by PCR using the pET21C-A-F and pET21C-S-R primers (Supplementary Table S4). These sequences were double-digested with *Aspl* and *SpeI* and ligated with T4 DNA ligase to generate the plasmid pT-21c. The ORF of *dxr* was amplified from the genome of *E. coli* with the *dxr*-N-F and *dxr*-X-R primers (Supplementary Table S4) and cloned into pT-21c *NheI*-*XhoI* sites to generate the plasmid pT-*dxr*. pT-*dxr* was transformed into *E. coli* JM109 (DE3). Then the chromosomal *dxr* gene sequence was deleted based on the Red system (Supplementary Figure S6) as previously described (2). The *dxr* gene in pT-*dxr* was under the control of the T7 promoter and leaking expression of this gene was sufficient to support growth. After eliminating the chromosomal *dxr* gene sequence, plasmids pO1-O3 and pO2 were transformed into the constructed strain and transformants were screened on LB medium containing 100 µg/mL ampicillin and 50 µg/mL kanamycin (without tetracycline). Because operon 1 and operon 2 could complement the deficiency of the MEP pathway (blocked in the *dxr* mutant) with the MVA pathway, the pT-*dxr*-deleted strain could be screened on the medium without tetracycline and confirmed with the loss of Tet^R. The resultant strain harboring the lycopene pathway genes is *dxr* deficient and named WW1.

PCR amplification of oligos

PCR of 50 μ L contained 1 ng of template oligos, 100 pmol of primers, 5 μ L of 2 mM dNTPs, 3 μ L of 25 mM MgSO₄, and 1 μ L of KOD plus DNA polymerase in 1 $\times$ reaction buffer. PCR parameters were set as follows: 94°C for 5 min, 30 cycles of 15 s at 94°C, 30 s at 50°C, 30 s at 68°C, and a final extension step of 10 min at 68°C. Amplified oligos were purified with the UNIQ-10 oligonucleotide kit (Sangon Biotech Co. (Shanghai, China)) according to the manufacturer's instructions.

PCR amplification of error-depleted fragments

The 50 μ L-PCR mixture contained 5 μ L of 10 $\times$ reaction buffer, 1 μ L of 10 mM dNTPs, 2 μ L of Pfu DNA polymerase (Biocolor BioScience & Technology Company, Shanghai, China), 1 μ L of eluted fraction, and 2 μ L of primer mixture (10 μ M). PCR parameters were: 94°C for 30 sec, 50°C for 30 sec, and 72°C for 30 sec for 30 cycles, followed by 72°C for 5 min. The PCR mixture was isolated on 3% (w/v) agarose gels and extracted with the Axygen gel extraction kit (TaKaRa Biotechnology (Dalian) Co. Ltd, Dalian, China) according to the manufacturer's instructions. Products were digested with the type IIS restriction enzyme *Bbs* I to remove the F-primer region for the following full-length DNA assembly. Cleaved short fragment of priming sites were removed with the UNIQ-10 oligonucleotide kit.

Gibson assemble of operons

Aliquots of 20 μL of PCR reaction mixture contained 0.75 μL 10 $\times$ Taq DNA ligase buffer, 0.2 μL dNTPs (2.5 mM each), 0.75 μL PEG6000 (50%), 4 μL MgCl_2 (25 mM), 0.04 U T5 exonuclease (New England Biolabs, Beverly, MA, USA), 0.25 U Phusion High-Fidelity DNA polymerase (New England Biolabs, Beverly, MA, USA), 40 U Taq DNA ligase, and 75 ng DNA. incubate at 50°C for 1 hour.

PCR amplification of full-length operons

The 50 μL -PCR mixture contained 10 μL of 5 $\times$ reaction buffer, 4 μL of 2.5 mM dNTPs, 0.5 μL of PrimeSTAR HS DNA polymerase, 1 μL of Gibson assembly product, and 1 μL of each primer (10 μM). PCR parameters were: 98°C for 10 sec, 55°C for 5 sec, and 72°C for 4.5 min for 30 cycles, followed by 72°C for 5 min. The PCR mixture was isolated on 1% (w/v) agarose gels and extracted with the Axygen gel extraction kit according to the manufacturer's instructions.

Supplementary data:

mvaE-1

mvaE-1_1-for

CACAGGAGTCCTCACACGCTCTGAAGACCCATGAAAACCGTTGTTATCATCGACGCGCTGCGCACCC
CGATCGGCAAATACAAAGGCTCTCAGGACTCCTCTG

mvaE-1_2-for

CACAGGAGTCCTCACCTCTGTCTCAGGTTTCTGCGGTTGACCTGGGTACCCACGTTACCACCCAGCTG
CTGCTCAGGACTCCTCTG

mvaE-1_3-for

CACAGGAGTCCTCACAAACGCCACTCTACCATCTCTGAAGAAATCGACCAGGTTATTTTCGGCAACG
TTCTGCAGGCGGCTCAGGACTCCTCTG

mvaE-1_4-for

CACAGGAGTCCTCACGCAACGGTCAGAACCCGGCGCGTCAGATCGCGATCAACTCTGGTCTGTCTCA
CTCAGGACTCCTCTG

mvaE-1_5-for

CACAGGAGTCCTCACCGAAATCCCGGCGATGACCGTTAACGAAGTTTGCGGCTCTGGCATGAAAGC
GGTTATCCTCAGGACTCCTCTG

mvaE-1_6-for

CACAGGAGTCCTCACCTGGCGAAACAGCTGATCCAGCTGGGTGAAGCGGAAGTTCTGATTGCGGGT
GGTATCCTGTCTTCTATCTCGCTCAGGACTCCTCTG

mvaE-1_1-rev

CACAGGAGTCCTCACGCAGCGCGTCGATGATAACAACGGTTTTTCATGGGTCTTCAGAGCGTCTCAG
GACTCCTCTG

mvaE-1_2-rev

CACAGGAGTCCTCACCCAGGTCAACCGCAGAAACCTGAGACAGAGAGCCTTTGTATTTGCCGATCG
GGGTGCCTCAGGACTCCTCTG

mvaE-1_3-rev

CACAGGAGTCCTCACTGGTCGATTTCTTCAGAGATGGTAGAGTGGCGTTTCAGCAGCTGGGTGGTA
ACGTGGGTACCTCAGGACTCCTCTG

mvaE-1_4-rev

CACAGGAGTCCTCACGCGCCGGGTTCTGACCGTTGCCCGCCTGCAGAACGTTGCCGAAAATAACCCT
CAGGACTCCTCTG

mvaE-1_5-rev

CACAGGAGTCCTCACTTCGTTAACGGTCATCGCCGGGATTTCTGTGAGACAGACCAGAGTTGATCGC
GATCTGACCTCAGGACTCCTCTG

mvaE-1_6-rev

CACAGGAGTCCTCACCCCAGCTGGATCAGCTGTTTCGCCAGGATAACCGCTTTCATGCCAGAGCCGC
AAACCTCAGGACTCCTCTG

mvaE-1_7-rev

CACAGGAGTCCTCACCGAGATAGAAGACAGGATACCACCCGCAATCAGAACTCCGCTTCACTCAG
GACTCCTCTG

mvaE-2

mvaE-2_1-for
CACAGGAGTCCTCACACGCTCTGAAGACCCGGAAGTTCTGATTGCGGGTGGTATCGAAAACATGTC
TCAGGCGCCGAAACTGCAGCGTTTCGTTGCGACTCGTAGG

mvaE-2_2-for
CACAGGAGTCCTCACAACACGAAACCGAATCTTACGACGCGCCGTTCTTCTATGATGTACGACG
GCCTGACCGACGTTGCGACTCGTAGG

mvaE-2_3-for
CACAGGAGTCCTCACGCGTTCTCTGGTCAGGCGATGGGTCTGACCGCGGAAAACGTTGCGGAAAAA
TATCACGGTTGCGACTCGTAGG

mvaE-2_4-for
CACAGGAGTCCTCACTTACCCGTGAAGAACAGGACCAGTTCTCTGTTCACTCTCAGCTGAAAGCGGC
GCAGGCGTTGCGACTCGTAGG

mvaE-2_5-for
CACAGGAGTCCTCACGCAGGCGGAAGGTATCTTCGCGGATGAAATTGCGCCGCTGGAAGTTTCTGG
CACCGTTGCGACTCGTAGG

mvaE-2_6-for
CACAGGAGTCCTCACCTGGTTGAAAAAGATGAAGGTATTCGCCCCGAACCTTTCTGTTGAAAAACTGG
GCACCCTGAAAACCGTTTTCAACTGTCTTCTATCTCGGTTGCGACTCGTAGG

mvaE-2_1-rev
CACAGGAGTCCTCACACATGTTTTGATACACCCGCAATCAGAACTTCCGGGTCTTCAGAGCGTGT
TGCGACTCGTAGG

mvaE-2_2-rev
CACAGGAGTCCTCACCGGCGCGTCGTAAGATTCGGTTTCGTAGTTGAAACGCTGCAGTTTCGGCGCC
TGAGGTTGCGACTCGTAGG

mvaE-2_3-rev
CACAGGAGTCCTCACAGACCCATCGCCTGACCAGAGAACGCGTCGGTCAGGCCGTCGTACATCATA
GAAGAGAAGTTGCGACTCGTAGG

mvaE-2_4-rev
CACAGGAGTCCTCACTGAACAGAGAACTGGTCCTGTTCTTCACGGGTAACGTGATATTTTCCGCAA
CGTTTTCCGCGGTCGTTGCGACTCGTAGG

mvaE-2_5-rev
CACAGGAGTCCTCACAATTTATCCGCGAAGATACCTTCCGCCTGCGCCTGCGCCGCTTTCAGCTGA
GAGGTTGCGACTCGTAGG

mvaE-2_6-rev
CACAGGAGTCCTCACGAAGAGTTCGGGCGAATACCTTCATCTTTTCAACCAGGGTGCCAGAACTT
CCAGCGGCGCGTTGCGACTCGTAGG

mvaE-2_7-rev
CACAGGAGTCCTCACCGAGATAGAAGACAGTTGAAAACGGTTTTTCAGGGTGCCAGTTTTTCAACA
GTTGCGACTCGTAGG

mvaE-3

mvaE-3_1-for
CACAGGAGTCCTCACACGCTCTGAAGACCCGGGCACCCTGAAAACCGTTTTCAAAGAAGATGGCAC
CGTTACCGCGGGTAACGCCAGACGACTCGAATG

mvaE-3_2-for
CACAGGAGTCCTCACGTCTACCATCAACGATGGTGCGTCTGCGCTGATTATTGCGTCTCAGGAATAC
GCGGAAGCCAGACGACTCGAATG

mvaE-3_3-for
CACAGGAGTCCTCACGCACGGTCTGCCGTACCTGGCGATCATTGCGGATTCTGTTGAAGTTGGTATC
GACCCAGACGACTCGAATG

mvaE-3_4-for
CACAGGAGTCCTCACCGGCGTACATGGGTATCTCTCCGATCAAAGCGATCCAGAACTGCTGGCGC
GCAGACGACTCGAATG

mvaE-3_5-for
CACAGGAGTCCTCACTAACCAGCTGACCACCGAAGAAATCGACCTGTACGAAATCAACGAAGCGTT
CGCGGCCAGACGACTCGAATG

mvaE-3_6-for
CACAGGAGTCCTCACGACCTCTATCGTTGTTGAGCGTGAAGTGGCGCTGCCGGAAGAAAAAGTTAA
CATCTACGGTGCAGACGACTCGAATG

mvaE-3_7-for
CACAGGAGTCCTCACGTGGTATCTCTCTGGGTACGCGATCGCTGTCTTCTATCTCGCAGACGACTC
GAATG

mvaE-3_1-rev
CACAGGAGTCCTCACCATCTTCTTTGAAAACGGTTTTAGGGTGCCCGGGTCTTCAGAGCGTCAGAC
GACTCGAATG

mvaE-3_2-rev
CACAGGAGTCCTCACCGCAGACGCACCATCGTTGATGGTAGACGCGTTACCCGCGGTAACGGTGCC
AGACGACTCGAATG

mvaE-3_3-rev
CACAGGAGTCCTCACGCCAGGTACGGCAGACCGTGCGCTTCCGCGTATTCTGAGACGCAATAATC
AGCAGACGACTCGAATG

mvaE-3_4-rev
CACAGGAGTCCTCACTTTGATCGGAGAGATACCCATGTACGCCGGGTCGATACCAACTTCAACAGAA
TCGCGAATGATCCAGACGACTCGAATG

mvaE-3_5-rev
CACAGGAGTCCTCACAGGTCGATTTCTTCGGTGGTCAGCTGGTTACGCGCCAGCAGTTTCTGGATCG
CCAGACGACTCGAATG

mvaE-3_6-rev
CACAGGAGTCCTCACGCCAGTTCACGCTGAACAACGATAGAGGTCGCCGGAACGCTTCGTTGATTT
CGTACCAGACGACTCGAATG

mvaE-3_7-rev
CACAGGAGTCCTCACCGAGATAGAAGACAGCGATCGCGTGACCCAGAGAGATACCACCACCGTAGA
TGTTAACTTTTTCTTCCGGCAGCCAGACGACTCGAATG

mvaE-4

mvaE-4_1-for
CACAGGAGTCCTCACACGCTCTGAAGACCCTATCTCTCTGGGTCACGCGATCGGTGCGACCGGTGCG
CGTCTGCTGACCGAAGGGACTCGTACG

mvaE-4_2-for
CACAGGAGTCCTCACTCTCTGTCTTACCAGCTGAACCAGAAAGAAAAAATACGGCGTTGCGTCTC
TGTGCATTGGTGGCGGGAAGGGACTCGTACG

mvaE-4_3-for
CACAGGAGTCCTCACTCTGGGTCTGGCGATGCTGCTGGAACGCCGCAGCAGAAAAAACTCTCG
CTTCTACGAAGGGACTCGTACG

mvaE-4_4-for
CACAGGAGTCCTCACCAGATGTCTCCGGAAGAACGTCTGGCGTCTCTGCTGAACGAAGGTCAGATC
TCTGCGGAGAAGGGACTCGTACG

mvaE-4_5-for
CACAGGAGTCCTCACCACCAAAAAAGAATTGAAAAACCCGCGCTGTCCTCTCAGATCGCGAACCAC
ATGATCGAAAACCAGATTGAAGGGACTCGTACG

mvaE-4_6-for
CACAGGAGTCCTCACTCTGAAACCGAAGTTCGGATGGGTGTTGGTCTGCACCTGACCGTTGACGAAA
CCGACTATCTGCTGTCTTCTATCTCGGAAGGGACTCGTACG

