**Table S1 Strains used in this study**

|  |  |  |
| --- | --- | --- |
| **Original Strains** | **Relevant characteristics** | **Sources** |
| *E. coli* DH5α | F- Φ80lacZΔM15, hsdR17 (rk-mk+)λ-, Δ(lacZYA-argF), U169, recA1, endA1, thi-1, gyrA96, relA, deoR, nupG,glnV44 | Lab stock |
| *Pseudomonas putida* KT2440 | mt-2 derivative, clearance of the TOL plasmid pWW0 | Lab stock |
| *Pseudomonas aeruginosa* PAO1 | Wild type | Lab stock |
| *Pseudomonas fluorescens* Pf-5 | Wild type | Lab stock |
| *Pseudomonas entomophila* L48 | Wild type | Lab stock |

**Table S2 Plasmids used in this study**

|  |  |  |
| --- | --- | --- |
| **Plasmids** | **Relevant characteristics** | **Sources** |
| pCAS-RK2T | oriRK2, TetR, Pcas-Cas9, ParaB-Red, PrhaB-sgRNA-pRO1600, SacB | Lab stock |
| pSEVA-gRNAF | oriPRO1600/ColE1, GmR, Pj23119-sgRNA-NicC | Lab stock |
| pSEVA-TtgA | oriPRO1600/ColE1, GmR, Pj23119-sgRNA-TtgA | This study |
| pUC57-eSpCas9pp | Plasmid carrying an enhanced specificity Cas9 nuclease gene eSpCas9pp (AmpR) | Genscript |
| pUC57-APOBEC1 | Plasmid carrying rat cytidine deaminase gene APOBEC1 (AmpR) | Genscript |
| pCMV-BE3 | Plasmid carrying rAPOBEC1-XTEN linker-SpCas9(D10A)-UGI-NLS (AmpR) | Lab stock |
| pVLT33 | oriRSF1010, KmR, lacI-Ptac | Lab stock |
| pSEVA-Module 1 | oriPRO1600/ColE1, GmR, Pj23119-sgRNA-TtgA, Pbs-APOBEC1-XTEN linker-SpCas9(D10A) | This study |
| pSEVA-Module 2 | oriPRO1600/ColE1, GmR, Pj23119-sgRNA-TtgA, AraC-ParaBAD-APOBEC1-XTEN linker-SpCas9(D10A) | This study |
| pSEVA-Module 3 | oriPRO1600/ColE1, GmR, Pj23119-sgRNA-TtgA, Pbs-APOBEC1-XTEN linker-eSpCas9pp(D10A) | This study |
| pSEVA-Module 4 | oriPRO1600/ColE1, GmR, Pj23119-sgRNA-TtgA, AraC-ParaBAD-APOBEC1-XTEN linker -eSpCas9pp(D10A) | This study |
| pSEVA-Module 5 | oriPRO1600/ColE1, GmR, Pj23119-sgRNA-TtgA, Xyls-Pm-APOBEC1-XTEN linker -eSpCas9pp(D10A) | This study |
| pSEVA-Module 6 /pSEVA6BE | oriPRO1600/ColE1, GmR, Pj23119-sgRNA-TtgA, AraC-ParaBAD-APOBEC1-XTEN linker -eSpCas9pp(D10A)-UGI | This study |
| pSEVA2BE | oriRSF1010, KmR, Pj23119-sgRNA-TtgA, AraC-ParaBAD-APOBEC1-XTEN linker -eSpCas9pp(D10A)-UGI | This study |
| pSEVA6BE-NG | oriPRO1600/ColE1, GmR, Pj23119-sgRNA-TtgA, AraC-ParaBAD-APOBEC1-XTEN linker -eSpCas9pp-NG(D10A, L1111R, D1135V, G1218R, E1219F, A1322R, R1335A and T1337R)-UGI | This study |
| pSEVA6BE-YE1 | oriPRO1600/ColE1, GmR, Pj23119-sgRNA-TtgA, AraC-ParaBAD-APOBEC1-YE1(W90Y and R126E)-XTEN linker -eSpCas9pp(D10A)-UGI | This study |
| pSEVA6BE-HmgA | pSEVA6BE containing HmgA spacer, GmR | This study |
| pSEVA6BE-PobA | pSEVA6BE containing PobA spacer, GmR | This study |
| pSEVA6BE-QuiC | pSEVA6BE containing QuiC spacer, GmR | This study |
| pSEVA6BE-TtgA | pSEVA6BE containing TtgA spacer, GmR | This study |
| pSEVA6BE-TtgA-2 | pSEVA6BE containing TtgA-2 spacer, GmR | This study |
| pSEVA6BE-PA1236 | pSEVA6BE containing PA1236 spacer, GmR | This study |
| pSEVA6BE-PA2018 | pSEVA6BE containing PA2018 spacer, GmR | This study |
| pSEVA6BE-PFL0054 | pSEVA6BE containing PFL0054 spacer, GmR | This study |
| pSEVA6BE-PFL0556 | pSEVA6BE containing PFL0556 spacer, GmR | This study |
| pSEVA6BE-L48glpR | pSEVA6BE containing PSEEN1196 spacer, GmR | This study |
| pSEVA6BE-L48pykF | pSEVA6BE containing PSEEN1668 spacer, GmR | This study |
| pSEVA2BE-QuiC-2 | pSEVA2BE containing QuiC-2 spacer, GmR | This study |
| pSEVA6BE-PobA-TrpE | pSEVA6BE containing spacers PobA and TrpE, GmR | This study |
| pSEVA6BE-S | oriPRO1600/ColE1, GmR, Pj23119-sgRNA-TtgA, AraC-ParaBAD-APOBEC1-XTEN linker -eSpCas9pp(D10A)-UGI, sacB | This study |
| pSEVA2BE-S | oriRSF1010, KmR, Pj23119-sgRNA-TtgA, AraC-ParaBAD-APOBEC1-XTEN linker -eSpCas9pp(D10A)-UGI, sacB | This study |
| pSEVA6BE-NG-S | pSEVA6BE-NG containing HexR-3 spacer, GmR, sacB | This study |
| pSEVA6BE-YE1-S | pSEVA6BE-YE1 containing TtgA spacer, GmR, sacB | This study |
| pSEVA6BE-PA2018-2 | pSEVA6BE containing PA2018-2 spacer, GmR | This study |
| pSEVA6BE-HexR-5 | pSEVA6BE containing HexR-5 spacer, GmR | This study |
| pSEVA6BE-HexR-4 | pSEVA6BE containing HexR-4 spacer, GmR | This study |
| pSEVA6BE-NG-HexR-2 | pSEVA6BE-NG containing HexR-2 spacer, GmR | This study |
| pSEVA6BE-NG-HexR-3 | pSEVA6BE-NG containing HexR-3 spacer, GmR | This study |
| pSEVA6BE-HexR-2 | pSEVA6BE containing HexR-2 spacer, GmR | This study |
| pSEVA6BE-HexR-3 | pSEVA6BE containing HexR-3 spacer, GmR | This study |
| pSEVA6BE-HexR | pSEVA6BE containing HexR spacer, GmR | This study |
| pSEVA6BE-YE-TtgA-2 | pSEVA6BE-YE containing TtgA-2 spacer, GmR | This study |
| pSEVA-Module 4-GllA | pSEVA-Module 4 containing GllA spacer, GmR | This study |
| pSEVA-Module 4-MexE | pSEVA-Module 4 containing MexE spacer, GmR | This study |
| pSEVA-Module 6-GllA | pSEVA-Module 6 containing GllA spacer, GmR | This study |
| pSEVA-Module 6-MexE | pSEVA-Module 6 containing MexE spacer, GmR | This study |
| pSEVA6BE-PobA-QuiC-2 | pSEVA6BE containing spacers PobA and QuiC-2, GmR | This study |
| pSEVA6BE-PobA-QuiC-2-TrpE | pSEVA6BE containing spacers PobA,QuiC-2 and TrpE, GmR | This study |
| pSEVA6BE-MexE | pSEVA6BE containing MexE spacer, GmR | This study |
| pSEVA6BE-MexE-QuiC-2 | pSEVA6BE containing spacers MexE and QuiC-2, GmR | This study |
| pSEVA6BE-NG-pcaHpykA-S | pSEVA6BE-NG-S containing spacers PcaH and PykA, GmR, sacB | This study |
| pSEVA6BE-NG-AF1-S | pSEVA6BE-NG-S containing spacers AF1, GmR, sacB | This study |

