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 Xiaolian¹,³, Hong Jiong¹*

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

| Primers ID  | Sequence                  |
|-------------|---------------------------|
| Mlyl_1F     | CACAGGAGTCCTCAC           |
| Mlyl_2F     | CCAAGGAGTCGCTAG           |
| Mlyl-3F     | CAGAGGAGTCCTGAG           |
| Mlyl-4F     | CCTACGAGTCGCAAC           |
| Mlyl-5F     | CATTTCAGAGTCGTCTG         |
| Mlyl-6F     | CGTACGAGTCCCTTC           |
| Mlyl-7F     | CTCGAGAGTCGTAT            |
| Mlyl-8F     | GGTACGAGTCAGTC            |
| Mlyl-9F     | CTTACGAGTCGTCTC           |
| Mlyl-10F    | GGATCGAGTCCTAC            |
| Mlyl-11F    | GGTGAGAGTCATATG           |
| Mlyl-12F    | GGATCAGTCAATTG            |
| Mlyl-13F    | CGTTGAGTCATCCCA           |
| Mlyl-14F    | GCATGGAGTCGATG            |
| xMlyl_1F    | GTATAGAGTCAGTC            |
| xMlyl-2F    | GTCACGAGTCATGGC           |
| xMlyl-3F    | GATAAGAGTCTCAGG           |
| xMlyl-4F    | GATGAGAGTCTACCGG          |
| Fra-F       | ACGCTCTGAGAGCC            |
| Fra-R       | CGAGATAAGAGACAG           |
| mvaE-F      | ATGAAAAACCTTGTGTTATCATCGAG|
| mvaE-2-R    | TGAAAAACCTTGTGTTTACGGGT  |
| mvaE-3-F    | GGCCACCTGAAAACCGTTTT     |
| mvaE-4-R    | CAGATAGTCGCTTCTGCTCA     |
| mvaE-5-F    | GACGTTGACGAAACCGGC       |
| mvaE-5-R    | ACAACGCTTTCGACATCG       |
| mvaE-6-F    | GGCTGATGGAAGCGGTT        |
| mvaE-6-R    | GTTCGCGCTCCAGGGTCC       |
| mvaE-7-F    | TGGACCCCTGGACCGGCAAC     |
| mvaE-R      | TTACTGTGTTCAGCAGTCTGTC   |
| mvaS-F      | ATGACATTGGCCATTTGATAAAATCCT|
| mvaS-2-R    | ACGGGTGCCGGGTCCGGG       |
| mvaS-3-R    | GCAGAGAAATCAGGCCCCAG     |
| mvaS-R      | TTAGTTACGGTAAAGAAGACCGGT |
| MvaK1-F     | ATGAATATCAAGAAGCAAGCTTG |
| MvaK1-2-R   | TAGTTACGGTAAAGAAGCAAGG  |
| MvaK1-3-F   | ACCGCTATGGCCAGACTAT      |