mvaE-4_1-rev
CACAGGAGTCCTCACGCACCGATCGCGTGACCCAGAGAGATAGGGTCTTCAGAGCGTGAAGGGAC
TCGTACG

mvaE-4_2-rev
CACAGGAGTCCTCACGCCGTATTTTTTTCTTTCTGGTTCAGCTGGTAAGACAGAGAGGTCAGCAGA
CGCGCACCGGTCGAAGGGACTCGTACG

mvaE-4_3-rev
CACAGGAGTCCTCACGTTCCAGCAGCATCGCCAGACCCAGACCGCCACCAATGCACAGAGACGCAA
CGAAGGGACTCGTACG

mvaE-4_4-rev
CACAGGAGTCCTCACACGCCAGACGTTCTTCCGGAGACATCTGGTAGAAGCGAGAGTTTTTTTCTG
CTGCGGGCGAAGGGACTCGTACG

mvaE-4_5-rev
CACAGGAGTCCTCACGGACAGCGCGGTGTTTTCGAATTCTTTTTTGGTGTCCGCAGAGATCTGACCT
TCGTTACAGAGGAAGGGACTCGTACG

mvaE-4_6-rev
CACAGGAGTCCTCACAGACCAACACCCATCGGAACTTCGGTTTCAGAAATCTGGTTTTCGATCATGT
GGTTCGCGATCTGAGAGAAGGGACTCGTACG

mvaE-4_7-rev
CACAGGAGTCCTCACCGAGATAGAAGACAGCAGATAGTCGGTTTCGTCAACGGTCAGGTGCGAAG
GGACTCGTACG

mvaE-5

mvaE-5_1-for
CACAGGAGTCCTCACACGCTCTGAAGACCCGACCGTTGACGAAACCGACTATCTGGTCCGATGGC
GACCGAAGAACCGTCTGTTATCGATACAGACTCGACAG

mvaE-5_2-for
CACAGGAGTCCTCACCGGCGCTGTCTAACGGTGCGAAAATCGCGCAGGGTTTCAAACCGTTAACCC
AGATACAGACTCGACAG

mvaE-5_3-for
CACAGGAGTCCTCACCAGCGTCTGATGCGTGCCAGATTGTTTTCTACGACGTTGCGGACCCGGAAT
CATACAGACTCGACAG

mvaE-5_4-for
CACAGGAGTCCTCACTCTGATCGACAACTGCAGGTTCTGTGAAGCGGAAATTTCCAGCAGGCGGA
ACTGTCTTACATACAGACTCGACAG

mvaE-5_5-for
CACAGGAGTCCTCACCCGTCTATCGTTAAACGTGGTGGTGGTCTGCGCGACCTGCAGTACCGTGCGA
TACAGACTCGACAG

mvaE-5_6-for
CACAGGAGTCCTCACTTCGATGAATCTTTCATCTCTGTTGACTTCCTGGTTGACGTTAAAGATGCGAT
GGGCGCGAACATCATACAGACTCGACAG

mvaE-5_7-for
CACAGGAGTCCTCACGTTAACGCGATGCTGGAAGGCGTTGTCTGTCTTCTATCTCGATACAGACTCG
ACAG

mvaE-5_1-rev
CACAGGAGTCCTCACGGAACCAGATAGTCGGTTTCGTCAACGGTCGGGTCTTCAGAGCGTATACAG
ACTCGACAG

mvaE-5_2-rev
CACAGGAGTCCTCACATTTTCGCACCGTTAGACAGCGCCGCGATAACAGACGGTTCTTCGGTCGCCA
TCATACAGACTCGACAG

mvaE-5_3-rev
CACAGGAGTCCTCACCAATCTGGCCACGCATCAGACGCTGCTGGTTAACGGTTTTGAAACCCTGCGC
GATACAGACTCGACAG

mvaE-5_4-rev
CACAGGAGTCCTCACGCTTCACGAACCTGCAGTTTGTGATCAGAGATTCCGGGTCCGCAACGTCGT
AGAAAAATACAGACTCGACAG

mvaE-5_5-rev
CACAGGAGTCCTCACCAGACCACCACCGTTTAACGATAGACGGGTAAGACAGTTCCGCCTGCTG
GAAAATTTCCATACAGACTCGACAG

mvaE-5_6-rev
CACAGGAGTCCTCACTCAACCAGGAAGTCAACAGAGATGAAAGATTCATCGAACGCACGGTACTGC
AGGTCGCGATACAGACTCGACAG

mvaE-5_7-rev
CACAGGAGTCCTCACCGAGATAGAAGACAGACAACGCCTTCCAGCATCGCGTTAACGATGTTGCGC
CCCATCGCATCTTTAACGATACAGACTCGACAG

mvaE-6

mvaE-6_1-for
CACAGGAGTCCTCACACGCTCTGAAGACCCGCGATGCTGGAAGGCGTTGTTGAACTGTTCCGTGAA
TGGTTCGCGGAACAGAAAATCCTGTTCTCTATGATCGGACTCGTACC