**Table S3 Primers used in this study**

|  |  |
| --- | --- |
| **Primers name** | **Primer sequence (5’ → 3’)** |
| S9-F | GATAAGAAATACTCAATAGGCTTAG |
| S9-R | TCAGTCACCTCCTAGCTGACTCAAATCAATG |
| U-F | TCTGGTGGTTCTACTAATCTGTCAGATATTATTG |
| U-R | AACAGGAGTCCAAGACTAGTTCAAGAACCACCAGAGAGCATC |
| eC9D10A-F | GGCCTGGCTATCGGCACCAACAGCG |
| eC9D10A-R | GTTGGTGCCGATAGCCAGGCCGATGCTG |
| C9D10A-F | CTTAGCTATCGGCACAAATAGCGTCGG |
| C9D10A-R | CTATTTGTGCCGATAGCTAAGCCTATTGAGTATTTC |
| 11-F | TGATCGCCCGCAAGAAGGACTGGGACCCGAAGAAGTACGGCGGCTTCGTCAGCCCGACCGTGGCC |
| 11-R | GTCCTTCTTGCGGGCGATCAGCTTGTCGCTGTTGCGCTTCGGCCGGATGCTTTCCTTGCTGAAGCC |
| 12-F | CAGCGCCCGCTTCCTGCAGAAGGGCAACGAAC |
| 12-R | TCTGCAGGAAGCGGGCGCTGGCCAGCATGCGC |
| 13-F | TTCGACACCACCATCGACCGCAAGGCCTACCGCAGCACCAAGGAAGTGC |
| 13-R | CGGTCGATGGTGGTGTCGAAGTACTTGAAGGCGCGCGGGGCGCCCAGG |
| YE-1F | CCGCTACCCGCACGTGACCCTGTTCATCTACATCGCCCGCCTGTACCACCACGCCGACCCGGAGAACCGCCAGGGCCTGCG |
| YE-1R | GGGTCACGTGCGGGTAGCGGCTCAGGAACTCGGTGATGGCGCGGCTGCATTCGCCGCACGGGCTATAGCTCAGGAACCAGG |
| eC9NG-1F | GACAAGAAGTACAGCATCGGCCTGGCTATCGGC |
| eC9NG-1R | CCGATGCTGTACTTCTTGTCACTTTCGGGTGTGGCGGACTC |
| eC9NG-2F | TCTGGTGGTTCTACTAATCTG |
| eC9NG-2R | AGATTAGTAGAACCACCAGAGTCGCCGCCCAGCTGGCTCAGG |
| BE-1F | TTAAGGGCGATAGGAGGAATATACCATGAGCAGCGAAACCGGCCCGG |
| BE-1R | TTCCTCCTATCGCCCTTAAGATGGAGAAACAGTAGAGAGTTG |
| BE-2F | GAGACTCCCGGGACCTCAGAGTCCGCCACACCCG |
| BE-2R | CTCTGAGGTCCCGGGAGTCTCGCTGCCGCTCTTCAGGCCGGTGGCCCACAGG |
| 62-1F | GGGTCCCCAATAATTACGATTTAAATTTGAC |
| 62-1R | ATCGTAATTATTGGGGACCCATCAAACAAAAGAGGAAAATAG |
| 62-2F | GCACCAGCGGCGCCTGAGAGGGGCGCGCCCAG |
| 62-2R | TCTCAGGCGCCGCTGGTGCTAAGCCATTGAATATAAAAGATAAAAATG |
| Sac-1F | CATTTTCTTTTGCGTTTTTATTTGTTAACTGTTAATTG |
| Sac-1R | AACAAATAAAAACGCAAAAGAAAATGCTGGATTCTCACCAATAAAAAACG |
| Sac-2F | GGGTCCCCAATAATTACGATTTAAATTTGACATAAGCC |
| Sac-2R | ATCGTAATTATTGGGGACCCATCAAACAAAAGAGGAAAATAG |
| C9-F | CCAAGAACCTGAGCGACGCCATCCTGC |
| C9-R | AGGCGTCGTGGGCGTGGTGGTAG |
| TtgA-gRNAF | TGCCAAACGATTGCAGGCTGGTTTTAGAGCTAGAAATAGCAAG |
| TtgA-gRNAR | CAGCCTGCAATCGTTTGGCAGCTAGCATTATACCTAGGAC |
| TtgA-2-gRNAF | CAAGCAACTGATTGACGAACGTTTTAGAGCTAGAAATAGCAAG |
| TtgA-2-gRNAR | GTTCGTCAATCAGTTGCTTGGCTAGCATTATACCTAGGAC |
| HmgA-gRNAF | GGGCAGAACTCCCCGCAGAGTTTTAGAGCTAGAAATAGCAAG |
| HmgA-gRNAR | TCTGCGGGGAGTTCTGCCCAGCTAGCATTATACCTAGGAC |
| PobA-gRNAF | AAAACTCAGGTTGCAATTATGTTTTAGAGCTAGAAATAGCAAG |
| PobA-gRNAR | ATAATTGCAACCTGAGTTTTGCTAGCATTATACCTAGGAC |
| QuiC-gRNAF | AACGTCCAGGCCGATGCCCTGTTTTAGAGCTAGAAATAGCAAG |
| QuiC-gRNAR | GGGCATCGGCCTGGACGTTGCTAGCATTATACCTAGGAC |
| PA1236-gRNAF | CTGCAGATAGTGCTGGAGGAGTTTTAGAGCTAGAAATAGCAAG |
| PA1236-gRNAR | TCCTCCAGCACTATCTGCAGGCTAGCATTATACCTAGGAC |
| PA2018-gRNAF | GTCAACCAAATGACCGCCACGTTTTAGAGCTAGAAATAGCAAG |
| PA2018-gRNAR | GTGGCGGTCATTTGGTTGACGCTAGCATTATACCTAGGAC |
| PFL0054-gRNAF | ATGCAGGACACCTACCCGGAGTTTTAGAGCTAGAAATAGCAAG |
| PFL0054-RNAR | TCCGGGTAGGTGTCCTGCATGCTAGCATTATACCTAGGAC |
| PFL0556-gRNAF | GTTGCAAGAGTTGCAGAACAGTTTTAGAGCTAGAAATAGCAAG |
| PFL0556-RNAR | TGTTCTGCAACTCTTGCAACGCTAGCATTATACCTAGGAC |
| L48glpR-gRNAF | CCAACAACAAATCCTCGAGCGTTTTAGAGCTAGAAATAGCAAG |
| L48glpR-gRNAR | GCTCGAGGATTTGTTGTTGGGCTAGCATTATACCTAGGAC |
| L48pykF-gRNAF | GGTGCAACTGCAACGCGGCCGTTTTAGAGCTAGAAATAGCAAG |
| L48pykF-gRNAR | GGCCGCGTTGCAGTTGCACCGCTAGCATTATACCTAGGAC |
| Quic2-gRNAF | TTACCAGCAAGTGTGGAACCGTTTTAGAGCTAGAAATAGCAAG |
| Quic2-gRNAR | GGTTCCACACTTGCTGGTAAGCTAGCATTATACCTAGGAC |
| TrpE-gRNAF | CAGGGCCAGGCACGTCTGCAGTTTTAGAGCTAGAAATAGCAAG |
| TrpE-gRNAR | TGCAGACGTGCCTGGCCCTGGCTAGCATTATACCTAGGAC |
| PA2018-2-RNAF | GTTGCAGGCGCTGCGCCGGGGTTTTAGAGCTAGAAATAGCAAG |
| PA2018-2-RNAR | CCCGGCGCAGCGCCTGCAACGCTAGCATTATACCTAGGAC |
| hexR-4-gRNAF | GCGCAGAGCCTGGCCAGTGGGTTTTAGAGCTAGAAATAGCAAG |
| hexR-4-gRNAR | CCACTGGCCAGGCTCTGCGCGCTAGCATTATACCTAGGAC |
| hexR-2-gRNAF | CAGATCCAGGGCCGCCTCGAGTTTTAGAGCTAGAAATAGCAAG |
| hexR-2-gRNAR | TCGAGGCGGCCCTGGATCTGGCTAGCATTATACCTAGGAC |
| hexR-3-gRNAF | GATCCAGGGCCGCCTCGACGGTTTTAGAGCTAGAAATAGCAAG |
| hexR-3-gRNAR | CGTCGAGGCGGCCCTGGATCGCTAGCATTATACCTAGGAC |
| hexR-5-gRNAF | GCAGTAGGTCAGCCGCGCCGGTTTTAGAGCTAGAAATAGCAAG |
| hexR-5-gRNAR | CGGCGCGGCTGACCTACTGCGCTAGCATTATACCTAGGAC |
| hexR-gRNAF | GCCCGGCAGATCCACTTCTTGTTTTAGAGCTAGAAATAGCAAG |
| hexR-gRNAR | AAGAAGTGGATCTGCCGGGCGCTAGCATTATACCTAGGAC |
| pykA-gF | CTTCCAGCGCTGCGACGAAGTTTTAGAGCTAGAAATAGCAAG |
| pykA-gR | TTCGTCGCAGCGCTGGAAGGGCTAGCATTATACCTAGGAC |
| PcaH-gF | TCACCCAGTTGTACTTCGAGTTTTAGAGCTAGAAATAGCAAG |
| PcaH-gR | TCGAAGTACAACTGGGTGATGCTAGCATTATACCTAGGAC |
| GllA-gF | ATCAGCCAGGTAATCACCTGTTTTAGAGCTAGAAATAGCAAG |
| GllA-gR | GGTGATTACCTGGCTGATCGCTAGCATTATACCTAGGAC |
| MexE-gF | GAACAACCGATCACCGAATGTTTTAGAGCTAGAAATAGCAAG |
| MexE-gR | TTCGGTGATCGGTTGTTCGGCTAGCATTATACCTAGGAC |
| AF1-gF | CATCAGCCCGCGAGACAAGGGTTTTAGAGCTAGAAATAGCAAG |
| AF1-gR | CCTTGTCTCGCGGGCTGATGGCTAGCATTATACCTAGGAC |

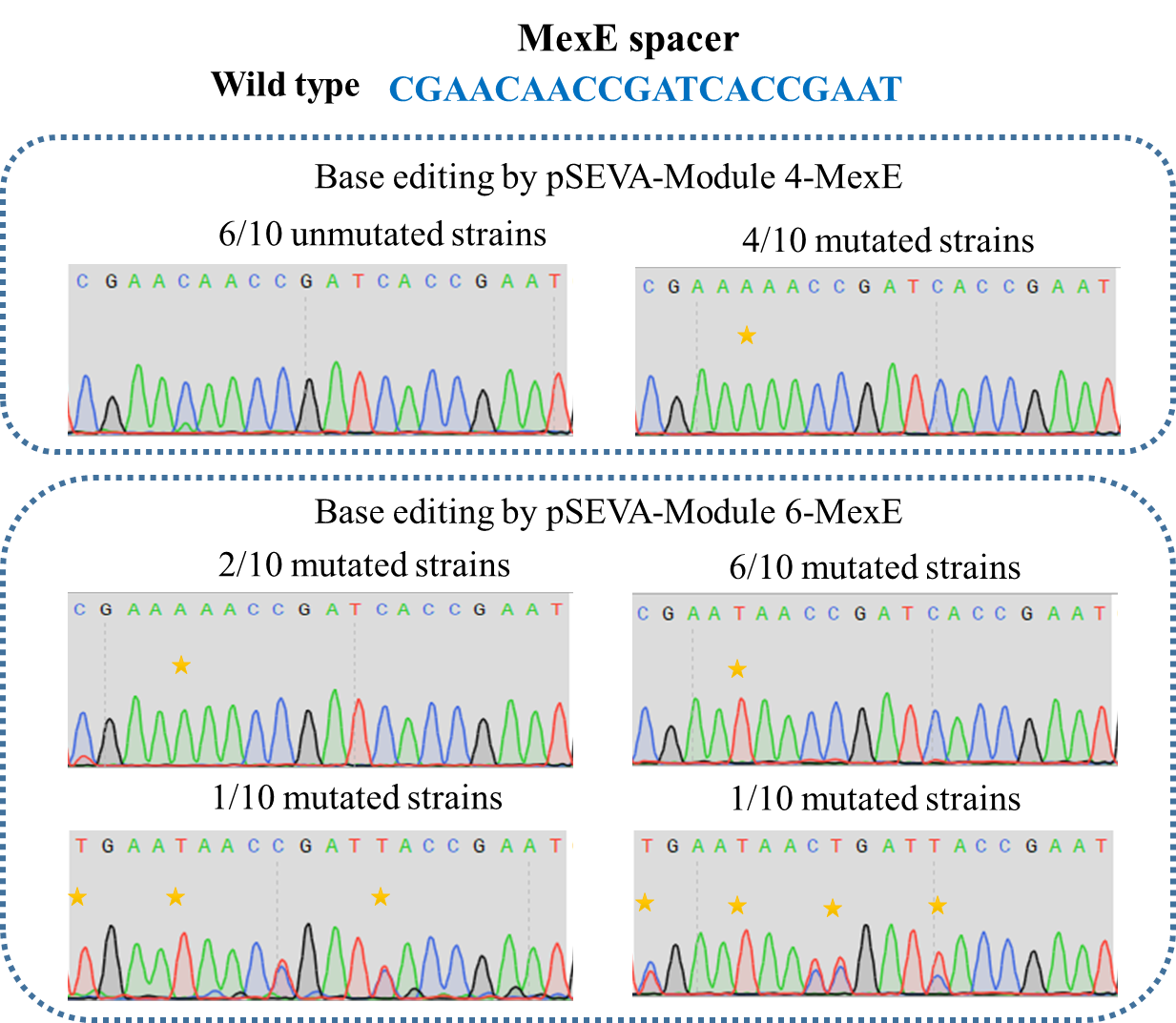
**Table S4. The sequences of base editing spacers used in this study.**

|  |  |
| --- | --- |
| **Spacer name** | **Sequence (5’ → 3’)** |
| TtgA (PP\_1386) | TGCCAAACGATTGCAGGCTG |
| HmgA (PP\_4621) | TGGGCAGAACTCCCCGCAGA |
| PobA (PP\_3537) | AAAACTCAGGTTGCAATTAT |
| QuiC (PP\_2554) | AACGTCCAGGCCGATGCCCT |
| TtgA-2 (PP\_1386) | CAAGCAACTGATTGACGAAC |
| PA1236 | CTGCAGATAGTGCTGGAGGA |
| PA2018 | GTCAACCAAATGACCGCCAC |
| PFL0054 | ATGCAGGACACCTACCCGGA |
| PFL0556 | GTTGCAAGAGTTGCAGAACA |
| PSEEN1196 | CCAACAACAAATCCTCGAGC |
| PSEEN1668 | GGTGCAACTGCAACGCGGCC |
| QuiC-2 (PP\_2554) | TTACCAGCAAGTGTGGAACC |
| TrpE (PP\_0417) | CAGGGCCAGGCACGTCTGCA |
| PA2018-2 | GTTGCAGGCGCTGCGCCGGG |
| HexR-5 (PP\_1021) | GCAGTAGGTCAGCCGCGCCG |
| HexR-4 (PP\_1021) | GCGCAGAGCCTGGCCAGTGG |
| HexR-2 (PP\_1021) | CAGATCCAGGGCCGCCTCGA |
| HexR-3 (PP\_1021) | GATCCAGGGCCGCCTCGACG |
| HexR (PP\_1021) | GCCCGGCAGATCCACTTCTT |
| PykA | CCTTCCAGCGCTGCGACGAA |
| PcaH | ATCACCCAGTTGTACTTCGA |
| GllA | GATCAGCCAGGTAATCACCT |
| MexE | CGAACAACCGATCACCGAAT |
| AF1 | CATCAGCCCGCGAGACAAGG |

**Figure S1 Base editing in GllA spacer by using pSEVA-Module 4 and pSEVA-Module 6**

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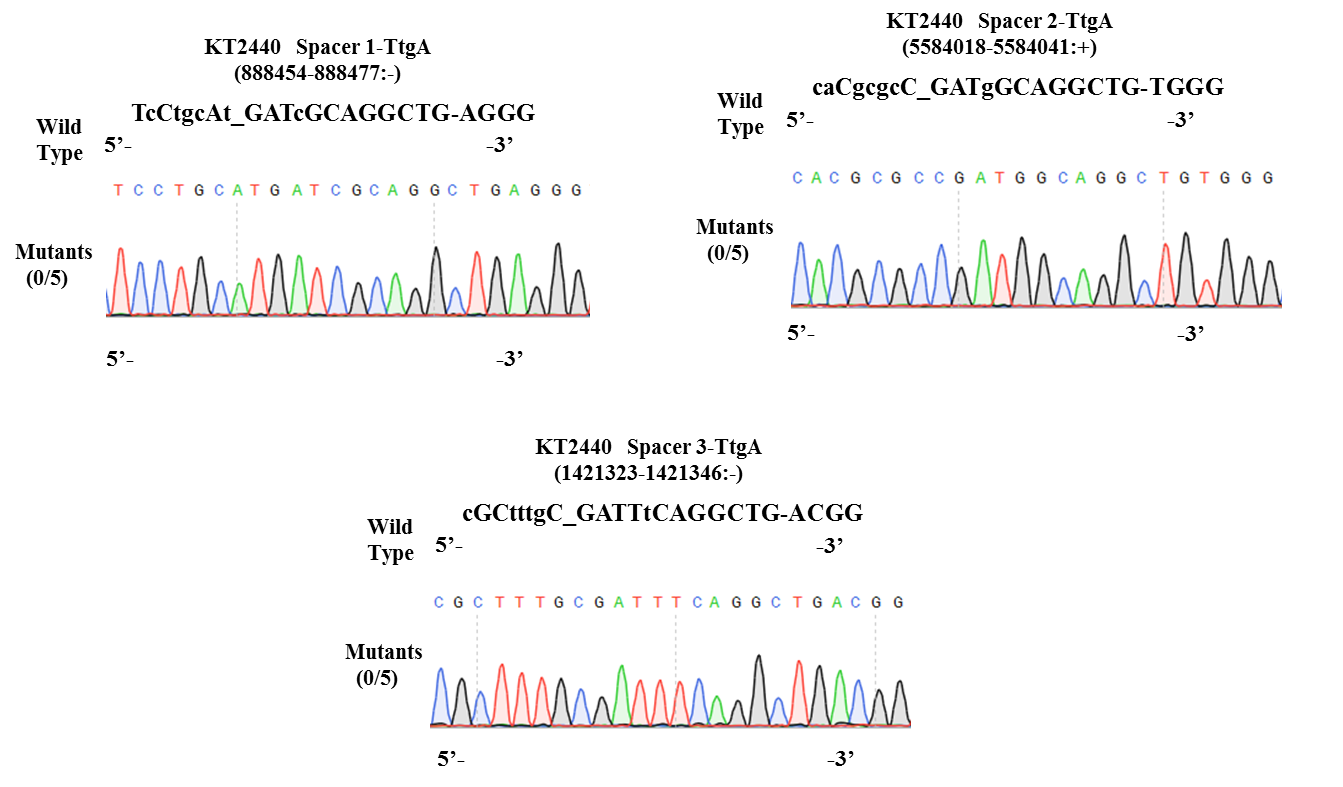
**Figure S2 Base editing in MexE spacer by using pSEVA-Module 4 and pSEVA-Module 6**