| MvaK1-R     | TTACTCTTTAACCTCCAGGTAC  |
| MvaK2-F     | ATGATCGAGTTACCACCCCG     |
| MvaK2-2-F   | GCAAATACGGTCTGGGCTT      |
| MvaK2-2-R   | TTTTTCTCTTTAGACGGT       |
| MvaK2-R     | TTAGCATTCTTTCTGGCCGTA    |
mvaD-F: ATGCTGTCTGGTAAAGCGCGT
MvaD-2-R: GCTTCGTGAACCTGAGAC
MvaD-2-F: CTCGGCTCTGGCCTGGCTG
MvaD-R: TTATTTGTCCATACCCCTGGTTCAG
idi-F: ATGAACCG AAAGATGAAACCTG
idi-1-R: CGAAGATCAGACGCGTCCG
idi-2-F: AAACCCGAGCGCTGATC
idi-2-R: GGCCCGACTCGTCCAGG
idi-3-F: TTTCTGGAGACACTGGGGGCA
idi-R: TTAGCGTTTCGCGAAACACGTTAG
IspA-F: ATGGATTTCCCGCAGCAGCTG
IspA-2-R: CTTTGTCGCCGCAAGACG
IspA-2-F: CTCTGCGTCTGGCCTGGCTG
crtE-2-F: ATGACCGTTTGTGCCGAAACACGTTAG
crtE-2-R: GTATGCGTG CATGGACG
crtE-R: TAGACCGCATCTGCATAGACG
crtI-F: ATGAACCGTACGACCGTAATTGG
crtI-2-F: GTGATGTAGAGGGCTATCGC
crtI-2-R: GGGCGACTACGACGCGTCCG
crtI-3-F: TGAAACCGGTCTCGTACG
crtI-3-R: AGCTGCCGAGCCCTCAG
crtI-R: TTAGGGCGACGTCCTCCAGCAT
T7F-H-F: ACCCAAGCTTGATCTCGATCCCGCGAAATTA
mS-X-R: ACTGTTTCTCAAGTATTTAGTGTAAGAAACGAACGCGTGT
mk1-N-F: CTAGCTAGCATGGATTTCCCGCAGCAGCTG
ii-H-R: ACTGTTAAGCTTTAGCGTTTCGCGAAAACGGTARG
iA-N-F: CTAGCTAGCATGGATTTCCCGCAGCAGCTG
T7T-H-R: ACCCAAGCTTGATCTGCGGCCGCACTCGACGCACCCACACCAACACACAC
RBS1b: ACGACCTCGTAAACAGTAAGGGAGATATTAGTAGACACCTTGCTGGTTAAAA (5'-3')
RBS2b: TGCTGGACCGCATTGGTATCTCCCTAAATCTACTGGTAAACGTTTTTT (3'-5')
RBS3b: CCGTGGAGGTTAAGAAGTAAAAAGAGGAGAAATACTAGATGCTGTGCTG (5'-3')
RBS4b: GGGACCTTCAATTCTACTTTTCTCTCTTTATGCTGCTAGACGACCATTTTG (3'-5')
RBS5b: AACAAGGATGGCAAAAATAGAGGAAGCATGATGACCTGGTAAACGTTTT (5'-3')
RBS6b: TTGGTTTCCATACCTGGTTTATCTCCTTCTCTCTCTCTCTTAAGTGGTG (3'-5')
RBS7b: ACGGCCGAAAGAAATCGTGAAGGAAGCATGCAAGCTGGTAAACGAAAA (5'-3')
RBS8b: TGCCGCTTCCTCTTACGATTCCTCCCTACTGCTATTGGG (3'-5')
RBS9b: TATATCTTATCGAGTAAACGCTGTTACTTTTCTCTTTCTCTCTCTCTTTT (5'-3')
RBS10b: ATATAGTTAAGCGTCTATTCTTCTCTCTCTCTCTTTTACTGACGCACGATCTG (3'-5')
Underline: the restriction enzyme site