mvaE-6_2-for
CACAGGAGTCCTCACCTGTCTAACTACGCGACCGAATCTGTTGTTACCATGAAAACCGCGATTCCG
GTTTCTCGCCTGTGATCGGACTCGTACC

mvaE-6_3-for
CACAGGAGTCCTCACCTAAAGGTTCTAACGGCCGTGAAATCGCGGAAAAAATTGTTCTGGCGTCTCG
TTACGCGTCTCTGGAGATCGGACTCGTACC

mvaE-6_4-for
CACAGGAGTCCTCACCCCGTACCGTGCGGTTACCCACAACAAAGGCATCATGAACGGCATTGAAGC
GGTTGTTGATCGGACTCGTACC

mvaE-6_5-for
CACAGGAGTCCTCACTGGCGACCGGTAACGACACCCGTGCGGTTTCTGCGTCTTGCCACGCGTTCGA
TCGGACTCGTACC

mvaE-6_6-for
CACAGGAGTCCTCACGCGGTTAAAGAAGGCCGTTACCAGGGTCTGACCTCTTGACCCCTGGACGGC
GAACCTGTCTTCTATCTCGGATCGGACTCGTACC

mvaE-6_1-rev
CACAGGAGTCCTCACGAACAGTTCAACAACGCCTTCAGCATCGCGGGTCTTCAGAGCGTGATCGG
ACTCGTACC

mvaE-6_2-rev
CACAGGAGTCCTCACCATGGTAACAACAGATTCGGTCGCGTAGTTAGACAGGATAGAGAACAGGAT
TTTCTGTTCCGGAACCATTCACGGATCGGACTCGTACC

mvaE-6_3-rev
CACAGGAGTCCTCACCAATTTTTTCCGCGATTTACGGCCGTTAGAACCTTTAGACAGGCGAGAAAC
CGGAATCGCGGTTTTGATCGGACTCGTACC

mvaE-6_4-rev
CACAGGAGTCCTCACTTTGTTGTGGGTAACCGCACGGTACGGGTCCAGAGACGCGTAACGAGACGC
CAGAAGATCGGACTCGTACC

mvaE-6_5-rev
CACAGGAGTCCTCACACGGGTGTCGTTACCGGTCGCCAGAACAAACCGCTTCAATGCCGTTTCATGAT
GCCGATCGGACTCGTACC

mvaE-6_6-rev
CACAGGAGTCCTCACAGACCCTGGTAACGGCCTTCTTTAACCGCGAACGCGTGGCAAGACGCAGAA
ACCGGATCGGACTCGTACC

mvaE-6_7-rev
CACAGGAGTCCTCACCGAGATAGAAGACAGGTTCCCGTCCAGGGTCCAAGAGGTCGATCGGACTC
GTACC

mvaE-7

mvaE-7_1-for
CACAGGAGTCCTCACACGCTCTGAAGACCCTGGACCCTGGACGGCGAACAGCTGATTGGTGAAATT
TCTGTTCCGCTGGCGGAGACGACTCGTAAG

mvaE-7_2-for
CACAGGAGTCCTCACCTGGCGACCGTTGGCGGTGCGACCAAAGTTCTGCCGAAATCTCAGGCGGAG
ACGACTCGTAAG

mvaE-7_3-for
CACAGGAGTCCTCACGCGGCGGACCTGCTGGCGGTTACCGACGCGAAAGAACTGTCTCGTGTGAGA
CGACTCGTAAG

mvaE-7_4-for
CACAGGAGTCCTCACTGTTGCGGCGGTTGGTCTGGCGCAGAACCTGGCGGCGCTGCGAGACGACTC
GTAAG

mvaE-7_5-for
CACAGGAGTCCTCACGCGCGCTGGTTTCTGAAGGTATCCAGAAAGGTCACATGGCGCTGCAGGCGA
GACGACTCGTAAG

mvaE-7_6-for
CACAGGAGTCCTCACGCGTTCTCTGGCGATGACCGTTGGCGCGACCGGCAAAGAAGTTGAAGCGGA
GACGACTCGTAAG

mvaE-7_7-for
CACAGGAGTCCTCACGTTGCGCAGCAGCTGAAACGTCAGAAAACCATGAACCAGGACCGTGCGCTG
GAGACGACTCGTAAG

mvaE-7_8-for
CACAGGAGTCCTCACGCGATCCTGAACGACCTGCGTAAACAGTAACTGTCTTCTATCTCGGAGACGA
CTCGTAAG

mvaE-7_1-rev
CACAGGAGTCCTCACGCTGTTGCGCGTCCAGGGTCCAGGGTCTTCAGAGCGTGAGACGACTCGTAA
G

mvaE-7_2-rev
CACAGGAGTCCTCACGCACCGCCAACGGTCGCCAGCGCCAGCGGAACAGAAATTCACCAATCAGA
GACGACTCGTAAG

mvaE-7_3-rev
CACAGGAGTCCTCACCGCCAGCAGGTCCGCCGCCGCTGAGATTTGGCAGAACTTTGGTCGAGAC
GACTCGTAAG

mvaE-7_4-rev
CACAGGAGTCCTCACGCCAGACCAACCGCCGCAACAACACGAGACAGTTCTTTGCGTCTGGTAACG
AGACGACTCGTAAG

mvaE-7_5-rev
CACAGGAGTCCTCACTCTGGATACCTTCAGAAACCAGCGCGCGCAGCGCCGCCAGGTTCTGCGAGA
CGACTCGTAAG

mvaE-7_6-rev
CACAGGAGTCCTCACCCAACGGTCATCGCCAGAGAACGCGCCTGCAGCGCCATGTGACCTTGAGAC
GACTCGTAAG

mvaE-7_7-rev

CACAGGAGTCCTCACTTTTCTGACGTTTCAGCTGCTGCGCAACCGCTTCAACTTCTTTGCCGGTCGCG
GAGACGACTCGTAAG

mvaE-7_8-rev

CACAGGAGTCCTCACCGAGATAGAAGACAGTTACTGTTTACGCAGGTCGTTTCAGGATCGCCAGCGC
ACGGTCCTGGTTCATGGGAGACGACTCGTAAG

mvaS-1

mvaS-1_1-for

GTATAGAGTCAGTCGACGCTCTGAAGACCCATGACCATTGGCATTGATAAAATCTCTTTCTTCGTTCC
GCCGTACTACATCGACATGACCGCGCTGGCCTCAGGACTCCTCTG

mvaS-1_2-for

GTATAGAGTCAGTCGGGAAGCGCGTAACGTTGATCCGGGTAAATCCACATCGGTATCGGTCAGGA
CCAGATGGCCTCAGGACTCCTCTG

mvaS-1_3-for

GTATAGAGTCAGTCGGGTAAACCCGATTTCTCAGGATATTGTTACCTTCGCGGCGAACGCGGCGGA
AGCGATCCCTCAGGACTCCTCTG

mvaS-1_4-for

GTATAGAGTCAGTCGTGACCAAAGAAGATAAAGAAGCGATTGACATGGTTATCGTTGGCACCGAAT
CTTCTATCGACGAATCTAAAGCGGCCTCAGGACTCCTCTG

mvaS-1_5-for

GTATAGAGTCAGTCGGGCGGTTGTTCTGCACCGTCTGATGGCTGTCTTCTATCTCGCTCAGGACTCCT
CTG

mvaS-1_1-rev

GTATAGAGTCAGTCGGCGGAACGAAGAAAGAGATTTTATCAATGCCAATGGTCATGGGTCTTCAGA
GCGTCTCAGGACTCCTCTG

mvaS-1_2-rev

GTATAGAGTCAGTCGGAATTTACCCGGATCAACGTTACGCGCTTCCGCCAGCGCGGTCATGTCGATG
TAGTACGCTCAGGACTCCTCTG

mvaS-1_3-rev

GTATAGAGTCAGTCGCGCGAAGGTAACAATATCCTGAGAAATCGGGTTAACCGCCATCTGGTCCTG
ACCGATACCGATGTGCTCAGGACTCCTCTG

mvaS-1_4-rev

GTATAGAGTCAGTCGCAACGATAACCATGTCAATCGCTTCTTATCTTCTTTGGTCAGGATCGCTTCC
GCCGCGTTTCGCCTCAGGACTCCTCTG

mvaS-1_5-rev

GTATAGAGTCAGTCGCGAGATAGAAGACAGCCATCAGACGGTGCAGAACAACCGCCGCCGCTTTAG
ATTCGTGATAGAAGATTGGTGCCTCAGGACTCCTCTG

mvaS-2

mvaS-2_1-for

GTATAGAGTCAGTCGACGCTCTGAAGACCCGGTTGTTCTGCACCGTCTGATGGGTATTCAGCCGTTCC
GCGCGTTCTTTCGAAATGTTGCGACTCGTAGG

mvaS-2_2-for
 GTATAGAGTCAGTCGCAAAGAAGCGTGCTACGGTGCGACCGCGGGTCTGCAGCTGGCGAAGTTGC
 GACTCGTAGG

mvaS-2_3-for
 GTATAGAGTCAGTCGAAACCACGTTGCGCTGCACCCGGACAAAAAAGTTCTGGTTGTTGCGGCGGA
 TATCGTTGCGACTCGTAGG

mvaS-2_4-for
 GTATAGAGTCAGTCGGCGAAATATGGTCTGAACTCTGGTGGTGAACCGACCCAGGGTGCGGGTGC
 GTTGC GACTCGTAGG

mvaS-2_5-for
 GTATAGAGTCAGTCGGGTTGCGATGCTGGTTGCGTCTGAACCGCGTATTCTGGCGCTGAAAGAAGA
 TAACGTTATGTTGCGACTCGTAGG

mvaS-2_6-for
 GTATAGAGTCAGTCGGCTGACCCAGGACATCTACGACTTCTGGCGTCCGACCGGCCACCCGTCTGTC
 TTCTATCTCGGTTGCGACTCGTAGG

mvaS_2_1-rev
 GTATAGAGTCAGTCGGAATACCCATCAGACGGTGCAGAACCAACCGGGTCTTCAGAGCGTGTTCGA
 CTCGTAGG

mvaS_2_2-rev
 GTATAGAGTCAGTCGGGTGCGACCGTAGCACGCTTCTTTGATTCGAAAGAACGCGCGAACGGCTG
 TTGCGACTCGTAGG

mvaS_2_3-rev
 GTATAGAGTCAGTCGCGGGTGCAGCGCAACGTGGTTTTTCGCCAGCTGCAGACCCGCGTTGCGACT
 CGTAGG

mvaS_2_4-rev
 GTATAGAGTCAGTCGGTTCACCACCAGAGTTCAGACCATATTTTCGCGATATCCGCCGCAACAACAG
 AACTTTTTTGTGCTTTCGACTCGTAGG

mvaS_2_5-rev
 GTATAGAGTCAGTCGGTTCAGACGCAACCAGCATCGCAACCGCACCCGCACCCTGGGTGCGTTGCG
 ACTCGTAGG

mvaS_2_6-rev
 GTATAGAGTCAGTCGCCAGAAGTCGTAGATGTCCTGGGTGAGCATAACGTTATCTTCTTCAGCGCC
 AGAATACGCGGTTGCGACTCGTAGG

mvaS_2_7-rev
 GTATAGAGTCAGTCGCGAGATAGAAGACAGACGGGTGGCCGGTCGGACGGTTGCGACTCGTAGG

mvaS-3

mvaS-3_1-for
 GTATAGAGTCAGTCGACGCTCTGAAGACCCCGACCGGCCACCCGTATCCGATGGTTGACGGTCCG
 CTGTCTAACGAAACCTACATCAGACGACTCGAATG

mvaS-3_2-for
 GTATAGAGTCAGTCGCCAGTCTTTTCGCGCAGGTTTGGGACGAACACAAAAACGCACCGGTCTGGA
 CTTGCCAGACGACTCGAATG

mvaS-3_3-for
 GTATAGAGTCAGTCGGGACTACGATGCGCTGGCGTTCCACATTCCGTACACCAAAATGGGCAAAA
 AGCGCTGCTCAGACGACTCGAATG

mvaS-3_4-for
 GTATAGAGTCAGTCGGGCGAAAATTTCTGACCAGACCGAAGCGGAACAGGAACGTATCCTGGCGC
 GTTACGAAGAATCTATCCAGACGACTCGAATG

mvaS-3_5-for
 GTATAGAGTCAGTCGGTTTATTCTCGTCGCGTTGGCAACCTGTACACCGGTTCTCTGTACCTGGGCCT
 GATTTCTCTGCCTGTCTTCTATCTCGCAGACGACTCGAATG

mvaS-3_1-rev
 GTATAGAGTCAGTCGATCGGATACGGGTGGCCGGTCGGGGGTCTTCAGAGCGTCAGACGACTCGA
 ATG

mvaS-3_2-rev
 GTATAGAGTCAGTCGTTTCGTCCCAAACCTGCGCGAAAGACTGGATGTAGGTTTCGTTAGACAGCGG
 ACCGTCAACCCAGACGACTCGAATG

mvaS-3_3-rev
 GTATAGAGTCAGTCGGAATGTGGAACGCCAGCGCATCGTAGTCCGCGAAGTCCAGACCGGTGCGTT
 TTTTGTGCAGACGACTCGAATG

mvaS-3_4-rev
 GTATAGAGTCAGTCGTTCCGCTTCGGTCTGGTCAGAAATTTTCGCCAGCAGCGCTTTTTTGCCATT
 TGGTGTACGCAGACGACTCGAATG

mvaS-3_5-rev
 GTATAGAGTCAGTCGGGTGTACAGGTTGCCAACGCGACGAGAATAAACGATAGATTCTTCGTAACG
 CGCCAGGATACGTTCTGCAGACGACTCGAATG

mvaS-3_6-rev
 GTATAGAGTCAGTCGCGAGATAGAAGACAGGCAGAGAAATCAGGCCCAGGTACAGAGAACCCAGA
 CGACTCGAATG

mvaS-4

mvaS-4_1-for
 GTATAGAGTCAGTCGACGCTCTGAAGACCCGTACCTGGGCCTGATTTCTCTGCTGGAAAACGCGACC
 ACCCTGACCGCGGGTAACCGAAGGGACTCGTACG

mvaS-4_2-for
 GTATAGAGTCAGTCGAGATCGGTCTGTTCTTTACGGCTCTGGTGCGGTTGCGGAATTCTTCACCGG
 TGAAGTGGTGAAGGGACTCGTACG

mvaS-4_3-for
 GTATAGAGTCAGTCGTGCGGGTTATCAGAACCACCTGCAGAAAGAAACCCACCTGGCGCTGCTGGA
 CAACCGAAGGGACTCGTACG

mvaS-4_4-for
 GTATAGAGTCAGTCGGTACCGAACTGTCTATCGCGGAATACGAAGCGATGTTTCGCGGAAACCTGG
 ACACCGAGAAGGGACTCGTACG

mvaS-4_5-for

GTATAGAGTCAGTCGCATCGACCAGACCCTGGAAGATGAACTGAAATACTCTATCTCTGCGATCAAC
AACACCGTTTCGTTCTTACCGTAACTAACTGTCTTCTATCTCGGAAGGGACTCGTACG