****

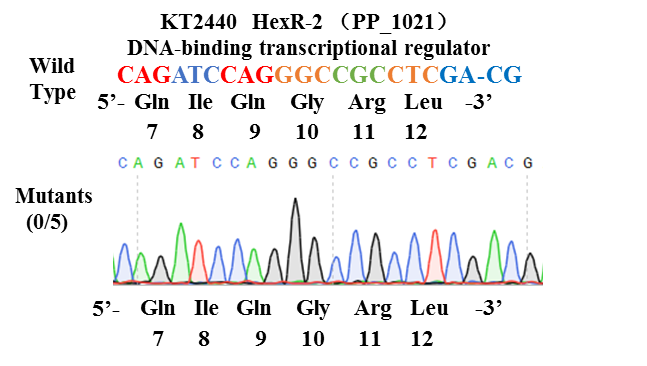
**Figure S3 Top three similar spacers of TtgA in the *P.putida* KT2440 genome and DNA sequencing results of these sites after base editing toward TtgA**

|  |  |
| --- | --- |
| **Spacer name** | **Sequence (5’-3’)** |
| **TtgA** | **TGCCAAACGATTGCAGGCTG** |
| **Spacer 1** | **TcCtgcAt\_GATcGCAGGCTG-AGGG (888454-888477:-)** |
| **Spacer 2** | **caCgcgcC\_GATgGCAGGCTG-TGGG (5584018-5584041:+)** |
| **Spacer 3** | **cGCtttgC\_GATTtCAGGCTG-ACGG (1421323-1421346:-)** |

**DNA sequencing of the top three similar spacers of TtgA**

****

**Figure S4 DNA sequencing of spacers HexR-2 and HexR-3 after base editing using NGG- recognizing plasmids pSEVA6BE-HexR-2 and pSEVA6BE-HexR-3**

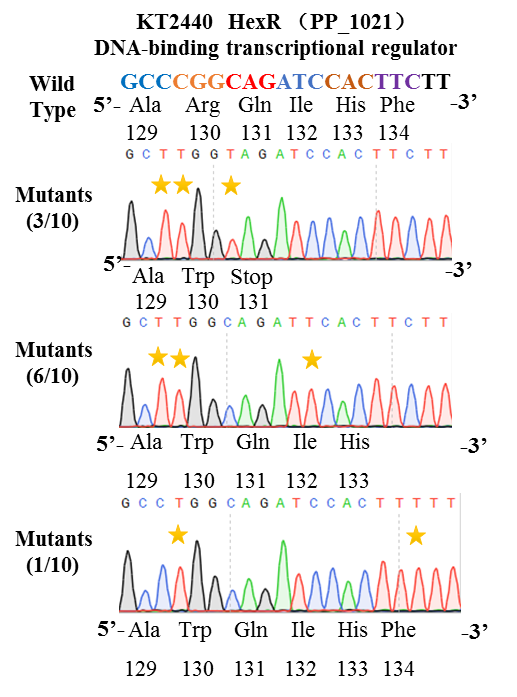
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**DNA sequencing of HexR-2 spacer after base editing using pSEVA6BE-HexR-2**

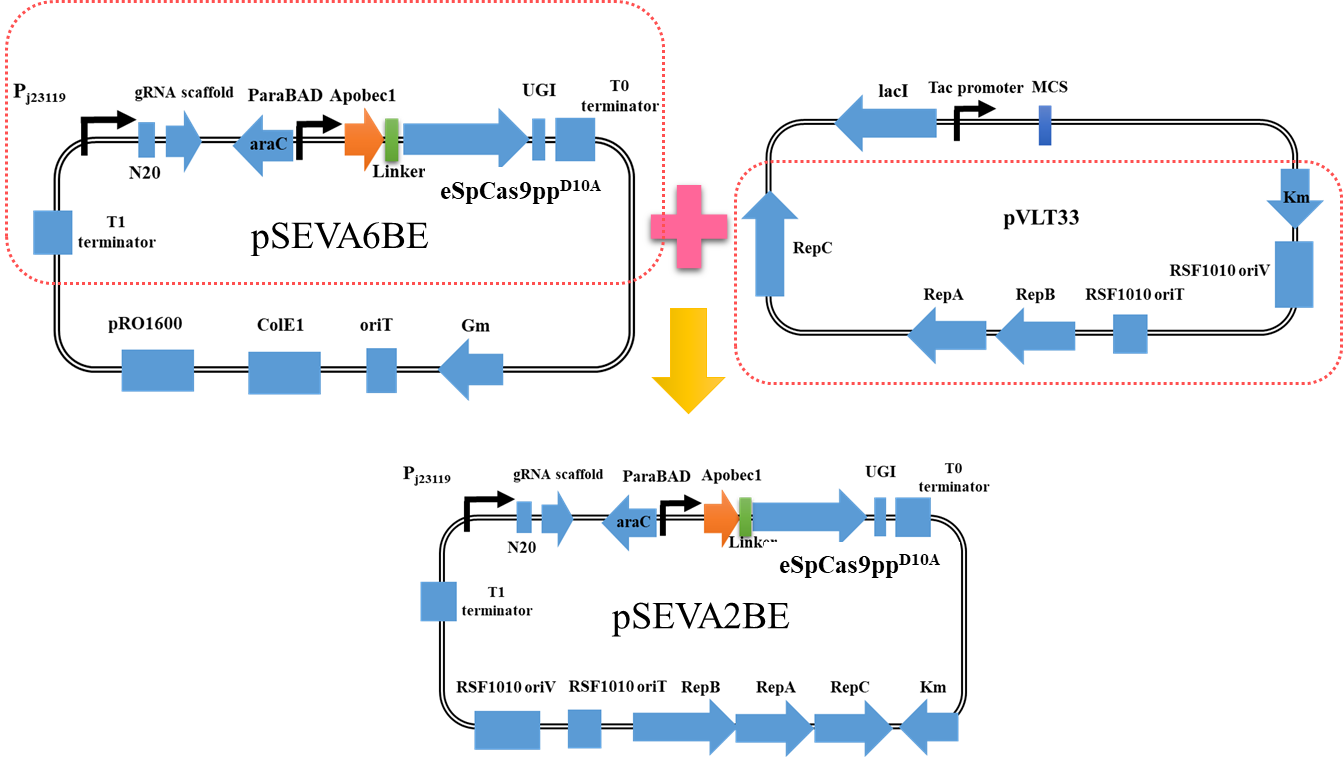
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**DNA sequencing of HexR-3 spacer after base editing using pSEVA6BE-HexR-3**

**Figure S5** **Base editing in a cytidine-rich HexR spacer**

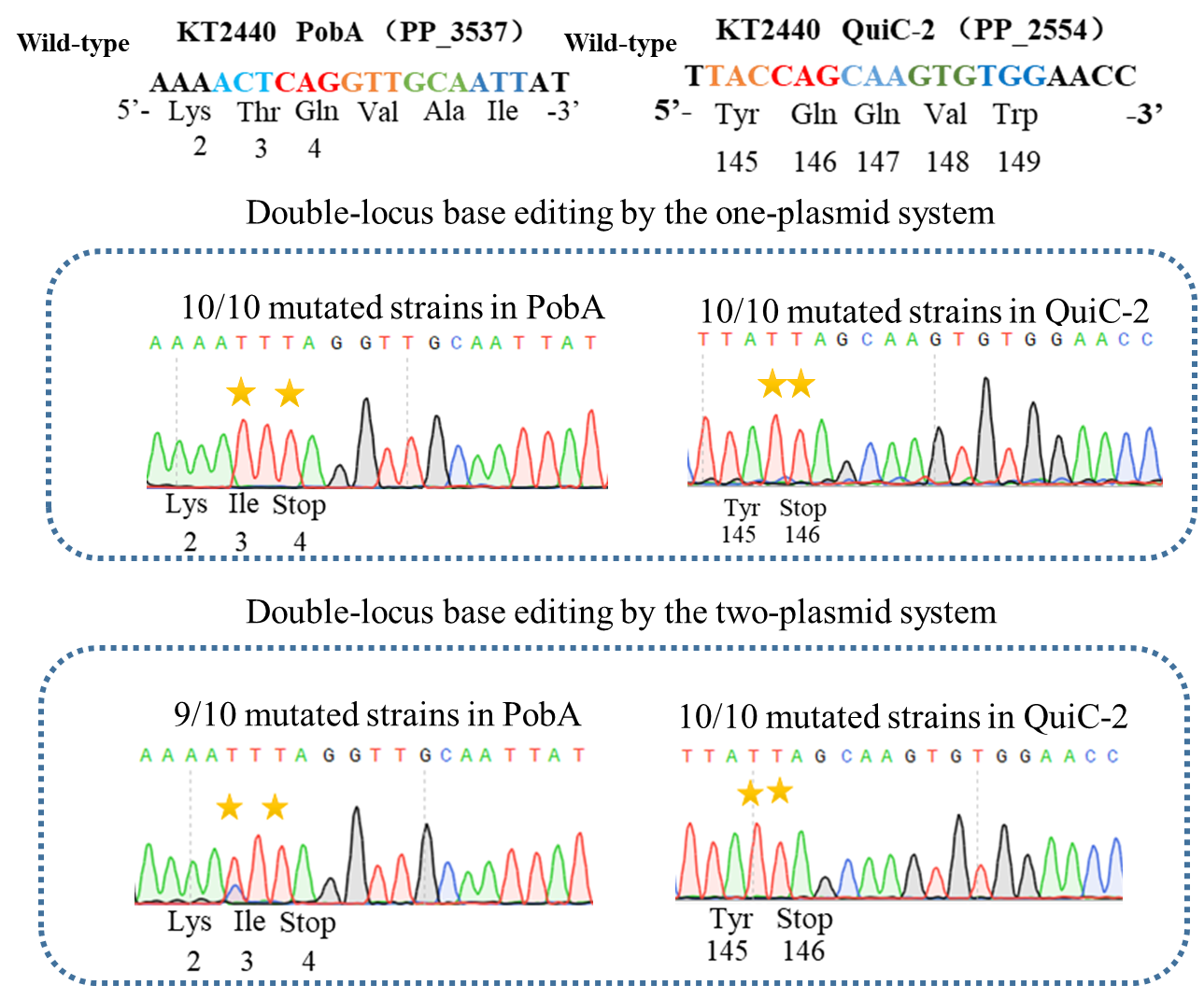


**Figure S6 The construction strategy of pSEVA2BE**

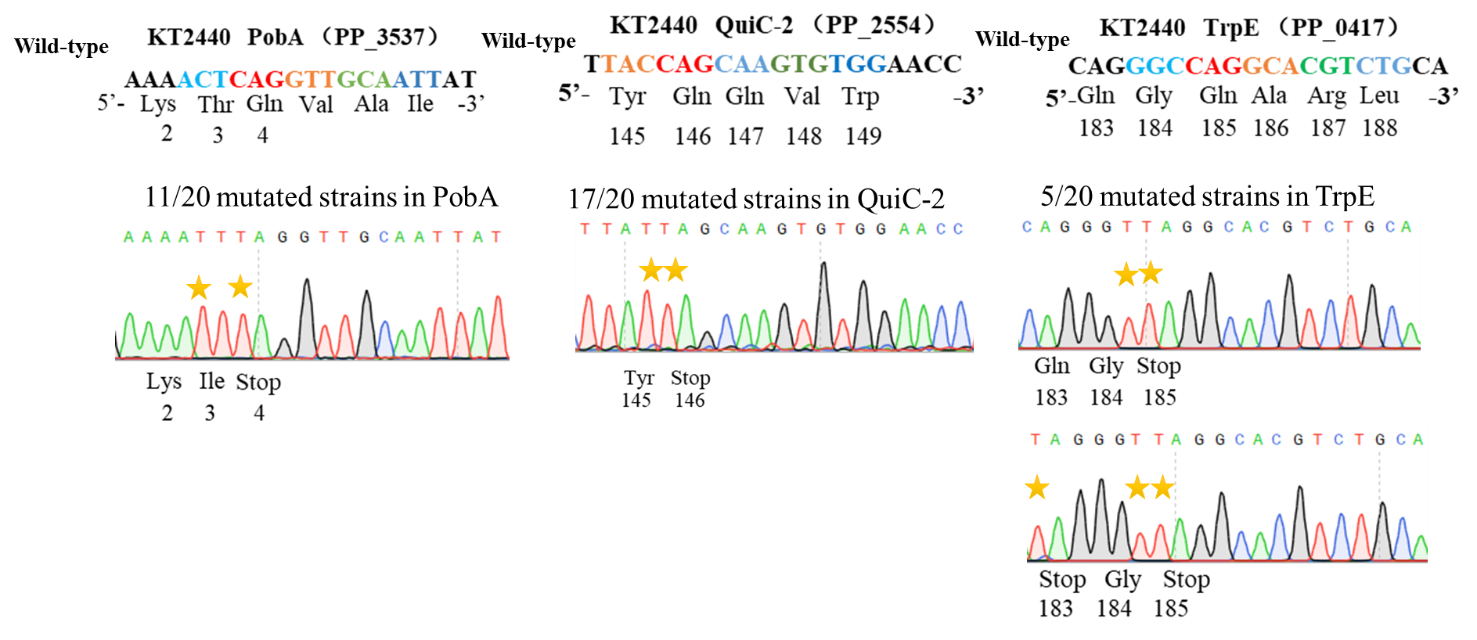
****

By connecting the base-editing cassette from pSEVA6BE with the broad-host-replicon RSF1010 and kanamycin-resistance marker from PVLT33, a kanamycin version of the base editing system pSEVA2BE (Figure S6) was constructed.