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

RBS6
CTGGAGGACCTGCTTAAGGATATTTAGATGGAAGTCGGTTCCAAGTC (5’-3’)
GACCTCTGGACCGGATTCCTCCTATAAATCTACTTTCA6GCAAGTTCAG (3’-5’)

RBS7
CTGGCGGCGGTTTTCTAAGGAGGATATTTAGATGGAACCGTACGACCCTTAAT (5’-3’)
GACCGCCCGAAGGAAATCCCTCCTATAAATCTACTTTGCATGCTGGCATT (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              | MlyI\(_1\)F | MlyI-3F | mvaE-F | Fra-R |
| mvaE-2              | MlyI\(_1\)F | MlyI-4F | Fra-F | mvaE-2-R |
| mvaE-3              | MlyI\(_1\)F | MlyI-5F | mvaE-3-F | Fra-R |
| mvaE-4              | MlyI\(_1\)F | MlyI-6F | Fra-F | mvaE-4-R |
| mvaE-5              | MlyI\(_1\)F | MlyI-7F | mvaE-5-F | Fra-R | mvaE-5-F | mvaE-5-R |
| mvaE-6              | MlyI\(_1\)F | MlyI-8F | Fra-F | mvaE-6-R | mvaE-6-F | mvaE-6-R |
| mvaE-7              | MlyI\(_1\)F | MlyI-9F | Fra-F | mvaE-9 | MvaE-7-F | mvaE-R |
| mvaS-1              | XMlyI\(_1\)F | MlyI-3F | mvaS-F | Fra-R |
| mvaS-2              | XMlyI\(_1\)F | MlyI-4F | Fra-F | mvaS-2-R |
| mvaS-3              | XMlyI\(_1\)F | MlyI-5F | Fra-F | mvaS-3-R |
| mvaS-4              | XMlyI\(_1\)F | MlyI-6F | Fra-F | mvaS-R |
| mvaK1-1             | MlyI\(_2\)F | MlyI-3F | MvaK1-F | Fra-R |
| mvaK1-2             | MlyI\(_2\)F | MlyI-4F | Fra-F | MvaK1-2-R |
| mvaK1-3             | MlyI\(_2\)F | MlyI-5F | Fra-F | MvaK1-R | MvaK1-3-F | MvaK1-R |
| mvaK2-1             | XMlyI\(_2\)F | MlyI-10F | MvaK2-F | Fra-R |
| mvaK2-2             | XMlyI\(_2\)F | MlyI-11F | MvaK2-2-F | Fra-R | MvaK2-2-F | MvaK2-2-R |
| mvaD-1              | XMlyI-3F | MlyI-10F | mvaD-F | Fra-R |
| mvaD-2              | XMlyI-3F | MlyI-11F | Fra-F | MvaD-2-R | MvaD-2-F | MvaD-2-R |
| mvaD-3              | XMlyI-3F | MlyI-12F | Fra-F | MvaD-R |
| idi-1               | XMlyI-4F | MlyI-12F | idi-F | Fra-R | idi-F | idi-1-R |
| idi-2               | XMlyI-4F | MlyI-13F | idi-2-F | Fra-R | idi-2-F | idi-2-R |
| idi-3               | XMlyI-4F | MlyI-14F | Fra-F | idi-R | idi-3-F | idi-R |
| ispA-1              | XMlyI\(_1\)F | MlyI-10F | IspA-F | Fra-R |
| ispA-2              | XMlyI\(_1\)F | MlyI-11F | Fra-F | IspA-2-R |
| ispA-3              | XMlyI\(_1\)F | MlyI-12F | Fra-F | IspA-R |
| crtE-1              | MlyI\(_1\)F | MlyI-10F | crtE-F | Fra-R |
| crtE-2              | MlyI\(_1\)F | MlyI-11F | Fra-F | CrtE-2-F | CrtE-2-R |
| crtE-3              | MlyI\(_1\)F | MlyI-12F | Fra-F | CrtE-R |
| crtB-1              | XMlyI\(_1\)F | MlyI-7F | crtB-F | Fra-R |
| crtB-2              | XMlyI\(_1\)F | MlyI-9F | crtB-2-F | Fra-R |
| crtB-3              | XMlyI\(_1\)F | MlyI-8F | Fra-F | crtB-R |
| crtI-1              | MlyI\(_2\)F | MlyI-6F | crtI-F | Fra-R |
| crtI-2              | MlyI\(_2\)F | MlyI-7F | Fra-F | crtI-2-R | crtI-2-F | crtI-2-R |
| crtI-3              | MlyI\(_2\)F | MlyI-8F | Fra-F | crtI-3-R | crtI-3-F | crtI-3-R |
| crtI-4              | MlyI\(_2\)F | MlyI-10F | Fra-F | crtI-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                        |
|--------------|---------------------------------|
| dxr-N-F      | CTAGCTAGCATGAAGCAACTCACCATTCTGG |
| dxr-X-R      | CGCTCGAGTCAGCTTGAGAGCATCAC      |
| Tc-A-F       | ACTTGCGCGCGCATATAAGTTGTAATTCTC  |
| Tc-S-R       | TTGGACTAGTTTCAGGCGAGGTCGCC      |
| Pet21c-A-F   | CACTGGCGCGCCACATTCCCCGAAAAAGTCCCA |
| Pet21c-S-R   | TTGGACTAGTCTGAGCAACAGTTTACCT    |