mvaS-4_1-rev

GTATAGAGTCAGTCGCGTTTTCCAGCAGAGAAATCAGGCCAGGTACGGGTCTTCAGAGCGTGAAG
GGACTCGTACG

mvaS-4_2-rev

GTATAGAGTCAGTCGGCACCAGAGCCGTAAGAGAACAGACCGATCTGGTTACCCGCGGTCAAGGT
GGTCGGAAGGGACTCGTACG

mvaS-4_3-rev

GTATAGAGTCAGTCGGTTTTCTTTCTGCAGGTGGTTCTGATAACCCGCAACCAGTTCACCGGTGAAGA
ATTCCGCAACCGAAGGGACTCGTACG

mvaS-4_4-rev

GTATAGAGTCAGTCGTCGCTTCGTATTCCGCGATAGACAGTTCGGTACGGTTGTCCAGCAGCGCCAG
GTGGGAAGGGACTCGTACG

mvaS-4_5-rev

GTATAGAGTCAGTCGAGATAGAGTATTTCAAGTTCATCTTCCAGGGTCTGGTCGATGTCGGTGTCCAG
GGTTTCCGCGAACAGAAGGGACTCGTACG

mvaS-4_6-rev

GTATAGAGTCAGTCGCGAGATAGAAGACAGTTAGTTACGGTAAGAACGAACGGTGTGTTGATCGC
AGGAAGGGACTCGTACG

mvaK1-1

mvaK1-1_1-for

CCAAGGAGTCGCTAGACGCTCTGAAGACCCATGAATATCAAGAAGCAAGGTCTGGGCCAGGCGACC
GGTAAATCATTCTGATGGGTGAGCACGCTCAGGACTCCTCTG

mvaK1-1_2-for

CCAAGGAGTCGCTAGCGGTGTTTTACGGTGAACCTGCGATTGCGTTCCCGTTCCAAGCGACTGAAAT
TACCGCCTCAGGACTCCTCTG

mvaK1-1_3-for

CCAAGGAGTCGCTAGTGTGTTACGCGCGCAAAGACCATGCAGATCGACTGCGCGTACTTCACGGG
TCTCAGGACTCCTCTG

mvaK1-1_4-for

CCAAGGAGTCGCTAGCTGCTGGAAGATGTCCCGCAGGAAGTGGCGAACATCAAGGAGGTGGTGCA
ACAAACCCTCAGGACTCCTCTG

mvaK1-1_5-for

CCAAGGAGTCGCTAGCTGCACTTCCTGAAGGAAGATACGTTCAAGGGCACCTGACGCTGACGTCT
ACCATTCCTCAGGACTCCTCTG

mvaK1-1_6-for

CCAAGGAGTCGCTAGGGCGGAGCGTGGTATGGGTTCTTCTGCTGTCTTCTATCTCGCTCAGGACTCC
TCTG

mvaK1-1_1-rev

CCAAGGAGTCGCTAGGCCTGGCCAGACCTTGCTTCTTGATATTCATGGGTCTTCAGAGCGTCTCAG
GACTCCTCTG

mvaK1-1_2-rev

CCAAGGAGTCGCTAGGCAATCGCAGGTTACCGTAAACGACCGCGTGCTACCCATCAGAATGATTT
TACCGGTCCTCAGGACTCCTCTG

mvaK1-1_3-rev

CCAAGGAGTCGCTAGGCATGGTCTTTGCCGGCGTGAACACAGCGGTAATTCAGTCGCTTGGAACG
GGAACCTCAGGACTCCTCTG

mvaK1-1_4-rev

CCAAGGAGTCGCTAGCAGTTCCTGCGGGACATCTTCAGCAGACCCGTGAAGTACGCGCAGTCGAT
CTCTCAGGACTCCTCTG

mvaK1-1_5-rev

CCAAGGAGTCGCTAGCCCTTGAACGTATCTTCCTCAGGAAGTGCAGGGTTTGTGTCACCACCTCCTT
GATGTTGCGCTCAGGACTCCTCTG

mvaK1-1_6-rev

CCAAGGAGTCGCTAGCGAGATAGAAGACAGCAGAAGAACCCATACCACGCTCCGCCGGAATGGTA
GACGTCAGCGTCAGGGTGCTCAGGACTCCTCTG

mvaK1-2

mvaK1-2_1-for

CCAAGGAGTCGCTAGACGCTCTGAAGACCCGGAGCGTGGTATGGGTTCTTCTGCGGCGACGGCGGT
GGCGATCGTACGCGTTGCGACTCGTAGG

mvaK1-2_2-for

CCAAGGAGTCGCTAGTCCCTGTTTGACTACTTCGATTACGCCTACACGTACCAAGAGCTGTTGAGC
TGTTTTCTGTCTGAAAAGATCGTTGCGACTCGTAGG

mvaK1-2_3-for

CCAAGGAGTCGCTAGGCACACGGTAACCCGTCTGGCATCGACGCGGCTGCCACGTCCGGTGGTTGC
GACTCGTAGG

mvaK1-2_4-for

CCAAGGAGTCGCTAGCGGACCCGCTGTTCTTACCCGTGGTTCCCGCCGACCCACTTCTCTATGAAT
CTGTGTTGCGACTCGTAGG

mvaK1-2_5-for

CCAAGGAGTCGCTAGCTAACGCGTACCTGGTCTTGCGGACACCGGTATCAAAGGTCAAACCCGCG
AGGCGGTTGCGACTCGTAGG

mvaK1-2_6-for

CCAAGGAGTCGCTAGGTTAAGGACATCGCCCAACTGGCTCAGAACAAACCCGACCGCCATCGCGGAG
ACTACTGTCTTCTATCTCGGTTGCGACTCGTAGG

mvaK1-2_1-rev

CCAAGGAGTCGCTAGGCCGAGAAGAACCCATACCACGCTCCGGGTCTTCAGAGCGTGTTGCGACT
CGTAGG

mvaK1-2_2-rev

CCAAGGAGTCGCTAGGTACGTGTAGGCGTAATCGAAGTAGTCAAACAGGGAGCGTACGATCGCCA
CCGCCGTCGTTGCGACTCGTAGG

mvaK1-2_3-rev

CCAAGGAGTCGCTAGTCGATGCCAGACGGGTACCCTGTGCGATCTTTTCAGACAGAGAAACCAGC
TCGAACAGCTCTTGTTGCGACTCGTAGG

mvaK1-2_4-rev

CCAAGGAGTCGCTAGCACGGGTGAAGAACAGCGGGTCCGCACCGGACGTGGCAGCCGCGGTTGCG
ACTCGTAGG

mvaK1-2_5-rev

CCAAGGAGTCGCTAGGTGTCCGCAACGACCAGGTACGCGTTAGACAGATTCATAGAGAAGTGGGTC
GGCGGGAAACGTTGCGACTCGTAGG

mvaK1-2_6-rev

CCAAGGAGTCGCTAGTTGTTCTGAGCCAGTTGGGCGATGTCCTTAACCGCCTCGCGGGTTTGACCTT
TGATACCGGTTGCGACTCGTAGG

mvaK1-2_7-rev

CCAAGGAGTCGCTAGCGAGATAGAAGACAGTAGTCTCCGCGATGGCGGTGCGGGTTGCGACTCGT
AGG

mvaK1-3

mvaK1-3_1-for

CCAAGGAGTCGCTAGACGCTCTGAAGACCCACCGCCATCGCGGAGACTATGAAACAGCTGGGCTCT
TTCACCAAGGAAGCACAGACGACTCGAATG

mvaK1-3_2-for

CCAAGGAGTCGCTAGGAAGCAAGCGATCCTGCAAGACGACAAGCAGAACTGGGTCAACTGATGAC
CCTGGCAGACGACTCGAATG

mvaK1-3_3-for

CCAAGGAGTCGCTAGCGCAGGAGCAACTGCAGCAGCTGACCGTTTCTAACGACATGCTGGACCGCA
GACGACTCGAATG

mvaK1-3_4-for

CCAAGGAGTCGCTAGCCTGGTAGCGCTGTCTTGGAACACGGTGCGCTGGGTGCGAACTGACAGA
CGACTCGAATG

mvaK1-3_5-for

CCAAGGAGTCGCTAGCCGGTGGTGGTCGTGGCGGTTGCATGATTGCCCTGACCGATAACAAGAAAA
CAGACGACTCGAATG

mvaK1-3_6-for

CCAAGGAGTCGCTAGCTGCACAGACCATTGCCCAAACGCTGGAGGAGAACGGTGCCGTTGCCAGAC
GACTCGAATG

mvaK1-3_7-for

CCAAGGAGTCGCTAGGACTTGGATTCACTCCCTGGAGGTTAAGAAGTAACTGTCTTCTATCTCGCAG
ACGACTCGAATG

mvaK1-3_1-rev

CCAAGGAGTCGCTAGTGTTCATAGTCTCCGCGATGGCGGTGGGTCTTCAGAGCGTCAGACGACTC
GAATG

mvaK1-3_2-rev

CCAAGGAGTCGCTAGCTTGTCTGTCAGGATCGCTTGCTTGCTTCCTTGGTGAAAGAGCCCAGC
CAGACGACTCGAATG

mvaK1-3_3-rev

CCAAGGAGTCGCTAGAGCTGCTGCAGTTGCTCCTGCGCCAGGGTCATCAGTTGACCCAGTTTCTGCA
GACGACTCGAATG

mvaK1-3_4-rev

CCAAGGAGTCGCTAGGTGTTCCAGAGACAGCGCTACCAGGCGGTCCAGCATGTCGTTAGAAACGGT
CCAGACGACTCGAATG

mvaK1-3_5-rev

CCAAGGAGTCGCTAGCCGCCACGACCACCACCGGTCACTTTCGCACCCAGCGCACCCAGACGACTC
GAATG

mvaK1-3_6-rev

CCAAGGAGTCGCTAGGCGTTTGGGCAATGGTCTGTGCAGTTTCTTGTTATCGGTCAAGGCAATCAT
GCAACAGACGACTCGAATG

mvaK1-3_7-rev

CCAAGGAGTCGCTAGCGAGATAGAAGACAGTTACTTCTTAACCTCCAGGGACTGAATCCAAGTCGC
AACGGCACCGTTCTCCTCCACAGACGACTCGAATG

mvaK2-1

mvaK2-1_1-for

GTCACGAGTCATGGCACGCTCTGAAGACCCATGATCGAAGTTACCACCCCGGGTAAACTGTTCAATG
CGGGCGAATATGCGGTTGTTGAAGTAGAGACTCGATCC

mvaK2-1_2-for

GTCACGAGTCATGGCCCGGGTCACCCGGCGATCATTGTTGCGGTTGATCAGTTGTTACCGTTACCG
TTGGTAGAGACTCGATCC

mvaK2-1_3-for

GTCACGAGTCATGGCAAGAAACCACCGATGAAGGTTCTATCCAGTCTGCGCAGTACTCTTCTCTGCC
GATCCGCTGGTAGAGACTCGATCC

mvaK2-1_4-for

GTCACGAGTCATGGCGACCCGTCGTAACGGCGAACTGGTTCTGGACATCCGCGAAAACCGTTCCA
CTAGTAGAGACTCGATCC

mvaK2-1_5-for

GTCACGAGTCATGGCCGTTCTGGCGGCGATTACCTGACCGAAAAATACGCGCAGGAACAGAACAA
AGAACTGTCTGTAGAGACTCGATCC

mvaK2-1_6-for

GTCACGAGTCATGGCTTCTATCACCTGAAAGTTACCTCTGAACTGGATTCTTCTAACGGCCGCAAATA
CGGTCTGGGTTCTTCTGGCTGTCTTCTATCTCGGTAGAGACTCGATCC

mvaK2-1_1-rev
GTCACGAGTCATGGCACAGTTTACCCGGGGTGGTAACTTCGATCATGGGTCTTCAGAGCGTGTAGA
GACTCGATCC

mvaK2-1_2-rev
GTCACGAGTCATGGCAACAATGATCGCCGGGTGACCCGGTTCACAACCGCATATTCGCCCGCAAT
GAGTAGAGACTCGATCC

mvaK2-1_3-rev
GTCACGAGTCATGGCGCAGACTGGATAGAACCTTCATCGGTGGTTTCTTCAACGGTAACGGTAACG
AACTGATCAACCGCGTAGAGACTCGATCC

mvaK2-1_4-rev
GTCACGAGTCATGGCGAACCAGTTCGCCGTTACGACGGGTCCAGCGGATCGGCAGAGAAGAGTAC
TGCGTAGAGACTCGATCC

mvaK2-1_5-rev
GTCACGAGTCATGGCGGTTCAGGTGAATCGCCGCCAGAACGTAGTGGAACGGGTTTTCGCGGATGTC
CAGTAGAGACTCGATCC

mvaK2-1_6-rev
GTCACGAGTCATGGCCGTTAGAAGAATCCAGTTCAGAGGTAACCTTCAGGTGATAGAAAGACAGTT
CTTTGTTCTGTTCTGCGCGTATTTTTCGTAGAGACTCGATCC