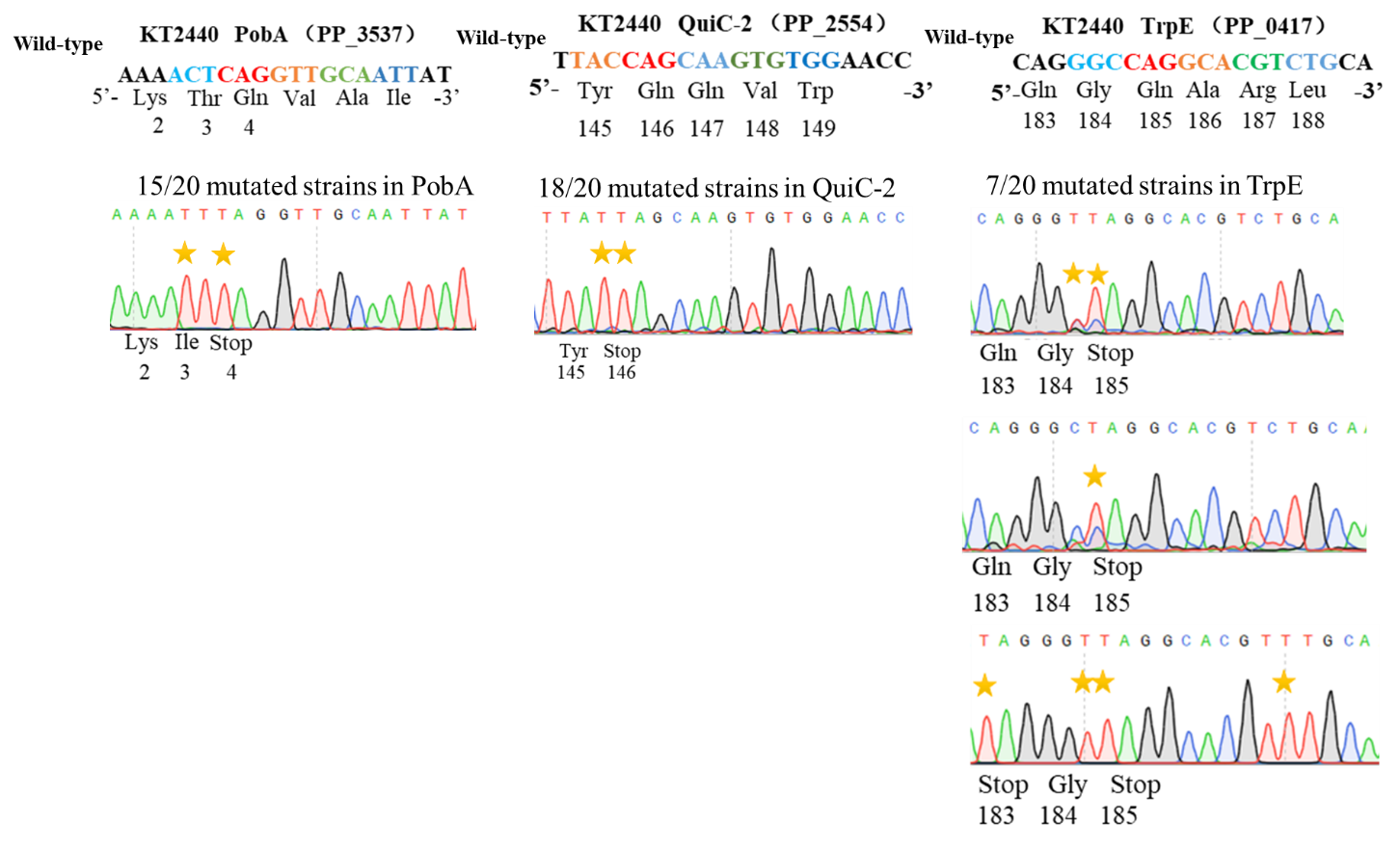
**Figure S7 Base editing in double-locus spacers PobA and QuiC-2**

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**Figure S8 Base editing in triple-locus spacers PobA, QuiC-2 and TrpE**

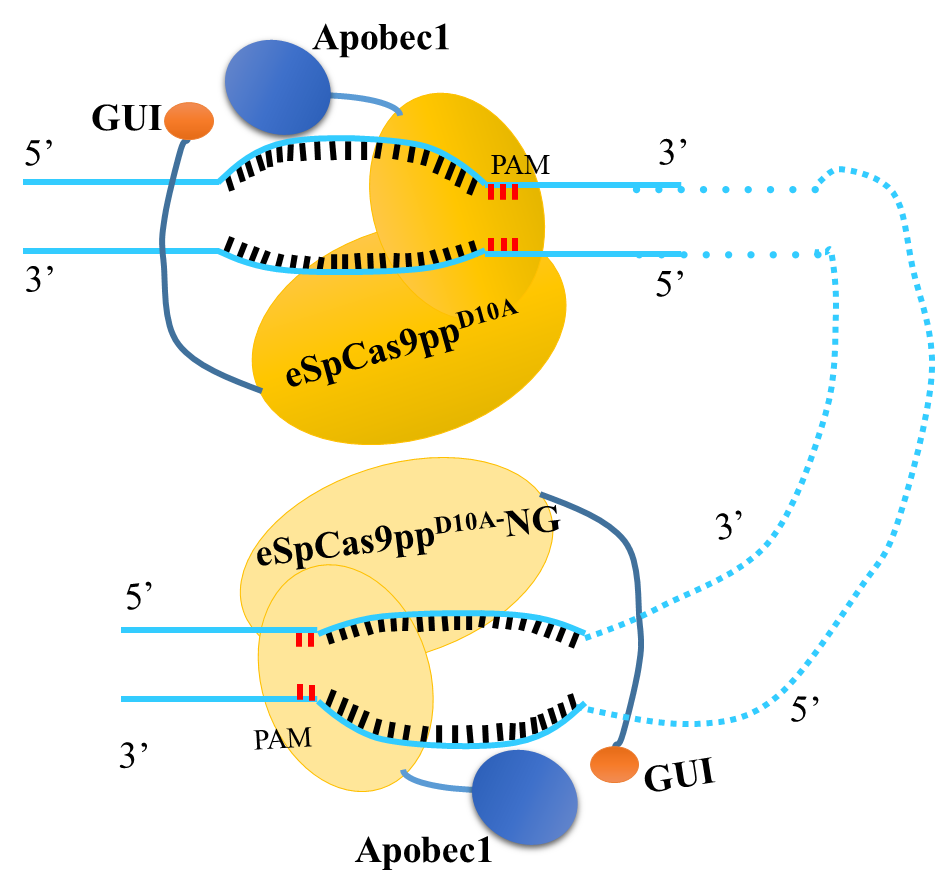
****

**DNA sequencing of triple-locus base editing in spacers PobA, QuiC-2 and TrpE using the one-plasmid system**

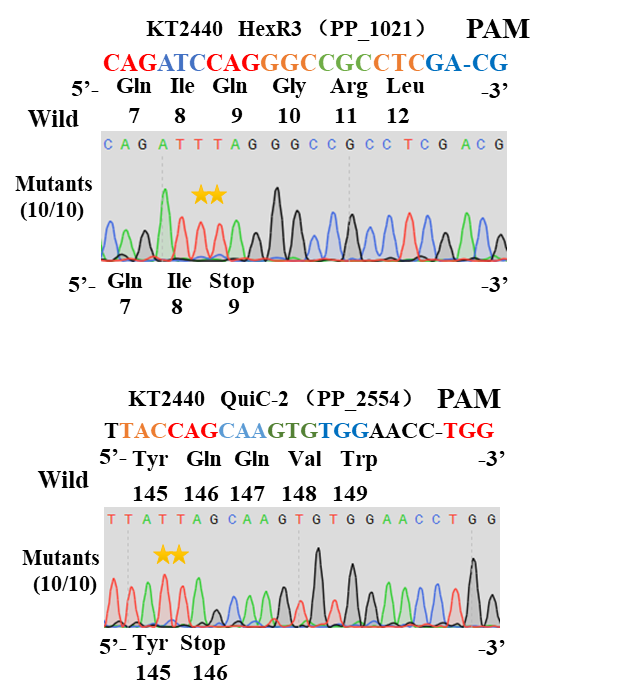
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**DNA sequencing of triple-locus base editing in spacers PobA, QuiC-2 and TrpE using the two-plasmid system**

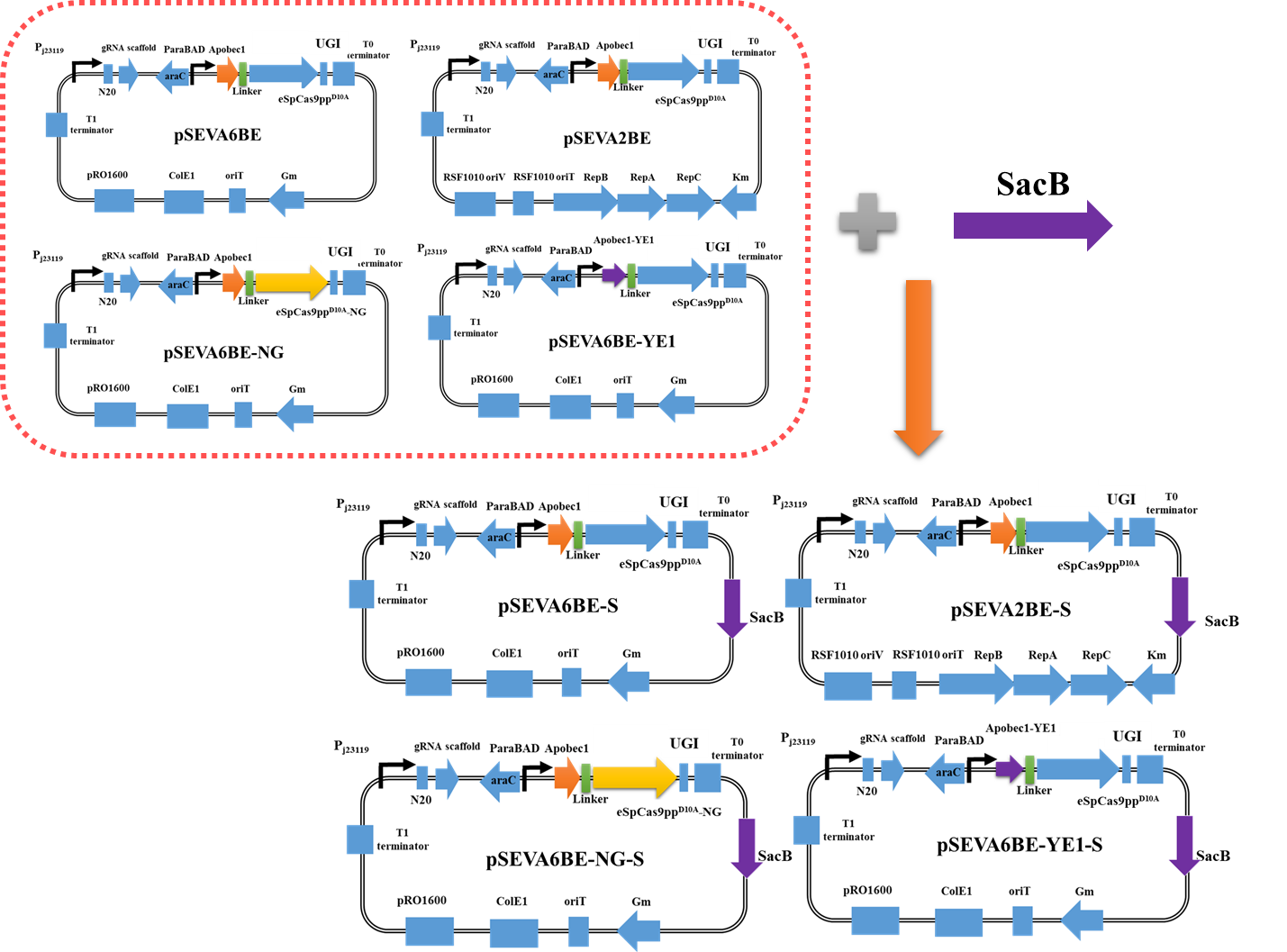
**Figure S9 Base editing of double-locus with different PAM sequences using a two-plasmid system**