*a* Underline: the restriction enzyme site
Supplementary Figure S1. Design of oligonucleotides of lycopene biosynthetic pathway genes for synthesis on microchips (mvaS oligonucleotides are described as an example).
Supplementary Figure S2. Schematic representation of the construction of the WW1 strain harboring the genes of the lycopene biosynthetic pathway.
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 Asp\(_I\) and Spe\(_I\) 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 µL contained 1 ng of template oligos, 100 pmol of primers, 5 µL of 2 mM dNTPs, 3 µL of 25 mM MgSO4, and 1 µL of KOD plus DNA polymerase in 1× 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 µL-PCR mixture contained 5 µL of 10× reaction buffer, 1 µL of 10 mM dNTPs, 2 µL of Pfu DNA polymerase (Biocolor BioScience & Technology Company, Shanghai, China), 1 µL of eluted fraction, and 2 µL of primer mixture (10 µM). 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 × Taq DNA ligase buffer, 0.2 µL dNTPs (2.5 mM each), 0.75 µL PEG6000 (50%), 4 µL MgCl₂ (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 × 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
CACAGGAGTCTCACCACGCTCTGAAAGGCTCTCTGGAACAACCCAGGCTGCGCAAGCGCTCG
mvaE-1_2-for
CACAGGAGTCTCACCACGCTCTGAAAGGCTCTCTGGAACAACCCAGGCTGCGCAAGCGCTCG
mvaE-1_3-for
CACAGGAGTCTCACCACGCTCTGAAAGGCTCTCTGGAACAACCCAGGCTGCGCAAGCGCTCG
mvaE-1_4-for
CACAGGAGTCTCACCACGCTCTGAAAGGCTCTCTGGAACAACCCAGGCTGCGCAAGCGCTCG
mvaE-1_5-for
CACAGGAGTCTCACCACGCTCTGAAAGGCTCTCTGGAACAACCCAGGCTGCGCAAGCGCTCG
mvaE-1_6-for
CACAGGAGTCTCACCACGCTCTGAAAGGCTCTCTGGAACAACCCAGGCTGCGCAAGCGCTCG
mvaE-1_7-for
CACAGGAGTCTCACCACGCTCTGAAAGGCTCTCTGGAACAACCCAGGCTGCGCAAGCGCTCG
mvaE-1_1-rev
CACAGGAGTCTCACCACGCTCTGAAAGGCTCTCTGGAACAACCCAGGCTGCGCAAGCGCTCG
mvaE-1_2-rev
CACAGGAGTCTCACCACGCTCTGAAAGGCTCTCTGGAACAACCCAGGCTGCGCAAGCGCTCG
mvaE-1_3-rev
CACAGGAGTCTCACCACGCTCTGAAAGGCTCTCTGGAACAACCCAGGCTGCGCAAGCGCTCG
mvaE-1_4-rev
CACAGGAGTCTCACCACGCTCTGAAAGGCTCTCTGGAACAACCCAGGCTGCGCAAGCGCTCG
mvaE-1_5-rev
CACAGGAGTCTCACCACGCTCTGAAAGGCTCTCTGGAACAACCCAGGCTGCGCAAGCGCTCG
mvaE-1_6-rev
CACAGGAGTCTCACCACGCTCTGAAAGGCTCTCTGGAACAACCCAGGCTGCGCAAGCGCTCG
mvaE-1_7-rev
CACAGGAGTCTCACCACGCTCTGAAAGGCTCTCTGGAACAACCCAGGCTGCGCAAGCGCTCG
mvaE-2
mvaE-2_1-for
CACAGGAGTCCTCACACGCTCTGAAGACCCGGAAGTTCTGATTGCGGGTGGTATCGAAAACATGTC
TCAGGCACCGGAAACTGCACTCGTAGG
mvaE-2_2-for
CACAGGAGTCCTCACAACTACGAAACCGAATCTTACGACGCGCCGTTCTCTTCTATGATGTACGACG
GCCTGACCGACGTTGCGACTCGTAGG
mvaE-2_3-for
CACAGGAGTCCTCACACGCTCTGAAGACCCGGAAGTTCTGATTGCGGGTGGTATCGAAAACATGTC
TCAGGCGCCGAAACTGCAGCGTTTCGTTGCGACTCGTAGG
mvaE-2_4-for
CACAGGAGTCCTCACACGCTCTGAAGACCCGGAAGTTCTGATTGCGGGTGGTATCGAAAACATGTC
TCAGGCGCCGAAACTGCAGCGTTTCGTTGCGACTCGTAGG
mvaE-2_5-for
CACAGGAGTCCTCACACGCTCTGAAGACCCGGAAGTTCTGATTGCGGGTGGTATCGAAAACATGTC
TCAGGCGCCGAAACTGCAGCGTTTCGTTGCGACTCGTAGG
mvaE-2_6-for
CACAGGAGTCCTCACACGCTCTGAAGACCCGGAAGTTCTGATTGCGGGTGGTATCGAAAACATGTC
TCAGGCGCCGAAACTGCAGCGTTTCGTTGCGACTCGTAGG
mvaE-2_1-rev
CACAGGAGTCCTCACACGCTCTGAAGACCCGGAAGTTCTGATTGCGGGTGGTATCGAAAACATGTC
TCAGGCGCCGAAACTGCAGCGTTTCGTTGCGACTCGTAGG
mvaE-2_2-rev
CACAGGAGTCCTCACACGCTCTGAAGACCCGGAAGTTCTGATTGCGGGTGGTATCGAAAACATGTC
TCAGGCGCCGAAACTGCAGCGTTTCGTTGCGACTCGTAGG