mvaK2-1_7-rev
GTCACGAGTCATGGCCGAGATAGAAGACAGCCAGAAGAACCAGACCGTATTTGCGGCGTAGAGA
CTCGATCC

mvaK2-2

mvaK2-2_1-for
GTCACGAGTCATGGCACGCTCTGAAGACCCGCAAATACGGTCTGGGTCTTCTGGCGCGGTTACCGT
TGGCACCGTTAAAGCGCTCATATGACTCCACAC

mvaK2-2_2-for
GTCACGAGTCATGGCGAACATTTTCTACGACCTGGGCCTGGAAAACGAAGAAATTTCAAAGTGTCT
GCGCTGGCGCACATATGACTCCACAC

mvaK2-2_3-for
GTCACGAGTCATGGCCCTGGCGGTTCAGGGCAACGGTTCTTGCGGTGACATCGCGGCGTCATATGA
CTCCACAC

mvaK2-2_4-for
GTCACGAGTCATGGCCTTGCTACGGTGGCTGGATCGCGTTCTCTACCTTCGACCACGACTGGGTAA
CCCATATGACTCCACAC

mvaK2-2_5-for
GTCACGAGTCATGGCAGAAAGTTGCGACCGAAACCCTGACCGACCTGCTGGCGATGGACTGGCCCA
TATGACTCCACAC

mvaK2-2_6-for
GTCACGAGTCATGGCGGAACTGATGATCTCCCGCTGAAAGTTCCGAAACAGCTGCGTCTGCTGATC
GGTTGGACCATATGACTCCACAC

mvaK2-2_7-for

GTCACGAGTCATGGCCGGCTCTCCGGCGTCTACCTCTGACCTGGTTGACCGTGTTCACCAGTCTAAA
GAAGAAAAACTGTCTTCTATCTCGCATATGACTCCACAC

mvaK2-2_1-rev

GTCACGAGTCATGGCGCGCCAGAAGAACCCAGACCGTATTTGCGGGTCTTCAGAGCGTCATATGAC
TCCACAC

mvaK2-2_2-rev

GTCACGAGTCATGGCCGTTTTCCAGGCCAGGTCGTAGAAAATGTTACGCGCTTTAACGGTGCCAAC
GGTAACCCATATGACTCCACAC

mvaK2-2_3-rev

GTCACGAGTCATGGCACC GTTGCCCTGAACCGCCAGGTGCGCCAGCGCAGACAGTTTGAAAATTTCT
TCATATGACTCCACAC

mvaK2-2_4-rev

GTCACGAGTCATGGCACGCGATCCAGCCACCGTAGCAAGACGCCGCGATGTCACCGCAAGACATAT
GACTCCACAC

mvaK2-2_5-rev

GTCACGAGTCATGGCCGGTCAGGGTTTCGGTCGCAACTTTCTGGTTAACCCAGTCGTGGTCTGAAGGT
AGAGACATATGACTCCACAC

mvaK2-2_6-rev

GTCACGAGTCATGGCTTTCGGAAC TTTAGCGGGAAGATCATCAGTTCCGGCCAGTCCATCGCCAGC
AGGTCATATGACTCCACAC

mvaK2-2_7-rev

GTCACGAGTCATGGCTCAGAGGTAGACGCCGGAGAGCCGGTCCAACCGATCAGCAGACGCAGCTG
CATATGACTCCACAC

mvaK2-2_8-rev

GTCACGAGTCATGGCCGAGATAGAAGACAGTTTTTCTTCTTTAGACTGGTGAACACGGTCAACCAGG
CATATGACTCCACAC

mvaK2-3

mvaK2-3_1-for

GTCACGAGTCATGGCACGCTCTGAAGACCCACCGTGTTACCAGTCTAAAGAAGAAAAACAGGCGG
CGTACGAACAGTTCCTGATGAAATCTCGTCGAATTGACTCGATCC

mvaK2-3_2-for

GTCACGAGTCATGGCTGTGCGTTGAAACCATGATCAACGGCTTCAACACCGGCAAAATCTCTGTTAT
CCAGAAACAGATTACCGAATTGACTCGATCC

mvaK2-3_3-for

GTCACGAGTCATGGCAAAAACCGTCAGCTGCTGGCGGAACTGTCCTCTCTGACCGGCGTTGTTATCG
AAACCGAATTGACTCGATCC

mvaK2-3_4-for

GTCACGAGTCATGGCGAAGCGCTGAAAAACCTGTGCGACCTGGCGGAATCTTATACCGGTGCGGCG
AAATCGAATTGACTCGATCC

mvaK2-3_5-for

GTCACGAGTCATGGCTTCTGGTGCGGGTGGCGGTGATTGCGGTATCGTTATCTTCCGTCAGAAATCT
GGTATCCTGGAATTGACTCGATCC

mvaK2-3_6-for

GTCACGAGTCATGGCCCGCTGATGACCGCGTGGGAAAAAGACGGCATTACCCCGCTGCCGCTGAAT
TGACTCGATCC

mvaK2-3_7-for

GTCACGAGTCATGGCGCACGTTTACACCTACGGCCAGAAAGAATGCTAACTGTCTTCTATCTCGGAA
TTGACTCGATCC

mvaK2-3_1-rev

GTCACGAGTCATGGCGCCTGTTTTCTTCTTTAGACTGGTGAACACGGTGGGTCTTCAGAGCGTGAA
TTGACTCGATCC

mvaK2-3_2-rev

GTCACGAGTCATGGCTGAAGCCGTTGATCATGGTTTCAACGCACAGACGAGATTTTCATCAGGAACT
GTTTCGTACGCCGAATTGACTCGATCC

mvaK2-3_3-rev

GTCACGAGTCATGGCCAGTTCGCCAGCAGCTGACGGTTTTTGGTAATCTGTTTCTGGATAACAGAG
ATTTTGCCGGTGTGAATTGACTCGATCC

mvaK2-3_4-rev

GTCACGAGTCATGGCCAGGTCGCACAGTTTTTCAGCGCTTCGGTTTCGATAACAACGCCGGTCAGA
GAGGAGAATTGACTCGATCC

mvaK2-3_5-rev

GTCACGAGTCATGGCCAATCACCGCCACCCGCACCAGAAGATTTGCGCCGACCGGTATAAGATTCCG
CGAATTGACTCGATCC

mvaK2-3_6-rev

GTCACGAGTCATGGCTCTTTTTCCACGCGGTCATCAGCGGCAGGATACCAGATTTCTGACGGAAGA
TAACGATACCGGAATTGACTCGATCC

mvaK2-3_7-rev

GTCACGAGTCATGGCCGAGATAGAAGACAGTTAGCATTCTTCTGGCCGTAGGTGTAAACGTGCAG
CGGCAGCGGGGTAATGCCGGAATTGACTCGATCC

mvaD-1

mvaD-1_1-for

GATAAGAGTCTCAGCACGCTCTGAAGACCCATGCTGTCTGGTAAAGCGCGTGCGCACACCAACATC
GCGCTGATCAAATACTGGGTAGAGACTCGATCC

mvaD-1_2-for

GATAAGAGTCTCAGCGGCAAAGCGAACGAAGAATACATCCTGCCGATGAACTCTTCTGTCTCTGA
CCCTGGATGGTAGAGACTCGATCC

mvaD-1_3-for

GATAAGAGTCTCAGCCGTTCTACACCGAAACCACCGTTACCTTCGACGCGCACTACTCTGAAGATGT
TTTCATCCGTAGAGACTCGATCC

mvaD-1_4-for

GATAAGAGTCTCAGCTGGACGGCATCCTGCAGAACGAGAAACAGACCAAGAAAGTTAAAGAATTCC
TGAACCTGGTGTAGAGACTCGATCC

mvaD-1_5-for

GATAAGAGTCTCAGCTCGCCAGCAGGCGGATTGTACCTGGTTCGCGAAAGTTGAATCTCAGAACTTC
GTTCTGTAGAGACTCGATCC

mvaD-1_6-for

GATAAGAGTCTCAGCCGACCGCAGCTGGTCTGGCGTCTCTGCGTCTGGCCTGGCTCTGTCTTCTAT
CTCGGTAGAGACTCGATCC

mvaD-1_1-rev

GATAAGAGTCTCAGCCGCACGCGCTTTACCAGACAGCATGGGTCTTCAGAGCGTGTAGAGACTCGA
TCC

mvaD-1_2-rev

GATAAGAGTCTCAGCGGCAGGATGTATTCTTCGTTTCGCTTTGCCCCAGTATTTGATCAGCGCGATGT
TGGTGTGGTAGAGACTCGATCC

mvaD-1_3-rev

GATAAGAGTCTCAGCGAAGGTAACGGTGGTTTCGGTGTAGAACGCATCCAGGGTCAGAGACAGAG
AAGAGTTCATCGTAGAGACTCGATCC

mvaD-1_4-rev

GATAAGAGTCTCAGCTCTCGTTCTGCAGGATGCCGTCCAGGATGAAAACATCTTCAGAGTAGTGCGC
GTCGTAGAGACTCGATCC

mvaD-1_5-rev

GATAAGAGTCTCAGCAGGTACAATCCGCTGCTGGCGAACCAGGTTTCAGGAATTCTTTAACTTTCTT
GGTCTGTTGTAGAGACTCGATCC

mvaD-1_6-rev

GATAAGAGTCTCAGCCGCCAGACCAGCTGCGGTCCGGAACGAAGTTCTGAGATTCAACTTTTCGCGAA
CCGTAGAGACTCGATCC

mvaD-1_7-rev

GATAAGAGTCTCAGCCGAGATAGAAGACAGAGCCAGGCCAGACGCAGAGGAGTAGAGACTCGATC
C

mvaD-2

mvaD-2_1-for

GATAAGAGTCTCAGCACGCTCTGAAGACCCCTCTGCGTCTGGCCTGGCTGCACTGGCGGGTGCGTG
CAACGTTGCCATATGACTCCACAC

mvaD-2_2-for

GATAAGAGTCTCAGCGCTGGGTCTGAACCTGTCTGCGAAAGACCTGTCTCGTCTGGCGCGTCGTGG
TCATATGACTCCACAC

mvaD-2_3-for

GATAAGAGTCTCAGCTCTGGTTCTGCGTGCCGTTCTATCTTCGGTGGTTTCGCGCAGTGGAACAAAG
GTCACTCATATGACTCCACAC

mvaD-2_4-for

GATAAGAGTCTCAGCCTGACGAAACCTCTTTCGCGGAAAACATCCCGGCGAACAACTGGGAAAACG
AACTGGCGATGCATATGACTCCACAC

mvaD-2_5-for

GATAAGAGTCTCAGCCTGTTTCATCCTGATCAACGACGGTGAAAAAGACGTTTCTTCTCGCGACGGCA
TGAAACGTACCGCATATGACTCCACAC

mvaD-2_6-for

GATAAGAGTCTCAGCTTGAAACCTCTTCTTTCTACCAGGGCTGGCTGGACAACGTTGAAAAAGATCT
GTCTCAGGTTACGAAGCCTGTCTTCTATCTCGCATATGACTCCACAC

mvaD-2_1-rev

GATAAGAGTCTCAGCGTGCAGCCAGGCCAGACGCAGAGGGGTCTTCAGAGCGTCATATGACTCCAC
AC

mvaD-2_2-rev

GATAAGAGTCTCAGCGGTCTTTCGAGACAGGTTTCAGACCCAGCGCAACGTTGCACGCACCCGCCA
CATATGACTCCACAC

mvaD-2_3-rev

GATAAGAGTCTCAGCCCAGATAGAACGGCACGCAGAACCCAGAACCCACGACGCGCCAGACGAGA
CACATATGACTCCACAC

mvaD-2_4-rev

GATAAGAGTCTCAGCCGGGATGTTTTCCGCGAAAAGAGGTTTCGTCAGAGTGACCTTTGTTCCACTGC
GCGAAACCACATATGACTCCACAC

mvaD-2_5-rev

GATAAGAGTCTCAGCACGTCTTTTTACCGTCGTTGATCAGGATGAACAGCATCGCCAGTTCGTTTTC
CCAGTTGTTCCGATATGACTCCACAC

mvaD-2_6-rev

GATAAGAGTCTCAGCCAGCCAGCCCTGGTAGAAAAGAAGAGGTTTCAACGGTACGTTTCATGCCGTC
GCGAGAAGAACATATGACTCCACAC

mvaD-2_7-rev

GATAAGAGTCTCAGCCGAGATAGAAGACAGGCTTCGTGAACCTGAGACAGATCTTTTTCAACGTTGT
CCATATGACTCCACAC

mvaD-3

mvaD-3_1-for

GATAAGAGTCTCAGCACGCTCTGAAGACCCAAAAAGATCTGTCTCAGGTTACGAAGCGATTAAAA
CCAAAGACTTCCCGCGCCTGGGTGAAATCATTGAGAATTGACTCGATCC

mvaD-3_2-for

GATAAGAGTCTCAGCAGCGAACGGCCTGCGTATGCACGGTACCACCCTGGGCGCGGTTCCGAATTG
ACTCGATCC

mvaD-3_3-for

GATAAGAGTCTCAGCGCCGTTACCTACTGGTCTCCGGGTTCTCTGCAGGCGATGGCGCTGGTTGAA
TTGACTCGATCC

mvaD-3_4-for

GATAAGAGTCTCAGCCGCCAGGCGCGTGCGAAAGGTATCCCGTGTTACTTCACCATGGACGCTGGT
CGAATTGACTCGATCC

mvaD-3_5-for

GATAAGAGTCTCAGCCGAACGTTAAAGTTCTGGTTGAAAAGAAGAACCTGGAAGCGCTGAAAACCT
TCCTGTCTGAACACTTCTCTAAAGAACAGGAATTGACTCGATCC

mvaD-3_6-for

GATAAGAGTCTCAGCCTGGTTCGGCGGTTCCGCGGGTCCGGGTATCGAACTGTTGAAACCAAAGGT