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**Figure S10 DNA sequencing results of base editing in NG-type HexR3 spacer and NGG-type QuiC-2 spacer using a two-plasmid system**

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**Figure S11 Construction of a plasmid-curing strategy by appending with a counter-selection marker *sacB***

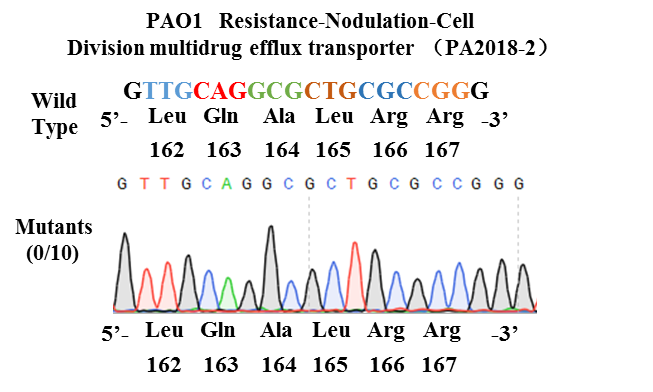
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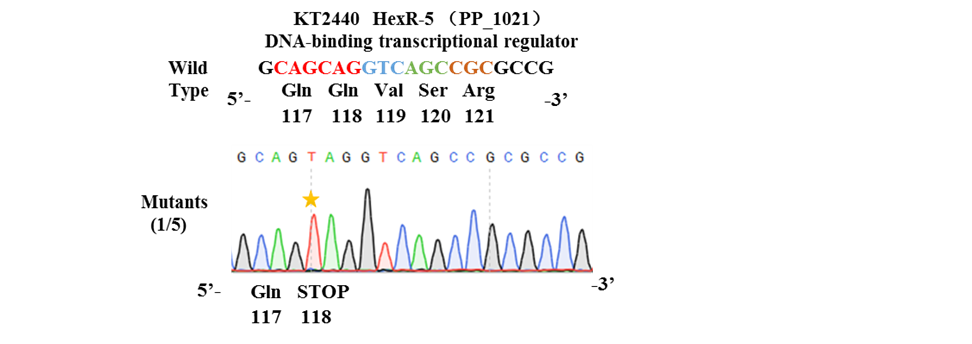
**Table S5 Potential off-target sites of spacers PA2018-2 and hexR-5**

|  |  |
| --- | --- |
| **Spacer name** | **Sequence** |
| **PA2018-2** | **GTTGCAGGCGCTGCGCCGGG** |
| **Spacer 1** | **cTgcgAGG\_CGCTGCGCCGcG-AGGT (104290-104313:+)** |
| **Spacer 2** | **GgcGgAtG\_CGCTGCGCCGGc-AGGC (351714-351737:+)** |
| **Spacer 3** | **cccGCAGG\_CGCTGCGCCGGG-AGGG (426820-426843:+)** |
| **Spacer 4** | **cTcGCAGt\_CGCTGCGCCaGG-AAGG (483385-483408:-)** |
| **Spacer 5** | **GTTGtgcG\_CGtTGCGCCGGG-CGGT (511033-511056:+)** |
| **Spacer 6** | **GTTGCtGG\_CGCTGCGCCaGG-CCGG (657777-657800:+)** |
| **Spacer 7** | **GcTcgAaG\_CGCTGCGCCGGt-TGGC (686520-686543:+)** |
| **Spacer 8** | **GcgcaAGG\_CGCTGCGCtGGG-CGGT (886710-886733:-)** |
| **Spacer 9** | **aTcGCtGG\_CGCcGCGCCGGG-TCGG (1173438-1173461:-)** |
| **Spacer 10** | **caTcCAGG\_CGCTGCtCCGGG-AAGT (1194962-1194985:+)** |
| **Spacer 11** | **cggtCtGc\_CGCTGCGCCGGG-GAGG (1442849-1442872:+)** |
| **Spacer 12** | **GcaGCAGG\_CGCTGCGCCaGG-CCGG (1490182-1490205:-)** |
| **Spacer 13** | **ccgaCAGG\_CGCTGCGCCaGG-CGGC (1754980-1755003:+)** |
| **Spacer 14** | **cggcCAGG\_CGCTGCGCCGGc-CGGC (1874807-1874830:-)** |
| **Spacer 15** | **tgTtCAGG\_CGCTGCGCCaGG-GCGG (2060512-2060535:-)** |
| **Spacer 16** | **GaTaCccG\_CGCTGCGCCtGG-AAGA (2259278-2259301:+)** |
| **Spacer 17** | **GcgGCgcG\_CGCTGCGCCGGG-TGGC (2306075-2306098:+)** |
| **Spacer 18** | **GcTGatGG\_CGCTGCGgCGGG-GAGA (2307769-2307792:+)** |
| **Spacer 19** | **ccTcCtGG\_CGCgGCGCCGGG-GTGG (2377911-2377934:+)** |
| **Spacer 20** | **GcaaCAGG\_CGCTGCGCCaGG-CGGA (2397940-2397963:+)** |
| **Spacer 21** | **GTcGtcGG\_CGaTGCGCCGGG-CCGG (2565637-2565660:-)** |
| **Spacer 22** | **cTcGgAGc\_CGCTGCGCCcGG-ACGG (2618888-2618911:+)** |
| **Spacer 23** | **cggGtAGt\_CGCTGCGCCGGG-TCGG (2864827-2864850:+)** |
| **Spacer 24** | **GcTGgAac\_CGCTGaGCCGGG-CGGC (3368924-3368947:+)** |
| **Spacer 25** | **tggcCAGG\_CGCTGCGCCGcG-CGGG (3723616-3723639:-)** |
| **Spacer 26** | **cTacCtGG\_CGCTGCGCCtGG-CGGC (3766330-3766353:-)** |
| **Spacer 27** | **GTTGCAGG\_CGCaGCGCCGGG-AAGC (3809914-3809937:+)** |
| **Spacer 28** | **GTcGgtGa\_CGCTGgGCCGGG-TGGC (3933993-3934016:-)** |
| **Spacer 29** | **GcgcCAGc\_CGtTGCGCCGGG-TCGG (3954388-3954411:-)** |
| **Spacer 30** | **ccTGCtGG\_CGCTGCGCCtGG-AGGA (4336248-4336271:-)** |
| **Spacer 31** | **GgaaCAGc\_CGCTGCGCCtGG-CTGG (4516598-4516621:-)** |
| **Spacer 32** | **GTTcgAtt\_gGCTGCGCCGGG-AGGC (4908305-4908328:+)** |
| **Spacer 33** | **GTTGagGc\_CGCTGCGCaGGG-CGGC (5089778-5089801:+)** |
| **Spacer 34** | **caccCAGG\_CGCTGCGCCtGG-CTGG (5288348-5288371:-)** |
| **Spacer 35** | **GcgGCcGG\_CGCTGCGCCtGG-AAGT (5321367-5321390:+)** |
| **Spacer 36** | **cTccgAGG\_CGCTGCGCCaGG-CGGC (5420357-5420380:-)** |
| **Spacer 37** | **ccgGCttG\_CGCTGCGCCGGG-AAGA (5673910-5673933:+)** |
| **Spacer 38** | **cTTGaAct\_CGCTGCGCCaGG-CGGT (5772477-5772500:+)** |

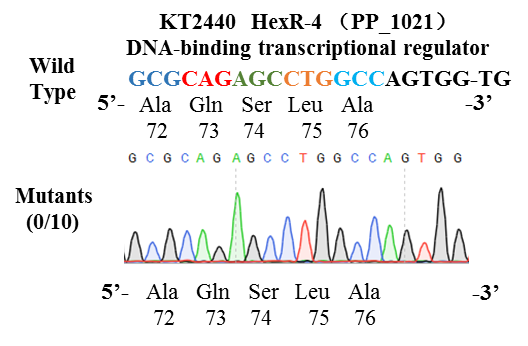
|  |  |
| --- | --- |
| **Spacer name** | **Sequence** |
| **HexR-5** | **GCAGCAGGTCAGCCGCGCCG** |
| **Spacer 1** | **cCtGaAGG\_TCAGCCGCGgCG-CGGT (5158966-5158989:+)** |
| **Spacer 2** | **cgAaCAGa\_TCcGCCGCGCCG-AGGC (2408182-2408205:-)** |
| **Spacer 3** | **aCAGCgtG\_TCAGCCGCGaCG-AAGC (4252595-4252618:+)** |
| **Spacer 4** | **GgAGCgta\_TCgGCCGCGCCG-TCGG (150576-150599:-)** |

**Figure S12** **DNA sequencing of spacers PA2018-2 and HexR-5**

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**Figure S13 Base editing in a NG PAM HexR-4 spacer**

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**DNA sequence of eSpCas9pp**

ATGGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACAGCGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCGAGCAAGAAGTTCAAGGTGCTGGGCAACACCGACCGCCACAGCATCAAGAAGAACCTGATCGGCGCCCTGCTGTTCGACAGCGGCGAGACCGCCGAAGCCACCCGCCTGAAGCGCACCGCCCGCCGCCGCTACACCCGTCGCAAGAACCGCATCTGCTACCTGCAGGAGATCTTCAGCAACGAAATGGCCAAGGTGGACGACAGCTTCTTCCACCGCCTGGAGGAAAGCTTCCTGGTGGAGGAAGACAAGAAGCACGAGCGCCACCCGATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAAAAGTACCCGACCATCTACCACCTGCGCAAGAAGCTGGTCGACAGCACCGACAAGGCCGACCTGCGCCTGATCTACCTGGCCCTGGCCCACATGATCAAGTTCCGCGGCCACTTCCTGATCGAAGGCGACCTGAACCCGGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCGATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGAGCGCCCGCCTGAGCAAGAGCCGCCGCCTGGAGAACCTGATCGCCCAGCTGCCGGGCGAAAAGAAGAACGGCCTGTTCGGCAACCTGATCGCCCTGAGCCTGGGCCTGACCCCGAACTTCAAGAGCAACTTCGACCTGGCCGAGGACGCCAAGCTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTCCTGGCCGCCAAGAACCTGAGCGACGCCATCCTGCTGAGCGACATCCTGCGCGTGAACACCGAGATCACCAAGGCCCCGCTGAGCGCCAGCATGATCAAGCGCTACGACGAACACCACCAGGACCTGACCCTGCTGAAGGCCCTGGTGCGCCAGCAGCTGCCGGAGAAGTACAAGGAAATCTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATCGACGGTGGCGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCGATCCTGGAGAAGATGGACGGCACCGAGGAACTGCTGGTGAAGCTGAACCGCGAAGACCTGCTGCGCAAGCAGCGCACCTTCGACAACGGCAGCATCCCGCACCAGATCCACCTGGGCGAGCTGCACGCCATCCTGCGTCGCCAGGAAGACTTCTACCCGTTCCTGAAGGACAACCGCGAGAAGATCGAAAAGATCCTGACCTTCCGCATCCCGTACTACGTGGGCCCGCTGGCCCGCGGCAACAGCCGCTTCGCCTGGATGACCCGCAAGAGCGAGGAAACCATCACCCCGTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCCAGCGCCCAGAGCTTCATCGAGCGCATGACCAACTTCGACAAGAACCTGCCGAACGAAAAGGTGCTGCCGAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTACAACGAACTGACCAAGGTGAAGTACGTGACCGAGGGCATGCGCAAGCCGGCCTTCCTGAGCGGCGAACAGAAGAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGCAAGGTGACCGTGAAGCAGCTGAAGGAAGACTACTTCAAGAAGATCGAATGCTTCGACAGCGTGGAGATCAGCGGCGTGGAAGACCGCTTCAACGCCAGCCTGGGCACCTACCACGACCTGCTGAAGATCATCAAGGACAAGGACTTCCTGGACAACGAGGAAAACGAGGACATCCTGGAAGACATCGTGCTGACCCTGACCCTGTTCGAGGACCGCGAAATGATCGAGGAACGCCTGAAGACCTACGCCCACCTGTTCGACGACAAGGTGATGAAGCAGCTGAAGCGCCGCCGCTACACCGGCTGGGGCCGCCTGAGCCGCAAGCTGATCAACGGCATCCGCGACAAGCAGAGCGGCAAGACCATCCTGGACTTCCTGAAGAGCGACGGCTTCGCCAACCGCAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTCAAGGAAGACATCCAGAAGGCCCAAGTGAGCGGCCAGGGCGACAGCCTGCACGAACACATCGCCAACCTGGCCGGCAGCCCGGCCATCAAGAAGGGCATCCTGCAGACCGTGAAGGTGGTGGACGAGCTGGTGAAGGTGATGGGCCGCCACAAGCCGGAAAACATCGTGATCGAGATGGCCCGCGAAAACCAGACCACCCAGAAGGGCCAGAAGAACAGCCGCGAGCGCATGAAGCGCATCGAGGAAGGCATCAAGGAACTGGGCAGCCAGATCCTGAAGGAGCACCCGGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAACGGCCGCGACATGTACGTGGACCAGGAACTGGACATCAACCGCCTGAGCGACTACGACGTGGACCACATCGTGCCGCAGAGCTTCCTGGCCGACGACAGCATCGACAACAAGGTGCTGACCCGCAGCGACAAGAACCGCGGCAAGAGCGACAACGTGCCGAGCGAGGAAGTGGTGAAGAAGATGAAGAACTACTGGCGCCAGCTGCTGAACGCCAAGCTGATCACCCAGCGCAAGTTCGACAACCTGACCAAGGCCGAGCGCGGCGGCCTGAGCGAACTGGACAAGGCCGGCTTCATCAAGCGCCAGCTGGTCGAGACCCGCCAGATCACCAAGCACGTGGCCCAGATCCTGGACAGCCGCATGAACACCAAGTACGACGAGAACGACAAGCTGATCCGCGAAGTGAAGGTGATCACCCTGAAGAGCAAGCTGGTCAGCGACTTCCGCAAGGACTTCCAGTTCTACAAGGTGCGCGAAATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTGGTGGGCACCGCCCTGATCAAGAAGTACCCGGCCCTGGAGAGCGAATTCGTGTACGGCGACTACAAGGTGTACGACGTGCGCAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCCACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTCTTCAAGACCGAGATCACCCTGGCCAACGGCGAAATCCGCAAGGCCCCGCTGATCGAGACCAACGGCGAGACCGGCGAAATCGTGTGGGACAAGGGCCGCGACTTCGCCACCGTGCGCAAGGTGCTGAGCATGCCGCAGGTGAACATCGTGAAGAAGACCGAGGTGCAGACCGGCGGCTTCAGCAAGGAAAGCATCCTGCCGAAGCGCAACAGCGACAAGCTGATCGCCCGCAAGAAGGACTGGGACCCGAAGAAGTACGGCGGCTTCGACAGCCCGACCGTGGCCTACAGCGTGCTGGTCGTGGCCAAGGTGGAGAAGGGCAAGAGCAAGAAGCTGAAGAGCGTGAAGGAACTGCTGGGCATCACCATCATGGAGCGCAGCAGCTTCGAAAAGAACCCGATCGACTTCCTGGAGGCCAAGGGCTACAAGGAAGTGAAGAAGGACCTGATCATCAAGCTGCCGAAGTACAGCCTGTTCGAGCTGGAAAACGGCCGCAAGCGCATGCTGGCCAGCGCCGGCGAGCTGCAGAAGGGCAACGAACTGGCCCTGCCGAGCAAGTACGTGAACTTCCTGTACCTGGCCTCGCACTACGAGAAGCTGAAGGGCAGCCCGGAGGACAACGAACAGAAGCAGCTGTTCGTGGAGCAGCACAAGCACTACCTGGACGAGATCATCGAACAGATCAGCGAATTCAGCAAGCGCGTGATCCTGGCCGACGCCAACCTGGACAAGGTGCTGAGCGCCTACAACAAGCACCGCGACAAGCCGATCCGCGAGCAGGCCGAAAACATCATCCACCTGTTCACCCTGACCAACCTGGGCGCCCCGGCCGCCTTCAAGTACTTCGACACCACCATCGACCGCAAGCGCTACACCAGCACCAAGGAAGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAAACCCGCATCGACCTGAGCCAGCTGGGCGGCGACTAG