mvaE-2_3-rev
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mvaE-2_4-rev
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mvaE-2_5-rev
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mvaE-2_6-rev
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mvaE-2_7-rev
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mvaE-3
mvaE-3_1-for
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CGTTACCGGGGTAACGCCAGACGACTCGAATG
mvaE-3_2-for
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mvaE-3_3-for
CACAGGAGTCTCAGCACGATGGTGCTGCTGATTATTGCGTCTCAGGAATAC
mvaE-3_4-for
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mvaE-3_5-for
CACAGGAGTCTCAGCACGATGGTGCTGCTGATTATTGCGTCTCAGGAATAC
mvaE-3_6-for
CACAGGAGTCTCAGCACGATGGTGCTGCTGATTATTGCGTCTCAGGAATAC
mvaE-3_7-for
CACAGGAGTCTCAGCACGATGGTGCTGCTGATTATTGCGTCTCAGGAATAC
mvaE-3_1-rev
CACAGGAGTCTCAGCACGATGGTGCTGCTGATTATTGCGTCTCAGGAATAC
mvaE-3_2-rev
CACAGGAGTCTCAGCACGATGGTGCTGCTGATTATTGCGTCTCAGGAATAC
mvaE-3_3-rev
CACAGGAGTCTCAGCACGATGGTGCTGCTGATTATTGCGTCTCAGGAATAC
mvaE-3_4-rev
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mvaE-3_5-rev
CACAGGAGTCTCAGCACGATGGTGCTGCTGATTATTGCGTCTCAGGAATAC
mvaE-3_6-rev
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mvaE-3_7-rev
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mvaE-4
mvaE-4_1-for
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mvaE-4_2-for
   CACAGGAGTCTCAGGATGCATGCTGGCTGACCTGACGCTCTGGTGAGATGATCCTGACCTGACGCTCTGCTGACCGTAAGGGACTCGTACG
mvaE-4_3-for
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mvaE-4_4-for
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mvaE-4_5-for
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mvaE-4_6-for
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mvaE-4_7-for
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mvaE-4_1-rev
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mvaE-4_2-rev
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mvaE-4_4-rev
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mvaE-4_5-rev
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mvaE-4_6-rev
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mvaE-4_7-rev
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mvaE-5
mvaE-5_1-for
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mvaE-5_2-for
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mvaE-5_3-for
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mvaE-5_4-for
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mvaE-5_5-for
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mvaE-5_6-for
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mvaE-5_7-for
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mvaE-5_1-rev
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mvaE-5_2-rev
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mvaE-5_5-rev
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mvaE-5_6-rev
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mvaE-6
mvaE-6_1-for
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mvaE-6_3-for
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mvaE-6_4-for
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mvaE-7