ATGGACAAATAACTGTCTTCTATCTCGGAATTGACTCGATCC

mvaD-3_1-rev

GATAAGAGTCTCAGCCTTTGGTTTTAATCGCTTCGTGAACCTGAGACAGATCTTTTTGGGTCTTCAGA
GCGTGAATTGACTCGATCC

mvaD-3_2-rev

GATAAGAGTCTCAGCCGTGCATACGCAGGCCGTTTCGCTTCAATGATTTACCCAGGCGCGGGAAGT
GAATTGACTCGATCC

mvaD-3_3-rev

GATAAGAGTCTCAGCACCCGGAGACCAGTAGGTGAACGGCGGAACCGCGCCCAGGGTGGTACGAA
TTGACTCGATCC

mvaD-3_4-rev

GATAAGAGTCTCAGCATACCTTTTCGCACGCGCCTGGCGAACCAGCGCCATCGCCTGCAGAGAGAAT
TGACTCGATCC

mvaD-3_5-rev

GATAAGAGTCTCAGCGCTTCCAGGTTCTTCTTTCAACCAGAACTTTAACGTTCCGACCAGCGTCCAT
GGTGAAGTAACACGGGGAATTGACTCGATCC

mvaD-3_6-rev

GATAAGAGTCTCAGCGACCCGCGAACGCCGGAACCAGCTGTTCTTTAGAGAAGTGTTTCAGACAGGA
AGGTTTTTCAGCGAATTGACTCGATCC

mvaD-3_7-rev

GATAAGAGTCTCAGCCGAGATAGAAGACAGTTATTTGTCCATACCTTTGGTTTCGAACAGTTTCGATA
CCCAGGAATTGACTCGATCC

idi-1

idi-1_1-for

GAGTGGAGTCTACCGACGCTCTGAAGACCCATGAACCGCAAAGATGAACACCTGTCTCTGGCGAAA
GCGTTCCACAAAAAAAATCTAACGACTTCGAGAATTGACTCGATCC

idi-1_2-for

GAGTGGAGTCTACCGCCGTGTTTCGTTTCGTTACCACTTTTCGCGGAATCTGCGGTTAACGAAGTT
GACATCTCTGAATTGACTCGATCC

idi-1_3-for

GAGTGGAGTCTACCGACCTTTTCCTGTCTTTCCAGCTGCCGCAGCCGTTCTATGTTAACGCGATGAC
CGGGAATTGACTCGATCC

idi-1_4-for

GAGTGGAGTCTACCGCGTTCTCAGCGTGCGAAAGAAATCAACCAGCAGCTGGGTATCATTGCGAA
AGAAACCGGAATTGACTCGATCC

idi-1_5-for

GAGTGGAGTCTACCGGCCTGCTGGTTGCGACCGTTCTGTTTCTGCGGCGCTGAAAGACGCGAATT
GACTCGATCC

idi-1_6-for

GAGTGGAGTCTACCGGTCTCTGGCGGACACCTACCAGATCATGCGTAAAGAAAACCCGGACGGTCT
GATCTTCGCTGTCTTCTATCTCGGAATTGACTCGATCC

idi-1_1-rev

GAGTGGAGTCTACCGCCAGAGACAGGTGTTTCATCTTTGCGGTTTCATGGGTCTTCAGAGCGTGAATT
GACTCGATCC

idi-1_2-rev

GAGTGGAGTCTACCGCGAAAGACTGGTGAACGAAACGAACACGGTCGAAGTCGTTAGATTTTTTTT
TGTGGAACGCTTTTCGGAATTGACTCGATCC

idi-1_3-rev

GAGTGGAGTCTACCGCGGCAGCTGGAAAGACAGGAAAGAGGTAGAGATGTCAACTTCGTTAACCG
CAGATTCCGGAATTGACTCGATCC

idi-1_4-rev

GAGTGGAGTCTACCGGGTTGATTTCTTCGCACGCTGAGAACCGCCGGTCATCGCGTTAACATAGAA
CGGCTGGAATTGACTCGATCC

idi-1_5-rev

GAGTGGAGTCTACCGGAACCGGTCGCAACCAGCAGGCCGTTTCTTTCGCAATGATACCCAGCTGC
TGAATTGACTCGATCC

idi-1_6-rev

GAGTGGAGTCTACCGCATGATCTGGTAGGTGTCCGCCAGAGACGCGTCTTTCAGCGCCGCAGAAAC
AGAATTGACTCGATCC

idi-1_7-rev

GAGTGGAGTCTACCGCGAGATAGAAGACAGCGAAGATCAGACCGTCCGGGTTTTCTTTACGGAATT
GACTCGATCC

idi-2

idi-2_1-for

GAGTGGAGTCTACCGACGCTCTGAAGACCCAAACCCGGACGGTCTGATCTTCGGAACATCGGTGC
GGGTCTGGGTGTTGATGGATGACTCGAACG

idi-2_2-for

GAGTGGAGTCTACCGAGAAGCGAAACGTGCGCTGGACCTGTTCCAGGCGAACGCGCTGCAGATCT
GGATGACTCGAACG

idi-2_3-for

GAGTGGAGTCTACCGCACGTTAACGTTCCGCAGGAACTGGTTATGCCGGAAGGCGATCGTGACTTC
ACCAACTGTGGATGACTCGAACG

idi-2_4-for

GAGTGGAGTCTACCGGCTGACCAAAATCGAAGCGATCGTTCAGGCGGTTGAAGTCCGGTTATTGT
TAAAGAAGTTGGCTTCGTGGATGACTCGAACG

idi-2_5-for

GAGTGGAGTCTACCGGCATGTCTCAGGAAACCCTGGAAAACTGACCTCTATCGGCGTTCAGGCGG
CGGATGGATGACTCGAACG

idi-2_6-for

GAGTGGAGTCTACCGCGTTTCTGGTCAGGGTGGTACCTCTTTCACCCAGATCGAAAACGCGCGTCGT
AAAAAACGTGATGGATGACTCGAACG

idi-2_7-for

GAGTGGAGTCTACCGACTGTCTTCTGGACGACTGGGGCCCTGTCTTCTATCTCGTGGATGACTCG
AACG

idi-2_1-rev

GAGTGGAGTCTACCGTCGCGAAGATCAGACCGTCCGGGTTTGGGTCTTCAGAGCGTTGGATGACTC
GAACG

idi-2_2-rev

GAGTGGAGTCTACCGCAGGTCCAGCGCACGTTTCGCTTCTTCAACACCCAGACCCGCACCGATGTTG
GATGACTCGAACG

idi-2_3-rev

GAGTGGAGTCTACCGGCATAACCAGTTCCTGCGGAACGTTAACGTGGATCTGCAGCGCGTTCGCCT
GGAATGGATGACTCGAACG

idi-2_4-rev

GAGTGGAGTCTACCGGCCTGAACGATCGCTTCGATTTTGGTCAGCCAGTTGGTGAAGTCACGATCG
CCTTCCGTGGATGACTCGAACG

idi-2_5-rev

GAGTGGAGTCTACCGGGTCAGTTTTTCCAGGGTTTCTGAGACATGCCGAAGCCAACTTCTTTAACA
ATAACCGGAACCTCAACCTGGATGACTCGAACG

idi-2_6-rev

GAGTGGAGTCTACCGGGTGAAAGAGGTACCACCCTGACCAGAAACGTCCGCCGCTGAACGCCGAT
AGATGGATGACTCGAACG

idi-2_7-rev

GAGTGGAGTCTACCGCGAGATAGAAGACAGGGCCCCAGTCGTCCAGGAAAGACAGTTCACGTTTTT
TACGACGCGCGTTTTTCGATCTGTGGATGACTCGAACG

idi-3

idi-3_1-for

GAGTGGAGTCTACCGACGCTCTGAAGACCCTTCTCTGGACGACTGGGGCCAGTCTACCGTTATCTCT
CTGCTGGAATCTCAGAACTGGCAGCATCCGACTCCATGC

idi-3_2-for

GAGTGGAGTCTACCGAAAAAACTGACCATTCTGGGTCTGGTGGCGTTCGTAACCTCTCTGGACATCG
TTAAAGGCCTGGCCATCCGACTCCATGC

idi-3_3-for

GAGTGGAGTCTACCGGCTGGGCGCGAAATCTATGGGCGTTGCGGGTACCATTCTGGCGTCTCTGAT
GTCATCCGACTCCATGC

idi-3_4-for

GAGTGGAGTCTACCGCTAAAAACGGTCTGGAAAACACCCTGGCGCTGGTTCAGCAGTGGCAGGAA
GAAGTTAAAATGCTCATCCGACTCCATGC

idi-3_5-for

GAGTGGAGTCTACCGGTATACCCTGCTGGGCAAAAAACCACCGAAGAACTGACCTCTACCGCGCT
GGTTCTGGATCCATCCGACTCCATGC

idi-3_6-for

GAGTGGAGTCTACCGCGTTCTGGTTAACTGGTGCCACAACCGTGGCATCGATTCTACCGTTTTCGC
GAAACGCTAACTGTCTTCTATCTCGCATCCGACTCCATGC

idi-3_1-rev

GAGTGGAGTCTACCGGTAGACTGGCCCCAGTCGTCCAGGAAAGGGTCTTCAGAGCGTCATCCGACT
CCATGC

idi-3_2-rev

GAGTGGAGTCTACCGAACGCCACCAGAACCAGAATGGTCAGTTTTTTCTGCCAGTTCTGAGATTCC
AGCAGAGAGATAACGCATCCGACTCCATGC

idi-3_3-rev

GAGTGGAGTCTACCGAACGCCATAGATTTTCGCGCCCAGCGCCAGGCCTTTAACGATGTCCAGAGA
GTTACGCATCCGACTCCATGC

idi-3_4-rev

GAGTGGAGTCTACCGGCGCCAGGGTGTTTTCCAGACCGTTTTTAGACATCAGAGACGCCAGAATGG
TACCCGCCATCCGACTCCATGC

idi-3_5-rev

GAGTGGAGTCTACCGTTCTTCGGTGGTTTTTTGCCAGCAGGGTATACAGCATTTTAACTTCTTCCT
GCCACTGCTGAACCACATCCGACTCCATGC

idi-3_6-rev

GAGTGGAGTCTACCGACGGTTGTGGCACCAGTTAACCAGAACCGGATCCAGAACCAGCGCGGTAG
AGGTCAGCATCCGACTCCATGC

idi-3_7-rev

GAGTGGAGTCTACCGCGAGATAGAAGACAGTTAGCGTTTCGCGAAAACGGTAGAATCGATGCCAT
CCGACTCCATGC

crtE-1

crtE-1_1-for

CACAGGAGTCCTCACACGCTCTGAAGACCCATGACCGTTTGTGCGAAAAAACACGTTACCTGACCC
GTGATGCGGCGGAACAGCGTAGAGACTCGATCC

crtE-1_2-for

CACAGGAGTCCTCACTGCTGGCGGACATCGACCGTCGTCTGGATCAGCTGCTGCCGGTTGAAGGGT
AGAGACTCGATCC

crtE-1_3-for

CACAGGAGTCCTCACTGAACGTGATGTTGTTGGTGCGGCGATGCGCGAAGGTGCGCTGGCGCGTA
GAGACTCGATCC

crtE-1_4-for

CACAGGAGTCCTCACCGGGCAAACGTATCCGTCCGATGCTGCTGCTGCTGACCGCGCGGAGTAGA
GACTCGATCC

crtE-1_5-for

CACAGGAGTCCTCACTCTGGGTTGTGCGGTTTCTCACGATGGCCTGCTGGATCTGGCGTGCGCGGG
TAGAGACTCGATCC

crtE-1_6-for

CACAGGAGTCCTCACTTGAAATGGTTCACGCGGCGTCTCTGATCCTGGACGATATGCCGTGCATGGA
CGACGCTGTCTTCTATCTCGGTAGAGACTCGATCC

crtE-1_1-rev

CACAGGAGTCCTCACAGGTGAACGTGTTTTTCGCACAAACGGTCATGGGTCTTCAGAGCGTGTAGA
GACTCGATCC

crtE-1_2-rev

CACAGGAGTCCTCACACGACGGTCGATGTCCGCCAGCAGCTGTTCCGCCGCATCACGGGTCGTAGA
GACTCGATCC

crtE-1_3-rev

CACAGGAGTCCTCACCATCGCCGCACCAACAACATCACGTTACCTTCAACCGGCAGCAGCTGATCC
AGGTAGAGACTCGATCC

crtE-1_4-rev

CACAGGAGTCCTCACCAGCATCGGACGGATACGTTTGCCCGGCCAGCGCACCTTCGCGGTAGAG
ACTCGATCC

crtE-1_5-rev

CACAGGAGTCCTCACGCCATCGTGAGAAACCGCACAAACCAGATCGCGCGCGGTACGACAGCAGGTA
GAGACTCGATCC

crtE-1_6-rev

CACAGGAGTCCTCACGGATCAGAGACGCCGCGTGAACCATTTCACCGCGCACGCCAGATCCAGCA
GGTAGAGACTCGATCC

crtE-1_7-rev

CACAGGAGTCCTCACCGAGATAGAAGACAGCGTCGTCCATGCACGGCATATCGTCCAGTAGAGACT
CGATCC

crtE-2

crtE-2_1-for

CACAGGAGTCCTCACACGCTCTGAAGACCCGATATGCCGTGCATGGACGACGCGAAACTGCGCCGT
GGTCGCCCCATATGACTCCACAC

crtE-2_2-for

CACAGGAGTCCTCACGACCATTCACTCTCACTACGGCGAACACGTTGCGATTCTGGCGGCGGTTGCA
TATGACTCCACAC

crtE-2_3-for