**DNA sequence of APOBEC1**

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**DNA sequence of eSpCas9ppD10A-NG**

ATGGACAAGAAGTACAGCATCGGCCTGGATATCGGCACCAACAGCGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCGAGCAAGAAGTTCAAGGTGCTGGGCAACACCGACCGCCACAGCATCAAGAAGAACCTGATCGGCGCCCTGCTGTTCGACAGCGGCGAGACCGCCGAAGCCACCCGCCTGAAGCGCACCGCCCGCCGCCGCTACACCCGTCGCAAGAACCGCATCTGCTACCTGCAGGAGATCTTCAGCAACGAAATGGCCAAGGTGGACGACAGCTTCTTCCACCGCCTGGAGGAAAGCTTCCTGGTGGAGGAAGACAAGAAGCACGAGCGCCACCCGATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAAAAGTACCCGACCATCTACCACCTGCGCAAGAAGCTGGTCGACAGCACCGACAAGGCCGACCTGCGCCTGATCTACCTGGCCCTGGCCCACATGATCAAGTTCCGCGGCCACTTCCTGATCGAAGGCGACCTGAACCCGGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCGATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGAGCGCCCGCCTGAGCAAGAGCCGCCGCCTGGAGAACCTGATCGCCCAGCTGCCGGGCGAAAAGAAGAACGGCCTGTTCGGCAACCTGATCGCCCTGAGCCTGGGCCTGACCCCGAACTTCAAGAGCAACTTCGACCTGGCCGAGGACGCCAAGCTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTCCTGGCCGCCAAGAACCTGAGCGACGCCATCCTGCTGAGCGACATCCTGCGCGTGAACACCGAGATCACCAAGGCCCCGCTGAGCGCCAGCATGATCAAGCGCTACGACGAACACCACCAGGACCTGACCCTGCTGAAGGCCCTGGTGCGCCAGCAGCTGCCGGAGAAGTACAAGGAAATCTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATCGACGGTGGCGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCGATCCTGGAGAAGATGGACGGCACCGAGGAACTGCTGGTGAAGCTGAACCGCGAAGACCTGCTGCGCAAGCAGCGCACCTTCGACAACGGCAGCATCCCGCACCAGATCCACCTGGGCGAGCTGCACGCCATCCTGCGTCGCCAGGAAGACTTCTACCCGTTCCTGAAGGACAACCGCGAGAAGATCGAAAAGATCCTGACCTTCCGCATCCCGTACTACGTGGGCCCGCTGGCCCGCGGCAACAGCCGCTTCGCCTGGATGACCCGCAAGAGCGAGGAAACCATCACCCCGTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCCAGCGCCCAGAGCTTCATCGAGCGCATGACCAACTTCGACAAGAACCTGCCGAACGAAAAGGTGCTGCCGAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTACAACGAACTGACCAAGGTGAAGTACGTGACCGAGGGCATGCGCAAGCCGGCCTTCCTGAGCGGCGAACAGAAGAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGCAAGGTGACCGTGAAGCAGCTGAAGGAAGACTACTTCAAGAAGATCGAATGCTTCGACAGCGTGGAGATCAGCGGCGTGGAAGACCGCTTCAACGCCAGCCTGGGCACCTACCACGACCTGCTGAAGATCATCAAGGACAAGGACTTCCTGGACAACGAGGAAAACGAGGACATCCTGGAAGACATCGTGCTGACCCTGACCCTGTTCGAGGACCGCGAAATGATCGAGGAACGCCTGAAGACCTACGCCCACCTGTTCGACGACAAGGTGATGAAGCAGCTGAAGCGCCGCCGCTACACCGGCTGGGGCCGCCTGAGCCGCAAGCTGATCAACGGCATCCGCGACAAGCAGAGCGGCAAGACCATCCTGGACTTCCTGAAGAGCGACGGCTTCGCCAACCGCAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTCAAGGAAGACATCCAGAAGGCCCAAGTGAGCGGCCAGGGCGACAGCCTGCACGAACACATCGCCAACCTGGCCGGCAGCCCGGCCATCAAGAAGGGCATCCTGCAGACCGTGAAGGTGGTGGACGAGCTGGTGAAGGTGATGGGCCGCCACAAGCCGGAAAACATCGTGATCGAGATGGCCCGCGAAAACCAGACCACCCAGAAGGGCCAGAAGAACAGCCGCGAGCGCATGAAGCGCATCGAGGAAGGCATCAAGGAACTGGGCAGCCAGATCCTGAAGGAGCACCCGGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAACGGCCGCGACATGTACGTGGACCAGGAACTGGACATCAACCGCCTGAGCGACTACGACGTGGACCACATCGTGCCGCAGAGCTTCCTGGCCGACGACAGCATCGACAACAAGGTGCTGACCCGCAGCGACAAGAACCGCGGCAAGAGCGACAACGTGCCGAGCGAGGAAGTGGTGAAGAAGATGAAGAACTACTGGCGCCAGCTGCTGAACGCCAAGCTGATCACCCAGCGCAAGTTCGACAACCTGACCAAGGCCGAGCGCGGCGGCCTGAGCGAACTGGACAAGGCCGGCTTCATCAAGCGCCAGCTGGTCGAGACCCGCCAGATCACCAAGCACGTGGCCCAGATCCTGGACAGCCGCATGAACACCAAGTACGACGAGAACGACAAGCTGATCCGCGAAGTGAAGGTGATCACCCTGAAGAGCAAGCTGGTCAGCGACTTCCGCAAGGACTTCCAGTTCTACAAGGTGCGCGAAATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTGGTGGGCACCGCCCTGATCAAGAAGTACCCGGCCCTGGAGAGCGAATTCGTGTACGGCGACTACAAGGTGTACGACGTGCGCAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCCACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTCTTCAAGACCGAGATCACCCTGGCCAACGGCGAAATCCGCAAGGCCCCGCTGATCGAGACCAACGGCGAGACCGGCGAAATCGTGTGGGACAAGGGCCGCGACTTCGCCACCGTGCGCAAGGTGCTGAGCATGCCGCAGGTGAACATCGTGAAGAAGACCGAGGTGCAGACCGGCGGCTTCAGCAAGGAAAGCATCCGGCCGAAGCGCAACAGCGACAAGCTGATCGCCCGCAAGAAGGACTGGGACCCGAAGAAGTACGGCGGCTTCGTCAGCCCGACCGTGGCCTACAGCGTGCTGGTCGTGGCCAAGGTGGAGAAGGGCAAGAGCAAGAAGCTGAAGAGCGTGAAGGAACTGCTGGGCATCACCATCATGGAGCGCAGCAGCTTCGAAAAGAACCCGATCGACTTCCTGGAGGCCAAGGGCTACAAGGAAGTGAAGAAGGACCTGATCATCAAGCTGCCGAAGTACAGCCTGTTCGAGCTGGAAAACGGCCGCAAGCGCATGCTGGCCAGCGCCCGCTTCCTGCAGAAGGGCAACGAACTGGCCCTGCCGAGCAAGTACGTGAACTTCCTGTACCTGGCCTCGCACTACGAGAAGCTGAAGGGCAGCCCGGAGGACAACGAACAGAAGCAGCTGTTCGTGGAGCAGCACAAGCACTACCTGGACGAGATCATCGAACAGATCAGCGAATTCAGCAAGCGCGTGATCCTGGCCGACGCCAACCTGGACAAGGTGCTGAGCGCCTACAACAAGCACCGCGACAAGCCGATCCGCGAGCAGGCCGAAAACATCATCCACCTGTTCACCCTGACCAACCTGGGCGCCCCGCGCGCCTTCAAGTACTTCGACACCACCATCGACCGCAAGGCCTACCGCAGCACCAAGGAAGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAAACCCGCATCGACCTGAGCCAGCTGGGCGGCGAC TAG

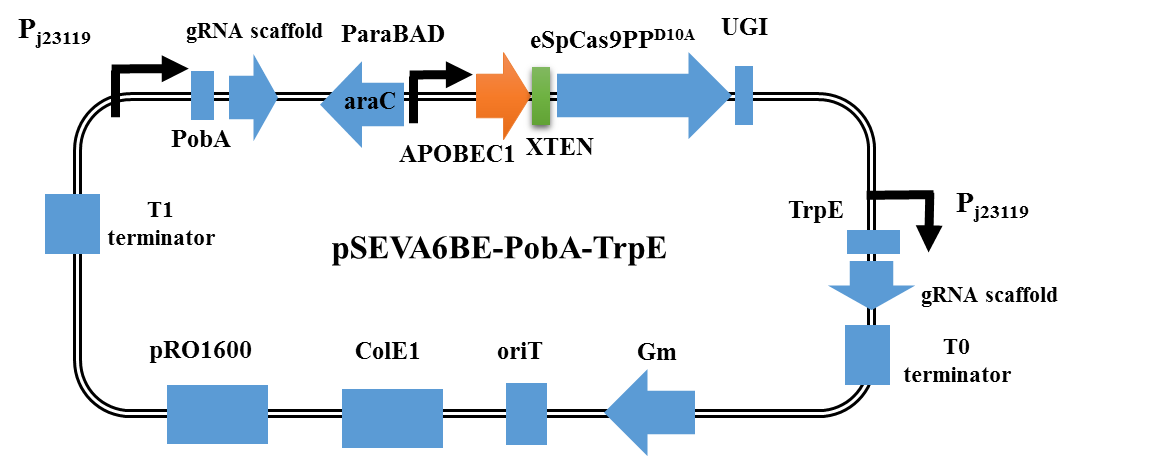
**DNA sequence of plasmid pSEVA6BE ( 9856 bp)**