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mvaE-7_1-for
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mvaE-7_2-for
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mvaE-7_3-for
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mvaE-7_4-for
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mvaE-7_5-for
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mvaE-7_6-for
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mvaE-7_7-for
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mvaE-7_8-for
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mvaE-7_4-rev
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mvaE-7_8-rev
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mvaE-7_7-rev
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GAGACGACTGTAAG
mvaE-7_8-rev
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mvaS-1
mvaS-1_1-for
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mvaS-1_2-for
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mvaS-1_3-for
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mvaS-1_4-for
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CTTCTACTGACGAGCTGCTGACTGCTCTCCTG
mvaS-1_5-for
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mvaS-1_1-rev
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mvaS-1_4-rev
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mvaS-1_5-rev
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mvaS-2
mvaS-2_1-for
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mvaS-2_2-for
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mvaS-2_3-for
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mvaS-2_5-for
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mvaS_2_7-rev
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mvaS-3_1-for
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mvaS-3_2-for
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mvaS-4_2-rev
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mvaS-4_6-rev
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mvaK1-1_1-for
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mvaK1-1_3-rev
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mvaK1-1_4-rev
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mvaK1-1_5-rev
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mvaK1-1_6-rev
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mvaK1-2_1-for
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mvaK1-2_2-for
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mvaK1-2_3-for
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mvaK1-2_5-for
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mvaK1-2_6-for
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mvaK1-1_3-for
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mvaK1-1_4-for
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mvaK1-1_5-for
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mvaK1-1_6-for
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mvaK1-2_3_rev
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mvaK1-2_4_rev
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mvaK1-2_5_rev
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mvaK1-2_6_rev
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mvaK1-2_7_rev
CCAGGAGTCGTAGCTGTTGCGACTCGTAGG
mvaK1-3
mvaK1-3_1_for
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mvaK1-3_2_for
CCAGGAGTCGTAGCTGTTGCGACTCGTAGG
mvaK1-3_3_for
CCAGGAGTCGTAGCTGTTGCGACTCGTAGG
mvaK1-3_4_for
CCAGGAGTCGTAGCTGTTGCGACTCGTAGG
mvaK1-3_5_for
CCAGGAGTCGTAGCTGTTGCGACTCGTAGG
mvaK1-3_6_for
CCAGGAGTCGTAGCTGTTGCGACTCGTAGG
mvaK1-3_7_for
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mvaK1-3_1-rev
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mvaK1-3_2-rev
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mvaK1-3_3-rev
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mvaK1-3_4-rev
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mvaK1-3_5-rev
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    GAATG
mvaK1-3_6-rev
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    GCACACGACTCGAATG
mvaK1-3_7-rev
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mvaK2-1
mvaK2-1_1-for
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    CGGGCGAATATGGCGGTTGTTGAAGTAGAGACTCGATCC
mvaK2-1_2-for
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    TTGGTAGAGACTCGATCC
mvaK2-1_3-for
    GTCA CGAGTCATGGGCAAGAACCACCGCATGAAAGTTCTATCCAGTCTGCGCAGTACTCTTCTGCC
    GATCCGCTGTAGAGACTCGATCC
mvaK2-1_4-for
    GTCA CGAGTCATGGCGACCCGTCGTAACGGCGAACTGGTTCTGGACATCCGCGAAAACCCGTTCCA
    CTAGT AAGAGACTCGATCC
mvaK2-1_5-for
    GTCA CGAGTCATGGCGGACCGCGGCTGTAACCGCGAATCTGGTTCTCTGGACATCCGCGAAGAACC
    GACGACTCGATCC
mvaK2-1_6-for
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GACTCGATCC
mvaK2-1_4-rev
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TGCGTAGAGACTCGATCC
mvaK2-1_5-rev
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CAGTAGAGACTCGATCC
mvaK2-1_6-rev
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CTTTGTTCTTCTGCTGCTGCTGATCC
mvaK2-1_7-rev
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CTCGATCC
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mvaK2-2_1-for
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mvaK2-2_5-for
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mvaK2-2_6-for
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mvaK2-3_5-for
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mvaK2-3_6-for
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mvaK2-3_7-for
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mvaK2-3_6-rev
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mvaK2-3_7-rev
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mvaD-1
mvaD-1_1-for
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mvaD-1_2-for
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mvaD-1_3-for
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mvaD-1_4-for
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mvaD-1_2-rev
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mvaD-1_4-rev
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mvaD-1_6-rev
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mvaD-1_7-rev
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GCTGTCAGAGACTCGATCC