CACAGGAGTCCTCACCGCTGCTGTCTAAAGCGTTCGGTGTTATCGCGGATGCGGACGGTCTGACCAT
ATGACTCCACAC

crtE-2_4-for

CACAGGAGTCCTCACCCCGCTGGCGAAAAACCGTGCGGTTTCTGAACTGTCTAACGCGATCGGTATG
CATATGACTCCACAC

crtE-2_5-for

CACAGGAGTCCTCACCCAGGGCCTGGTTCAGGGCCAGTTCAAAGATCTGTCTGAAGGCGACAAACCG
CATATGACTCCACAC

crtE-2_6-for

CACAGGAGTCCTCACCGCTCTGCGGAAGCGATCCTGATGACCAACCACTTCAAAACCTCTACCCTGT
TCCATATGACTCCACAC

crtE-2_7-for

CACAGGAGTCCTCACTGCGCGTCTATGCAGATGGCGTCTACTGTCTTCTATCTCGCATATGACTCCAC
AC

crtE-2_1-rev

CACAGGAGTCCTCACCGCGTCGTCCATGCACGGCATATCGGGTCTTCAGAGCGTCATATGACTCCAC
AC

crtE-2_2-rev

CACAGGAGTCCTCACGTGTTTCGCCGTAGTGAGAGTGAATGGTCGGGCGACCACGGCGCAGTTTCAT
ATGACTCCACAC

crtE-2_3-rev

CACAGGAGTCCTCACATAACACCGAACGCTTTAGACAGCAGCGCAACCGCCGCCAGAATCGCAACC
ATATGACTCCACAC

crtE-2_4-rev

CACAGGAGTCCTCACGCACGGTTTTTCGCCAGCGGGGTCAGACCGTCCGCATCCGCGCATATGACTC
CACAC

crtE-2_5-rev

CACAGGAGTCCTCACTGGCCCTGAACCAGGCCCTGCATACCGATCGCGTTAGACAGTTCAGAAACCC
ATATGACTCCACAC

crtE-2_6-rev

CACAGGAGTCCTCACATCAGGATCGCTTCCGCAGAGCGCGGTTTGTCGCCTTCAGACAGATCTTTGA
ACCATATGACTCCACAC

crtE-2_7-rev

CACAGGAGTCCTCACCGAGATAGAAGACAGTAGACGCCATCTGCATAGACGCGCAGAACAGGGTA
GAGGTTTTGAAGTGGTTGGTCCATATGACTCCACAC

crtE-3

crtE-3_1-for

CACAGGAGTCCTCACACGCTCTGAAGACCCCGCTCTATGCAGATGGCGTCTATTGTTGCGAACGCG
TCCTCTGAAGCGCGTGATTGGAATTGACTCGATCC

crtE-3_2-for

CACAGGAGTCCTCACCTGCACCGTTTCTCTCTGGACCTGGGCCAGGCGTTCCAGCTGCTGGACGGA
ATTGACTCGATCC

crtE-3_3-for

CACAGGAGTCCTCACATCTGACCGATGGCATGACCGACACCGGCAAAGATTCTAACCAGGACGCGG
GTAAATCTACCGAATTGACTCGATCC

crtE-3_4-for

CACAGGAGTCCTCACCTGGTTAACCTGCTGGGTCCGCGTGCGGTTGAAGAACGTCTGCGTCAGCAC
CTGAATTGACTCGATCC

crtE-3_5-for

CACAGGAGTCCTCACGCAGCTGGCGTCTGAACACCTGTCTGCGGCGTGCCAGCACGGCCAGAATTG
ACTCGATCC

crtE-3_6-for

CACAGGAGTCCTCACCGCGACCCAGCACTTCATCCAGGCGTGGTTCGATAAAAACTGGCGGCGGT
TTCTTAAGTGTCTTCTATCTCGGAATTGACTCGATCC

crtE-3_1-rev

CACAGGAGTCCTCACGCAACAATAGACGCCATCTGCATAGACGCGGGGTCTTCAGAGCGTGAATTG
ACTCGATCC

crtE-3_2-rev

CACAGGAGTCCTCACCCCAGGTCCAGAGAGAAACGGTGCAGGCAATCACGCGCTTCAGAGGACGC
GTTTGAATTGACTCGATCC

crtE-3_3-rev

CACAGGAGTCCTCACCGGTGTCGGTCATGCCATCGGTTCAGATCGTCCAGCAGCTGGAACGCCTGGG
AATTGACTCGATCC

crtE-3_4-rev

CACAGGAGTCCTCACACGCGGACCCAGCAGGTTAACCAGGGTAGATTTACCCGCGTCCTGGTTAG
AATCTTTGCGAATTGACTCGATCC

crtE-3_5-rev

CACAGGAGTCCTCACAGACAGGTGTTTCAGACGCCAGCTGCAGGTGCTGACGCAGACGTTCTTCAA
CCGGAATTGACTCGATCC

crtE-3_6-rev

CACAGGAGTCCTCACGCCTGGATGAAGTGCTGGGTGCGTGGCCGTGCTGGCACGCCGGAATTGAC
TCGATCC

crtE-3_7-rev

CACAGGAGTCCTCACCGAGATAGAAGACAGTTAAGAAACCGCCGCCAGTTTTTTATCGAACCACGA
ATTGACTCGATCC

crtB-1

crtB-1_1-for

GTATAGAGTCAGTCGACGCTCTGAAGACCCATGGAAGTCGGTTCCAAGTCCTTCGCGACGGCGTCT
AAGCTGTTTCGACGCGAAAACATACAGACTCGACAG

crtB-1_2-for

GTATAGAGTCAGTCGGCGCCGCTCCGTTCTGATGCTGTACGCGTGGTGCCGCCACTGCGATACAGA
CTCGACAG

crtB-1_3-for

GTATAGAGTCAGTCGACGACGTGATCGACGACCAGGTGCTGGGCTTCTCCAATGACACCCCGTCCAT
ACAGACTCGACAG

crtB-1_4-for

GTATAGAGTCAGTCGCTGCAATCCGCTGAGCAGCGCCTGGCCCAACTGGAAATGAAAACGCGCCAT
ACAGACTCGACAG

crtB-1_5-for

GTATAGAGTCAGTCGAGGCTTACGCGGGCTCTCAGATGCACGAACCGGCGTTCGCGGCCATACAGA
CTCGACAG

crtB-1_6-for

GTATAGAGTCAGTCGTTCCAAGAAGTGGCGATGGCTCACGACATCCTGCCGGCCTACGCATTTGACC
ATCCTGTCTTCTATCTCGATACAGACTCGACAG

crtB-1_1-rev

GTATAGAGTCAGTCGTCGGAAGGACTTGGAACCGACTTCCATGGGTCTTCAGAGCGTATACAGAC
TCGACAG

crtB-1_2-rev

GTATAGAGTCAGTCGGTACAGCATCAGAACGGAGCGGCGCGTTTTTCGCGTCGAACAGCTTAGACGC
CGATACAGACTCGACAG

crtB-1_3-rev

GTATAGAGTCAGTCGAGCACCTGGTCGTCGATCACGTCGTCGAGTGGCGGCACCACGCATACAGA
CTCGACAG

crtB-1_4-rev

GTATAGAGTCAGTCGAGGCGCTGCTCAGCGGATTGCAGGGACGGGGTGTCATTGGAGAAGCCCAT
ACAGACTCGACAG

crtB-1_5-rev

GTATAGAGTCAGTCGTGCATCTGAGAGCCCGCGTAAGCCTGGCGCGTTTTTCATTTCAGTTGGGCCA
TACAGACTCGACAG

crtB-1_6-rev

GTATAGAGTCAGTCGATGTCGTGAGCCATCGCCACTTCTTGGAAGGCCGCGAACGCCGGTTCGATA
CAGACTCGACAG

crtB-1_7-rev

GTATAGAGTCAGTCGCGAGATAGAAGACAGGATGGTCAAATGCGTAGGCCGGCAGGATACAGACT
CGACAG

crtB-2

crtB-2_1-for

GTATAGAGTCAGTCGACGCTCTGAAGACCCCGGCCTACGCATTTGACCATCTGGCCGGTTTCGCGA
TGGACGTGCATGAAACCCGAGACGACTCGTAAG

crtB-2_2-for

GTATAGAGTCAGTCGGCTACCAGACGCTGGACGACACCCTGCGCTACTGCTACCACGTCGCTGGTGT
GGAGACGACTCGTAAG

crtB-2_3-for

GTATAGAGTCAGTCGGTCGGCCTGATGATGGCGCAGATCATGGGTGTGCGTGACAACGCCACTCTG
GATCGGAGACGACTCGTAAG

crtB-2_4-for

GTATAGAGTCAGTCGTGCGTGCGACCTGGGTCTGGCGTTCCAGCTGACCAACATCGCCGCGGAGA
CGACTCGTAAG

crtB-2_5-for

GTATAGAGTCAGTCGACATCGTAGAGGACGCCGAAGCAGGTCGTTGCTACCTGCCTGCGGCATGGC
TGGAGACGACTCGTAAG

crtB-2_6-for

GTATAGAGTCAGTCGGCCGAAGAAGGTCTGACGCGCGAGAATCTGGCGGACCCACAGAATCGCAA
GGCTCCTGTCTTCTATCTCGGAGACGACTCGTAAG

crtB-2_1-rev

GTATAGAGTCAGTCGGGCCAGATGGTCAAATGCGTAGGCCGGGGGTCTTCAGAGCGTGAGACGAC
TCGTAAG

crtB-2_2-rev

GTATAGAGTCAGTCGCAGGGTGTCGTCCAGCGTCTGGTAGCGGGTTTCATGCACGTCCATCGCGAA
ACCGAGACGACTCGTAAG

crtB-2_3-rev

GTATAGAGTCAGTCGCCATGATCTGCGCCATCATCAGGCCGACCACACCAGCGACGTGGTAGCAGT
AGCGGAGACGACTCGTAAG

crtB-2_4-rev

GTATAGAGTCAGTCGCGCCAGACCCAGGTCGCACGCACGATCCAGAGTGGCGTTGTCACGCACACG
AGACGACTCGTAAG

crtB-2_5-rev

GTATAGAGTCAGTCGCGACCTGCTTCGGCGTCCTCTACGATGTCGCGGGCGATGTTGGTCAGCTGG
AAGAGACGACTCGTAAG

crtB-2_6-rev

GTATAGAGTCAGTCGAGATTCTCGCGCGTCAGACCTTCTTCGGCCAGCCATGCCGCAGGCAGGTAG
CAAGAGACGACTCGTAAG

crtB-2_7-rev

GTATAGAGTCAGTCGCGAGATAGAAGACAGGAGCCTTGCGATTCTGTGGGTCCGCCGAGACGACTC
GTAAG

crtB-3

crtB-3_1-for

GTATAGAGTCAGTCGACGCTCTGAAGACCCGACCCACAGAATCGCAAGGCTCTGTCCCGTGTGCTC
GCCGTCTGGTGGATCGGACTCGTACC

crtB-3_2-for
 GTATAGAGTCAGTCGGAAACCGCGGAGCCATACTACCGCAGCGCTCCGCAGGTCTGCGATCGGAC
 TCGTACC

crtB-3_3-for
 GTATAGAGTCAGTCGCTGGTCTGCCTCTGCGCTCTGCTTGGGCAATCGCAACGGCGCAGATCGGACT
 CGTACC

crtB-3_4-for
 GTATAGAGTCAGTCGGCAAGTGTACCGCAAGATCGGCATGAAGGTCGTGCAGGCGGGTCCCGATC
 GGACTCGTACC

crtB-3_5-for
 GTATAGAGTCAGTCGAGGCGTGGGAACAGCGCCAAAGCACCTCCACGCCGAAAAAGCTGGGATCG
 GACTCGTACC

crtB-3_6-for
 GTATAGAGTCAGTCGCACTGCTGGTTGCTGCCAGCGGTCAAGCCGTGACCTCTCGCGTAGGATCGG
 ACTCGTACC

crtB-3_7-for
 GTATAGAGTCAGTCGCCCCTCATGCGCCTCGTTCTGCGGATCTGTGGCAGCGTCCGGTTTAACTGTC
 TTCTATCTCGGATCGGACTCGTACC

crtB-3_1-rev
 GTATAGAGTCAGTCGGACAGAGCCTTGCATTCTGTGGGTCGGGTCTTCAGAGCGTGATCGGACTC
 GTACC

crtB-3_2-rev
 GTATAGAGTCAGTCGGCGGTAGTATGGCTCCGCGGTTTCCACCAGACGGCGAGCAACACGGGATCG
 GACTCGTACC

crtB-3_3-rev
 GTATAGAGTCAGTCGGCAGAGCGCAGAGGCAGACCAGGCAGACCTGCGGACGCGCTGATCGGACT
 CGTACC

crtB-3_4-rev
 GTATAGAGTCAGTCGTTTCATGCCGATCTTGCGGTACACTTGCTGCGCCGTTGCGATTGCCCAAGATC
 GGACTCGTACC

crtB-3_5-rev
 GTATAGAGTCAGTCGCTTTGGCGCTGTTCCACGCCTGGGAACCCGCCTGCACGACCGATCGGACTC
 GTACC

crtB-3_6-rev
 GTATAGAGTCAGTCGCGCTGGCAGCAACCAGCAGTGCCAGCTTTTCCGGCGTGAGGTGGATCGGA
 CTCGTACC

crtB-3_7-rev
 GTATAGAGTCAGTCGGCAGAACGAGGCGCATGACGGGCTACGCGAGAGGTCACGGCTTGACGATC
 GGACTCGTACC

crtB-3_8-rev
 GTATAGAGTCAGTCGCGAGATAGAAGACAGTTAAACCGGACGCTGCCACAGATCCGATCGGACTCG
 TACC

crt1-1
 crt1-1_1-for