**TTAATTAATGACACCATGAATTCTTGACAGCTAGCTCAGTCCTAGGTATAATGCTAGCTGCCAAACGATTGCAGGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTTGAGGAGCTCGGTCACCGTTACATATCAAAGGGAAAACTGTCCATACCCATGGGGCATGGCGAATTATGACAACTTGACGGCTACATCATTCACTTTTTCTTCACAACCGGCACGGAACTCGCTCGGGCTGGCCCCGGTGCATTTTTTAAATACCCGCGAGAAGTAGAGTTGATCGTCAAAACCAACATTGCGACCGACGGTGGCGATAGGCATCCGGGTGGTGCTCAAAAGCAGCTTCGCCTGGCTGATACGTTGGTCCTCGCGCCAGCTTAAGACGCTAATCCCTAACTGCTGGCGGAAAAGATGTGACAGACGCGACGGCGACAAGCAAACATGCTGTGCGACGCTGGCGATATCAAAATTGCTGTCTGCCAGGTGATCGCTGATGTACTGACAAGCCTCGCGTACCCGATTATCCATCGGTGGATGGAGCGACTCGTTAATCGCTTCCATGCGCCGCAGTAACAATTGCTCAAGCAGATTTATCGCCAGCAGCTCCGAATAGCGCCCTTCCCCTTGCCCGGCGTTAATGATTTGCCCAAACAGGTCGCTGAAATGCGGCTGGTGCGCTTCATCCGGGCGAAAGAACCCCGTATTGGCAAATATTGACGGCCAGTTAAGCCATTCATGCCAGTAGGCGCGCGGACGAAAGTAAACCCACTGGTGATACCATTCGCGAGCCTCCGGATGACGACCGTAGTGATGAATCTCTCCTGGCGGGAACAGCAAAATATCACCCGGTCGGCAAACAAATTCTCGTCCCTGATTTTTCACCACCCCCTGACCGCGAATGGTGAGATTGAGAATATAACCTTTCATTCCCAGCGGTCGGTCGATAAAAAAATCGAGATAACCGTTGGCCTCAATCGGCGTTAAACCCGCCACCAGATGGGCATTAAACGAGTATCCCGGCAGCAGGGGATCATTTTGCGCTTCAGCCATACTTTTCATACTCCCGCCATTCAGAGAAGAAACCAATTGTCCATATTGCATCAGACATTGCCGTCACTGCGTCTTTTACTGGCTCTTCTCGCTAACCAAACCGGTAACCCCGCTTATTAAAAGCATTCTGTAACAAAGCGGGACCAAAGCCATGACAAAAACGCGTAACAAAAGTGTCTATAATCACGGCAGAAAAGTCCACATTGATTATTTGCACGGCGTCACACTTTGCTATGCCATAGCATTTTTATCCATAAGATTAGCGGATCCTACCTGACGCTTTTTATCGCAACTCTCTACTGTTTCTCCATCTTAAGGGCGATAGGAGGAATATACCATGAGCAGCGAAACCGGCCCGGTGGCCGTGGACCCGACCCTGCGTCGCCGCATCGAGCCGCACGAGTTCGAAGTGTTCTTCGACCCGCGCGAGCTGCGCAAGGAAACCTGCCTGCTGTACGAAATCAACTGGGGCGGCCGCCACAGCATCTGGCGCCACACCAGCCAGAACACCAACAAGCACGTGGAGGTGAACTTCATCGAAAAGTTCACCACCGAGCGCTACTTCTGCCCGAACACCCGCTGCAGCATCACCTGGTTCCTGAGCTGGAGCCCGTGCGGCGAATGCAGCCGCGCCATCACCGAGTTCCTGAGCCGCTACCCGCACGTGACCCTGTTCATCTACATCGCCCGCCTGTACCACCACGCCGACCCGCGCAACCGCCAGGGCCTGCGCGACCTGATCAGCAGCGGCGTGACCATCCAGATCATGACCGAGCAGGAAAGCGGCTACTGCTGGCGCAACTTCGTGAACTACAGCCCGAGCAACGAAGCCCACTGGCCGCGCTACCCGCACCTGTGGGTGCGCCTGTACGTGCTGGAGCTGTACTGCATCATCCTGGGCCTGCCGCCGTGCCTGAACATCCTGCGTCGCAAGCAGCCGCAGCTGACCTTCTTCACCATCGCCCTGCAGAGCTGCCACTACCAGCGCCTGCCGCCGCACATCCTGTGGGCCACCGGCCTGAAGAGCGGCAGCGAGACTCCCGGGACCTCAGAGTCCGCCACACCCGAAAGTGACAAGAAGTACAGCATCGGCCTGGCTATCGGCACCAACAGCGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCGAGCAAGAAGTTCAAGGTGCTGGGCAACACCGACCGCCACAGCATCAAGAAGAACCTGATCGGCGCCCTGCTGTTCGACAGCGGCGAGACCGCCGAAGCCACCCGCCTGAAGCGCACCGCCCGCCGCCGCTACACCCGTCGCAAGAACCGCATCTGCTACCTGCAGGAGATCTTCAGCAACGAAATGGCCAAGGTGGACGACAGCTTCTTCCACCGCCTGGAGGAAAGCTTCCTGGTGGAGGAAGACAAGAAGCACGAGCGCCACCCGATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAAAAGTACCCGACCATCTACCACCTGCGCAAGAAGCTGGTCGACAGCACCGACAAGGCCGACCTGCGCCTGATCTACCTGGCCCTGGCCCACATGATCAAGTTCCGCGGCCACTTCCTGATCGAAGGCGACCTGAACCCGGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCGATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGAGCGCCCGCCTGAGCAAGAGCCGCCGCCTGGAGAACCTGATCGCCCAGCTGCCGGGCGAAAAGAAGAACGGCCTGTTCGGCAACCTGATCGCCCTGAGCCTGGGCCTGACCCCGAACTTCAAGAGCAACTTCGACCTGGCCGAGGACGCCAAGCTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTCCTGGCCGCCAAGAACCTGAGCGACGCCATCCTGCTGAGCGACATCCTGCGCGTGAACACCGAGATCACCAAGGCCCCGCTGAGCGCCAGCATGATCAAGCGCTACGACGAACACCACCAGGACCTGACCCTGCTGAAGGCCCTGGTGCGCCAGCAGCTGCCGGAGAAGTACAAGGAAATCTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATCGACGGTGGCGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCGATCCTGGAGAAGATGGACGGCACCGAGGAACTGCTGGTGAAGCTGAACCGCGAAGACCTGCTGCGCAAGCAGCGCACCTTCGACAACGGCAGCATCCCGCACCAGATCCACCTGGGCGAGCTGCACGCCATCCTGCGTCGCCAGGAAGACTTCTACCCGTTCCTGAAGGACAACCGCGAGAAGATCGAAAAGATCCTGACCTTCCGCATCCCGTACTACGTGGGCCCGCTGGCCCGCGGCAACAGCCGCTTCGCCTGGATGACCCGCAAGAGCGAGGAAACCATCACCCCGTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCCAGCGCCCAGAGCTTCATCGAGCGCATGACCAACTTCGACAAGAACCTGCCGAACGAAAAGGTGCTGCCGAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTACAACGAACTGACCAAGGTGAAGTACGTGACCGAGGGCATGCGCAAGCCGGCCTTCCTGAGCGGCGAACAGAAGAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGCAAGGTGACCGTGAAGCAGCTGAAGGAAGACTACTTCAAGAAGATCGAATGCTTCGACAGCGTGGAGATCAGCGGCGTGGAAGACCGCTTCAACGCCAGCCTGGGCACCTACCACGACCTGCTGAAGATCATCAAGGACAAGGACTTCCTGGACAACGAGGAAAACGAGGACATCCTGGAAGACATCGTGCTGACCCTGACCCTGTTCGAGGACCGCGAAATGATCGAGGAACGCCTGAAGACCTACGCCCACCTGTTCGACGACAAGGTGATGAAGCAGCTGAAGCGCCGCCGCTACACCGGCTGGGGCCGCCTGAGCCGCAAGCTGATCAACGGCATCCGCGACAAGCAGAGCGGCAAGACCATCCTGGACTTCCTGAAGAGCGACGGCTTCGCCAACCGCAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTCAAGGAAGACATCCAGAAGGCCCAAGTGAGCGGCCAGGGCGACAGCCTGCACGAACACATCGCCAACCTGGCCGGCAGCCCGGCCATCAAGAAGGGCATCCTGCAGACCGTGAAGGTGGTGGACGAGCTGGTGAAGGTGATGGGCCGCCACAAGCCGGAAAACATCGTGATCGAGATGGCCCGCGAAAACCAGACCACCCAGAAGGGCCAGAAGAACAGCCGCGAGCGCATGAAGCGCATCGAGGAAGGCATCAAGGAACTGGGCAGCCAGATCCTGAAGGAGCACCCGGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAACGGCCGCGACATGTACGTGGACCAGGAACTGGACATCAACCGCCTGAGCGACTACGACGTGGACCACATCGTGCCGCAGAGCTTCCTGGCCGACGACAGCATCGACAACAAGGTGCTGACCCGCAGCGACAAGAACCGCGGCAAGAGCGACAACGTGCCGAGCGAGGAAGTGGTGAAGAAGATGAAGAACTACTGGCGCCAGCTGCTGAACGCCAAGCTGATCACCCAGCGCAAGTTCGACAACCTGACCAAGGCCGAGCGCGGCGGCCTGAGCGAACTGGACAAGGCCGGCTTCATCAAGCGCCAGCTGGTCGAGACCCGCCAGATCACCAAGCACGTGGCCCAGATCCTGGACAGCCGCATGAACACCAAGTACGACGAGAACGACAAGCTGATCCGCGAAGTGAAGGTGATCACCCTGAAGAGCAAGCTGGTCAGCGACTTCCGCAAGGACTTCCAGTTCTACAAGGTGCGCGAAATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTGGTGGGCACCGCCCTGATCAAGAAGTACCCGGCCCTGGAGAGCGAATTCGTGTACGGCGACTACAAGGTGTACGACGTGCGCAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCCACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTCTTCAAGACCGAGATCACCCTGGCCAACGGCGAAATCCGCAAGGCCCCGCTGATCGAGACCAACGGCGAGACCGGCGAAATCGTGTGGGACAAGGGCCGCGACTTCGCCACCGTGCGCAAGGTGCTGAGCATGCCGCAGGTGAACATCGTGAAGAAGACCGAGGTGCAGACCGGCGGCTTCAGCAAGGAAAGCATCCTGCCGAAGCGCAACAGCGACAAGCTGATCGCCCGCAAGAAGGACTGGGACCCGAAGAAGTACGGCGGCTTCGACAGCCCGACCGTGGCCTACAGCGTGCTGGTCGTGGCCAAGGTGGAGAAGGGCAAGAGCAAGAAGCTGAAGAGCGTGAAGGAACTGCTGGGCATCACCATCATGGAGCGCAGCAGCTTCGAAAAGAACCCGATCGACTTCCTGGAGGCCAAGGGCTACAAGGAAGTGAAGAAGGACCTGATCATCAAGCTGCCGAAGTACAGCCTGTTCGAGCTGGAAAACGGCCGCAAGCGCATGCTGGCCAGCGCCGGCGAGCTGCAGAAGGGCAACGAACTGGCCCTGCCGAGCAAGTACGTGAACTTCCTGTACCTGGCCTCGCACTACGAGAAGCTGAAGGGCAGCCCGGAGGACAACGAACAGAAGCAGCTGTTCGTGGAGCAGCACAAGCACTACCTGGACGAGATCATCGAACAGATCAGCGAATTCAGCAAGCGCGTGATCCTGGCCGACGCCAACCTGGACAAGGTGCTGAGCGCCTACAACAAGCACCGCGACAAGCCGATCCGCGAGCAGGCCGAAAACATCATCCACCTGTTCACCCTGACCAACCTGGGCGCCCCGGCCGCCTTCAAGTACTTCGACACCACCATCGACCGCAAGCGCTACACCAGCACCAAGGAAGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAAACCCGCATCGACCTGAGCCAGCTGGGCGGCGACTCTGGTGGTTCTACTAATCTGTCAGATATTATTGAAAAGGAAACCGGTAAGCAACTGGTTATCCAGGAATCCATCCTCATGCTCCCAGAGGAGGTGGAAGAAGTCATTGGGAACAAGCCGGAAAGCGATATACTCGTGCACACCGCCTACGACGAGAGCACCGACGAGAATGTCATGCTTCTGACTAGCGACGCCCCTGAATACAAGCCTTGGGCTCTGGTCATACAGGATAGCAACGGTGAGAACAAGATTAAGATGCTCTCTGGTGGTTCTTGAACTAGTCTTGGACTCCTGTTGATAGATCCAGTAATGACCTCAGAACTCCATCTGGATTTGTTCAGAACGCTCGGTTGCCGCCGGGCGTTTTTTATTGGTGAGAATCCAGGGGTCCCCAATAATTACGATTTAAATTTGACATAAGCCTGTTCGGTTCGTAAACTGTAATGCAAGTAGCGTATGCGCTCACGCAACTGGTCCAGAACCTTGACCGAACGCAGCGGTGGTAACGGCGCAGTGGCGGTTTTCATGGCTTGTTATGACTGTTTTTTTGTACAGCCTATGCCTCGGGCATCCAAGCAGCAAGCGCGTTACGCCGTGGGTCGATGTTTGATGTTATGGAGCAGCAACGATGTTACGCAGCAGCAACGATGTTACGCAGCAGGGCAGTCGCCCTAAAACAAAGTTAGGTGGCTCAAGTATGGGCATCATTCGCACATGTAGGCTCGGCCCTGACCAAGTCAAATCCATGCGGGCTGCTCTTGATCTTTTCGGTCGTGAGTTCGGAGACGTAGCCACCTACTCCCAACATCAGCCGGACTCCGATTACCTCGGGAACTTGCTCCGTAGTAAGACATTCATCGCGCTTGCTGCCTTCGACCAAGAAGCGGTTGTTGGCGCTCTCGCGGCTTACGTTCTGCCCAAGTTTGAGCAGCCGCGTAGTGAGATCTATATCTATGATCTCGCAGTCTCCGGAGAGCACCGGAGGCAGGGCATTGCCACCGCGCTCATCAATCTCCTCAAGCATGAGGCCAACGCGCTTGGTGCTTATGTGATCTACGTGCAAGCAGATTACGGTGACGATCCCGCAGTGGCTCTCTATACAAAGTTGGGCATACGGGAAGAAGTGATGCACTTTGATATCGACCCAAGTACCGCCACCTAACAATTCGTTCAAGCCGAGATCGGCTTCCCGGCCGCGGAGTTGTTCGGTAAATTGGACAACGGTCCGCGCGTTGTCCTTTTCCGCTGCATAACCCTGCTTCGGGGTCATTATAGCGATTTTTTCGGTATATCCATCCTTTTTCGCACGATATACAGGATTTTGCCAAAGGGTTCGTGTAGACTTTCCTTGGTGTATCCAACGGCGTCAGCCGGGCAGGATAGGTGAAGTAGGCCCACCCGCGAGCGGGTGTTCCTTCTTCACTGTCCCTTATTCGCACCTGGCGGTGCTCAACGGGAATCCTGCTCTGCGAGGCTGGCCGTAGGCCGGCCGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGCATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCGTGAAAGGCAGGCCGGTCCGTGGTGGCCACGGCCTCTAGGCCAGATCCAGCGGCATCTGGGTTAGTCGAGCGCGGGCCGCTTCCCATGTCTCACCAGGGCGAGCCTGTTTCGCGATCTCAGCATCTGAAATCTTCCCGGCCTTGCGCTTCGCTGGGGCCTTACCCACCGCCTTGGCGGGCTTCTTCGGTCCAAAACTGAACAACAGATGTGTGACCTTGCGCCCGGTCTTTCGCTGCGCCCACTCCACCTGTAGCGGGCTGTGCTCGTTGATCTGCGTCACGGCTGGATCAAGCACTCGCAACTTGAAGTCCTTGATCGAGGGATACCGGCCTTCCAGTTGAAACCACTTTCGCAGCTGGTCAATTTCTATTTCGCGCTGGCCGATGCTGTCCCATTGCATGAGCAGCTCGTAAAGCCTGATCGCGTGGGTGCTGTCCATCTTGGCCACGTCAGCCAAGGCGTATTTGGTGAACTGTTTGGTGAGTTCCGTCAGGTACGGCAGCATGTCTTTGGTGAACCTGAGTTCTACACGGCCCTCACCCTCCCGGTAGATGATTGTTTGCACCCAGCCGGTAATCATCACACTCGGTCTTTTCCCCTTGCCATTGGGCTCTTGGGTTAACCGGACTTCCCGCCGTTTCAGGCGCAGGGCCGCTTCTTTGAGCTGGTTGTAGGAAGATTCGATAGGGACACCCGCCATCGTCGCTATGTCCTCCGCCGTCACTGAATACATCACTTCATCGGTGACAGGCTCGCTCCTCTTCACCTGGCTAATACAGGCCAGAACGATCCGCTGTTCCTGAACACTGAGGCGATACGCGGCCTCGACCAGGGCATTGCTTTTGTAAACCATTGGGGGTGAGGCCACGTTCGACATTCCTTGTGTATAAGGGGACACTGTATCTGCGTCCCACAATACAACAAATCCGTCCCTTTACAACAACAAATCCGTCCCTTCTTAACAACAAATCCGTCCCTTAATGGCAACAAATCCGTCCCTTTTTAAACTCTACAGGCCACGGATTACGTGGCCTGTAGACGTCCTAAAAGGTTTAAAAGGGAAAAGGAAGAAAAGGGTGGAAACGCAAAAAACGCACCACTACGTGGCCCCGTTGGGGCCGCATTTGTGCCCCTGAAGGGGCGGGGGAGGCGTCTGGGCAATCCCCGTTTTACCAGTCCCCTATCGCCGCCTGAGAGGGCGCAGGAAGCGAGTAATCAGGGTATCGAGGCGGATTCACCCTTGGCGTCCAACCAGCGGCACCAGCGGCGCCTGAGAGGGGCGCGCCCAGCTGTCTAGGGCGGCGGATTTGTCCTACTCAGGAGAGCGTTCACCGACAAACAACAGATAAAACGAAAGGCCCAGTCTTTCGACTGAGCCTTTCGTTTTATTTGATGCCT**