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mvaD-2_2-for
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mvaD-2_3-for
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mvaD-2
mvaD-2_1-for
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mvaD-2_2-for
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mvaD-2_3-for
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    CGAATTGACTCGATCC
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mvaD-3_4-rev
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mvaD-3_6-rev
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    GCGTGAATTGACTCGATCC
mvaD-3_7-rev
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    GCGTGAATTGACTCGATCC

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idi-1_1-for
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idi-1_4-for
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idi-1_5-for
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idi-1_6-for
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idi-1_1-rev
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idi-1_2-rev
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idi-1_3-rev
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idi-1_5-rev
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idi-1_6-rev
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idi-1_7-rev
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idi-2
idi-2_1-for
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idi-2_2-for
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idi-2_3-for
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 idi-2
idi-2_1-for
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idi-2_2-for
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idi-2_3-for
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 idi-2
idi-2_4-for
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idi-2_5-for
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idi-2_6-for
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idi-3_1-for
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idi-3_2-for
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idi-3_3-for
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idi-3_4-for
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idi-3_5-for
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idi-3_6-for
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idi-3_1-rev
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CCATGC
idi-3_2-rev
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idi-3_3-rev
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idi-3_4-rev
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idi-3_5-rev
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idi-3_6-rev
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idi-3_7-rev
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crtE-1
crtE-1_1-for
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GAGTCACGATCCGACTCCATGC
crtE-1_2-for
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| Sequence | Description |
|----------|-------------|
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| ... | CACAGGAGTCCTCAGTCGGCGCTGATGCGCGGAGGTGCGCTGGCGCGTA | GAGACTCGATCC |
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| ... | CACAGGAGTCCTCAGTCGGCGCTGATGCGCGGAGGTGCGCTGGCGCGTA | GAGACTCGATCC |
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| ... | crtE-2_1-for |
| ... | CACAGGAGTCCTCAGTCGGCGCTGATGCGCGGAGGTGCGCTGGCGCGTA | GAGACTCGATCC |
| ... | crtE-2_2-for |
| ... | CACAGGAGTCCTCAGTCGGCGCTGATGCGCGGAGGTGCGCTGGCGCGTA | GAGACTCGATCC |

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crtE-2_3-for
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crtE-2_4-for
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crtE-2_5-for
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crtE-2_6-for
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crtE-2_7-for
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crtE-2_2-rev
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crtE-2_3-rev
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ATGACTCACCAC

crtE-2_4-rev
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ATGACTCACCAC

crtE-2_5-rev
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ATGACTCACCAC

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ATGACTCACCAC

crtE-2_7-rev
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ATGACTCACCAC

crtE-3
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crtE-3_1-for
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crtE-3_2-for
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crtE-3_3-for
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crtE-3_4-for
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crtE-3_5-for
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crtE-3_6-for
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crtE-3_4-rev
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crtE-3_5-rev
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crtE-3_6-rev
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crtE-3_7-rev
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crtB-1

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ATTGACTCGATCC

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crtB-2_7-rev
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  CGTACC
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  GACTCGTACC
crtB-3_5-for
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crtB-3_6-for
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    CTTGGGGAAGGGACTCGTACG
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crtI-2

crtI-2_1-for

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crtI-2_7-for

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crtI-2_8-rev
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   TCGACAG

crtI-3

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crtI-3_4_for
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crtl-3_8-rev
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crtl-4
crtl-4_1-for
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TTCCGCACCTGGGTTGAGAGACTCGATCC
crtl-4_2-for
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crtl-4_3-for
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crtl-4_7-for
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  AGAGACTCGATCC

crtl-4_8-rev
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  TCGATCC
Supplementary references

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