 CCAAGGAGTCGCTAGACGCTCTGAAGACCCATGAACCGTACGACCGTAATTGGTGCGGGCTTCGGT
 GGCCTGGCACTGGCGGAAGGGACTCGTACG
 crt1-1_2-for
 CCAAGGAGTCGCTAGATCCGTCTGCAAGCCTCTGGTGTCCCTACTCGTCTGCTGGAACAGCGCGACA
 GAAGGGACTCGTACG
 crt1-1_3-for
 CCAAGGAGTCGCTAGAACAGGCGGTCTGTCTTACGTGTACCAAGATCAGGGTTTCACCTTCGACG
 CTGGTGAAGGGACTCGTACG
 crt1-1_4-for
 CCAAGGAGTCGCTAGCCGACTGTCATCACCGATCCATCTGCGATCGAAGAACTGTTTACTCTGGCCG
 GCAAGAAGAAGGGACTCGTACG
 crt1-1_5-for
 CCAAGGAGTCGCTAGGCTGTCTGACTACGTGGAAGTATGCCAGTTAAACCATTTTATCGTCTGTGC
 TGGGAATCTGGTAAGGTATTGAAGGGACTCGTACG
 crt1-1_6-for
 CCAAGGAGTCGCTAGCAGCTACGACAACGATCAACCGGCCCTGGAAGCGCAGATTGCGGCCTTCAA
 CCGAAGGGACTCGTACG
 crt1-1_7-for
 CCAAGGAGTCGCTAGCGCGTGATGTAGAGGGCTATCGCCGTTCTGTCTTCTATCTCGGAAGGGACTC
 GTACG
 crt1-1_1-rev
 CCAAGGAGTCGCTAGCCCGCACCAATTACGGTCGTACGGTTCATGGGTCTTCAGAGCGTGAAGGGA
 CTCGTACG
 crt1-1_2-rev
 CCAAGGAGTCGCTAGGGGACACCAGAGGCTTGACAGACGGATCGCCAGTGCCAGGCCACCGAAGGA
 AGGGACTCGTACG
 crt1-1_3-rev
 CCAAGGAGTCGCTAGGGTACACGTAAGCACGACCGCCTGGTTTGTGCGGCTGTTCCAGCAGACGAG
 TAGAAGGGACTCGTACG
 crt1-1_4-rev
 CCAAGGAGTCGCTAGTCGCAGATGGATCGGTGATGACAGTCGGACCAGCGTGAAGGTGAAACCC
 TGATCTTGAAGGGACTCGTACG
 crt1-1_5-rev
 CCAAGGAGTCGCTAGACTGGCATCAGTTCCACGTAGTCAGACAGCTTCTTGCCGGCCAGAGTAAAC
 AGTTCTTCGAGAAGGGACTCGTACG
 crt1-1_6-rev
 CCAAGGAGTCGCTAGAGGGCCGGTTGATCGTTGTCGTAGCTGAATACCTTACCAGATTCCCAGCACA
 GACGATAAAATGGTTTAGAAGGGACTCGTACG
 crt1-1_7-rev
 CCAAGGAGTCGCTAGCGAGATAGAAGACAGAACGGCGATAGCCCTCTACATCACGCGGGTTGAAG
 GCCGCAATCTGCGCTTCCGAAGGGACTCGTACG

crtl-2

crtl-2_1-for
CCAAGGAGTCGCTAGACGCTCTGAAGACCCGTGATGTAGAGGGCTATCGCCGTTTTCTGGCGTATTC
TCGCGCGGTCTTTGCGGAAGGTTAATACAGACTCGACAG

crtl-2_2-for
CCAAGGAGTCGCTAGCCTGAAGCTGGGCACTGTGCCATTCTGTCTTTCCGTGACATGCTGCGTGCT
GCATACAGACTCGACAG

crtl-2_3-for
CCAAGGAGTCGCTAGACCGCAACTGGCTAAACTGCAGGCTTGGCGCTCCGTATATTCTAAAGTTGCG
TCTTACATCGAGATACAGACTCGACAG

crtl-2_4-for
CCAAGGAGTCGCTAGGACGAGCACCTGCGTCAAGCGTTCTCTTTTACAGCCTGCTGGTCGGCGGAT
ACAGACTCGACAG

crtl-2_5-for
CCAAGGAGTCGCTAGTAACCCGTTTGCGACCTCTTCCATCTATACGCTGATCCACGCACTGGAACGC
GAGTGGATACAGACTCGACAG

crtl-2_6-for
CCAAGGAGTCGCTAGGGTGTGTGGTTCCCTCGTGGCGGTACGGGTGCCCTGGTGCAAGGCATATAC
AGACTCGACAG

crtl-2_7-for
CCAAGGAGTCGCTAGGGTAAAGCTGTTGAGGATCTGGGTGGTGAAGTTGAGCTGAACGCGTCTGT
AGCTCGCCCTGTCTTCTATCTCGATACAGACTCGACAG

crtl-2_1-rev
CCAAGGAGTCGCTAGGCCAGAAAACGGCGATAGCCCTCTACATCACGGGTCTTCAGAGCGTATACA
GACTCGACAG

crtl-2_2-rev
CCAAGGAGTCGCTAGAGGAATGGCACAGTGCCCAGCTTCAGGTAACCTCCGCAAAGACCGCGCGA
GAATACATACAGACTCGACAG

crtl-2_3-rev
CCAAGGAGTCGCTAGCAAGCCTGCAGTTTAGCCAGTTGCGGTGCAGCACGCAGCATGTCACGGAAA
GACATACAGACTCGACAG

crtl-2_4-rev
CCAAGGAGTCGCTAGGAGAACGCTTGACGCAGGTGCTCGTCCTCGATGTAAGACGCAACTTTAGAA
TATACGGAGCGCATACAGACTCGACAG

crtl-2_5-rev
CCAAGGAGTCGCTAGAGCGTATAGATGGAAGAGGTCGCAAACGGGTTACCGCCGACCAGCAGGCT
GTGAAAAATACAGACTCGACAG

crtl-2_6-rev
CCAAGGAGTCGCTAGCCGCCACGAGGGAACACACACCCCACTCGCGTTCCAGTGCGTGGATCATA
CAGACTCGACAG

crtl-2_7-rev

CCAAGGAGTCGCTAGCTTCACCACCCAGATCCTCGAACAGCTTTACCATGCCTTGCACCAGGGCACC
CGTAATACAGACTCGACAG

crtl-2_8-rev

CCAAGGAGTCGCTAGCGAGATAGAAGACAGGGCGAGCTACAGACGCGTTCAGCTCAAATACAGAC
TCGACAG

crtl-3

crtl-3_1-for

CCAAGGAGTCGCTAGACGCTCTGAAGACCCTGAACGCGTCTGTAGCTCGCCTGGAAACTCAAGAAA
ACCGCATCACGGCAGTGCGATCGGACTCGTACC

crtl-3_2-for

CCAAGGAGTCGCTAGATCTGAAAGACGGTCGCGTGTTCCTCAACTCGTGCAGTTGCCTCCAATGCCGA
CGGATCGGACTCGTACC

crtl-3_3-for

CCAAGGAGTCGCTAGTGGTTCATACTTATCGTGAGCTGCTGTCTCAACACCCTGCTTCTCAGGCCCA
GGGTCGATCGGACTCGTACC

crtl-3_4-for

CCAAGGAGTCGCTAGGCTCTCTGCAAAACAAGCGTATGTCTAATAGCCTGTTTGTAAATTTACTTCGG
CCTGAACCATCACCACGATCGATCGGACTCGTACC

crtl-3_5-for

CCAAGGAGTCGCTAGAGCTGGCGCACCACACCGTCTGTTTTGGCCCGCGCTACCGCGAGATCGGAC
TCGTACC

crtl-3_6-for

CCAAGGAGTCGCTAGGCTGATTGACGAAATCTTCAACAAAGATGGTCTGGCGGAGGATTTCTCTCT
GTACCTGCACGCTCGATCGGACTCGTACC

crtl-3_7-for

CCAAGGAGTCGCTAGCTTGCCTTACTGACCCGTCCCTGGCCCCTGAGGGCTGCGGCAGCTCTGTCTT
CTATCTCGGATCGGACTCGTACC

crtl-3_1-rev

CCAAGGAGTCGCTAGTTCAGGCGAGCTACAGACGCGTTCAGGGTCTTCAGAGCGTGATCGGACTC
GTACC

crtl-3_2-rev

CCAAGGAGTCGCTAGGAGTTGGAAACACGCGACCGTCTTTCAGATGCACTGCCGTGATGCGGTTTT
CTTGAGTGATCGGACTCGTACC

crtl-3_3-rev

CCAAGGAGTCGCTAGTGTGAGACAGCAGCTCACGATAAGTATGAACCACGTCGGCATTGGAGGCA
ACTGCACGATCGGACTCGTACC

crtl-3_4-rev

CCAAGGAGTCGCTAGAACAGGCTATTAGACATACGCTTGTGTTTGCAGAGAGCGACCTGGGCCTGA
GAAGCAGGGGATCGGACTCGTACC

crtl-3_5-rev

CCAAGGAGTCGCTAGCAGACGGTGTGGTGCGCCAGCTGATCGTGGTGATGGTTCAGGCCGAAGTA
AATTACAGATCGGACTCGTACC

crtl-3_6-rev

CCAAGGAGTCGCTAGGCCAGACCATCTTTGTTGAAGATTTCTGCAATCAGCTCGCGGTAGCGCGGG
CCAAAAGATCGGACTCGTACC

crtl-3_7-rev

CCAAGGAGTCGCTAGGCCAGGGACGGGTACAGTAACGCAAGGAGCGTGACGGTACAGAGAGAAAT
CCTCCGATCGGACTCGTACC

crtl-3_8-rev

CCAAGGAGTCGCTAGCGAGATAGAAGACAGAGCTGCCGAGCCCTCAGGGGATCGGACTCGTACC

crtl-4

crtl-4_1-for

CCAAGGAGTCGCTAGACGCTCTGAAGACCCCTGAGGGCTGCGGCAGCTACTACGTCTGGCTCCTG
TTCCGCACCTGGGGTAGAGACTCGATCC

crtl-4_2-for

CCAAGGAGTCGCTAGTACGGCGGACATCGACTGGGCGGTTGAGGGTCCGCGCCTGCGTGAGTAGA
GACTCGATCC

crtl-4_3-for

CCAAGGAGTCGCTAGCCGCATTTTCGACTATCTGGAGCAGCACTACATGCCTGGCCTGCGCAGCCAA
CTGGGTAGAGACTCGATCC

crtl-4_4-for

CCAAGGAGTCGCTAGTGACCCACCGTATTTTCACGCCATTCGATTTTCGTGACGAAGTGAATGCCTAC
CAGGGTTCTGCGTAGAGACTCGATCC

crtl-4_5-for

CCAAGGAGTCGCTAGCTTTTCCGTTGAACCAATTCTGACCCAAAGCGCATGGTTCGGTCCGCACAAT
CGTGACAAGAACATTAAGTAGAGACTCGATCC

crtl-4_6-for

CCAAGGAGTCGCTAGCAACCTGTATCTGGTTGGTGCCGGTACGCACCCAGGCGCCGGTATTCCGGG
GTAGAGACTCGATCC

crtl-4_7-for

CCAAGGAGTCGCTAGCGTTATTGGCTCTGCGAAAGCGACCGCGGGTCTGATGCTGGAGGACCTGGC
CTAACTGTCTTCTATCTCGGTAGAGACTCGATCC

crtl-4_1-rev

CCAAGGAGTCGCTAGACGTAGTAGCTGCCGAGCCCTCAGGGGTCTTCAGAGCGTGTAGAGACTCG
ATCC

crtl-4_2-rev

CCAAGGAGTCGCTAGCCGCCAGTCGATGTCCGCGTACCCAGGTGCGGAACAGGAGCCAGGGTA
GAGACTCGATCC

crtl-4_3-rev

CCAAGGAGTCGCTAGCATGTAGTGCTGCTCCAGATAGTCGAAAATGCGGTACGCAGGCGCGGACC
CTCAAGTAGAGACTCGATCC

crtl-4_4-rev

CCAAGGAGTCGCTAGCGAAAATCGAATGGCGTGAAAATACGGTGGGTCACCAGTTGGCTGCGCAG
GCCAGGGTAGAGACTCGATCC

crtl-4_5-rev

CCAAGGAGTCGCTAGGCGCTTTGGGTCAGAATTGGTTCAACGGAAAAGGCAGAACCCTGGTAGGC
ATTCAGTTCGTCAGTAGAGACTCGATCC

crtl-4_6-rev

CCAAGGAGTCGCTAGGCGTACCGGCACCAACCAGATACAGGTTGTTAATGTTCTTGTCACGATTGTG
CGGACGGAACCATGTAGAGACTCGATCC

crtl-4_7-rev

CCAAGGAGTCGCTAGGCGGTGCTTTCGCAGAGCCAATAACGCCCAGGAATACCGGCGCCTGGGTGT
AGAGACTCGATCC

crtl-4_8-rev

CCAAGGAGTCGCTAGCGAGATAGAAGACAGTTAGGCCAGGTCCTCCAGCATCAGACCCGTAGAGAC
TCGATCC

Supplementary references

1. Martin, V.J., Pitera, D.J., Withers, S.T., Newman, J.D. and Keasling, J.D. (2003) Engineering a mevalonate pathway in *Escherichia coli* for production of terpenoids. *Nature biotechnology*, **21**, 796-802.
2. Datsenko, K.A. and Wanner, B.L. (2000) One-step inactivation of chromosomal genes in *Escherichia coli* K-12 using PCR products. *P Natl Acad Sci USA*, **97**, 6640-6645.