**DNA sequence of plasmid pSEVA6BE-S**

TTAATTAATGACACCATGAATTCTTGACAGCTAGCTCAGTCCTAGGTATAATGCTAGCTGCCAAACGATTGCAGGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTTGAGGAGCTCGGTCACCGTTACATATCAAAGGGAAAACTGTCCATACCCATGGGGCATGGCGAATTATGACAACTTGACGGCTACATCATTCACTTTTTCTTCACAACCGGCACGGAACTCGCTCGGGCTGGCCCCGGTGCATTTTTTAAATACCCGCGAGAAGTAGAGTTGATCGTCAAAACCAACATTGCGACCGACGGTGGCGATAGGCATCCGGGTGGTGCTCAAAAGCAGCTTCGCCTGGCTGATACGTTGGTCCTCGCGCCAGCTTAAGACGCTAATCCCTAACTGCTGGCGGAAAAGATGTGACAGACGCGACGGCGACAAGCAAACATGCTGTGCGACGCTGGCGATATCAAAATTGCTGTCTGCCAGGTGATCGCTGATGTACTGACAAGCCTCGCGTACCCGATTATCCATCGGTGGATGGAGCGACTCGTTAATCGCTTCCATGCGCCGCAGTAACAATTGCTCAAGCAGATTTATCGCCAGCAGCTCCGAATAGCGCCCTTCCCCTTGCCCGGCGTTAATGATTTGCCCAAACAGGTCGCTGAAATGCGGCTGGTGCGCTTCATCCGGGCGAAAGAACCCCGTATTGGCAAATATTGACGGCCAGTTAAGCCATTCATGCCAGTAGGCGCGCGGACGAAAGTAAACCCACTGGTGATACCATTCGCGAGCCTCCGGATGACGACCGTAGTGATGAATCTCTCCTGGCGGGAACAGCAAAATATCACCCGGTCGGCAAACAAATTCTCGTCCCTGATTTTTCACCACCCCCTGACCGCGAATGGTGAGATTGAGAATATAACCTTTCATTCCCAGCGGTCGGTCGATAAAAAAATCGAGATAACCGTTGGCCTCAATCGGCGTTAAACCCGCCACCAGATGGGCATTAAACGAGTATCCCGGCAGCAGGGGATCATTTTGCGCTTCAGCCATACTTTTCATACTCCCGCCATTCAGAGAAGAAACCAATTGTCCATATTGCATCAGACATTGCCGTCACTGCGTCTTTTACTGGCTCTTCTCGCTAACCAAACCGGTAACCCCGCTTATTAAAAGCATTCTGTAACAAAGCGGGACCAAAGCCATGACAAAAACGCGTAACAAAAGTGTCTATAATCACGGCAGAAAAGTCCACATTGATTATTTGCACGGCGTCACACTTTGCTATGCCATAGCATTTTTATCCATAAGATTAGCGGATCCTACCTGACGCTTTTTATCGCAACTCTCTACTGTTTCTCCATCTTAAGGGCGATAGGAGGAATATACCATGAGCAGCGAAACCGGCCCGGTGGCCGTGGACCCGACCCTGCGTCGCCGCATCGAGCCGCACGAGTTCGAAGTGTTCTTCGACCCGCGCGAGCTGCGCAAGGAAACCTGCCTGCTGTACGAAATCAACTGGGGCGGCCGCCACAGCATCTGGCGCCACACCAGCCAGAACACCAACAAGCACGTGGAGGTGAACTTCATCGAAAAGTTCACCACCGAGCGCTACTTCTGCCCGAACACCCGCTGCAGCATCACCTGGTTCCTGAGCTGGAGCCCGTGCGGCGAATGCAGCCGCGCCATCACCGAGTTCCTGAGCCGCTACCCGCACGTGACCCTGTTCATCTACATCGCCCGCCTGTACCACCACGCCGACCCGCGCAACCGCCAGGGCCTGCGCGACCTGATCAGCAGCGGCGTGACCATCCAGATCATGACCGAGCAGGAAAGCGGCTACTGCTGGCGCAACTTCGTGAACTACAGCCCGAGCAACGAAGCCCACTGGCCGCGCTACCCGCACCTGTGGGTGCGCCTGTACGTGCTGGAGCTGTACTGCATCATCCTGGGCCTGCCGCCGTGCCTGAACATCCTGCGTCGCAAGCAGCCGCAGCTGACCTTCTTCACCATCGCCCTGCAGAGCTGCCACTACCAGCGCCTGCCGCCGCACATCCTGTGGGCCACCGGCCTGAAGAGCGGCAGCGAGACTCCCGGGACCTCAGAGTCCGCCACACCCGAAAGTGACAAGAAGTACAGCATCGGCCTGGCTATCGGCACCAACAGCGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCGAGCAAGAAGTTCAAGGTGCTGGGCAACACCGACCGCCACAGCATCAAGAAGAACCTGATCGGCGCCCTGCTGTTCGACAGCGGCGAGACCGCCGAAGCCACCCGCCTGAAGCGCACCGCCCGCCGCCGCTACACCCGTCGCAAGAACCGCATCTGCTACCTGCAGGAGATCTTCAGCAACGAAATGGCCAAGGTGGACGACAGCTTCTTCCACCGCCTGGAGGAAAGCTTCCTGGTGGAGGAAGACAAGAAGCACGAGCGCCACCCGATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAAAAGTACCCGACCATCTACCACCTGCGCAAGAAGCTGGTCGACAGCACCGACAAGGCCGACCTGCGCCTGATCTACCTGGCCCTGGCCCACATGATCAAGTTCCGCGGCCACTTCCTGATCGAAGGCGACCTGAACCCGGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCGATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGAGCGCCCGCCTGAGCAAGAGCCGCCGCCTGGAGAACCTGATCGCCCAGCTGCCGGGCGAAAAGAAGAACGGCCTGTTCGGCAACCTGATCGCCCTGAGCCTGGGCCTGACCCCGAACTTCAAGAGCAACTTCGACCTGGCCGAGGACGCCAAGCTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTCCTGGCCGCCAAGAACCTGAGCGACGCCATCCTGCTGAGCGACATCCTGCGCGTGAACACCGAGATCACCAAGGCCCCGCTGAGCGCCAGCATGATCAAGCGCTACGACGAACACCACCAGGACCTGACCCTGCTGAAGGCCCTGGTGCGCCAGCAGCTGCCGGAGAAGTACAAGGAAATCTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATCGACGGTGGCGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCGATCCTGGAGAAGATGGACGGCACCGAGGAACTGCTGGTGAAGCTGAACCGCGAAGACCTGCTGCGCAAGCAGCGCACCTTCGACAACGGCAGCATCCCGCACCAGATCCACCTGGGCGAGCTGCACGCCATCCTGCGTCGCCAGGAAGACTTCTACCCGTTCCTGAAGGACAACCGCGAGAAGATCGAAAAGATCCTGACCTTCCGCATCCCGTACTACGTGGGCCCGCTGGCCCGCGGCAACAGCCGCTTCGCCTGGATGACCCGCAAGAGCGAGGAAACCATCACCCCGTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCCAGCGCCCAGAGCTTCATCGAGCGCATGACCAACTTCGACAAGAACCTGCCGAACGAAAAGGTGCTGCCGAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTACAACGAACTGACCAAGGTGAAGTACGTGACCGAGGGCATGCGCAAGCCGGCCTTCCTGAGCGGCGAACAGAAGAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGCAAGGTGACCGTGAAGCAGCTGAAGGAAGACTACTTCAAGAAGATCGAATGCTTCGACAGCGTGGAGATCAGCGGCGTGGAAGACCGCTTCAACGCCAGCCTGGGCACCTACCACGACCTGCTGAAGATCATCAAGGACAAGGACTTCCTGGACAACGAGGAAAACGAGGACATCCTGGAAGACATCGTGCTGACCCTGACCCTGTTCGAGGACCGCGAAATGATCGAGGAACGCCTGAAGACCTACGCCCACCTGTTCGACGACAAGGTGATGAAGCAGCTGAAGCGCCGCCGCTACACCGGCTGGGGCCGCCTGAGCCGCAAGCTGATCAACGGCATCCGCGACAAGCAGAGCGGCAAGACCATCCTGGACTTCCTGAAGAGCGACGGCTTCGCCAACCGCAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTCAAGGAAGACATCCAGAAGGCCCAAGTGAGCGGCCAGGGCGACAGCCTGCACGAACACATCGCCAACCTGGCCGGCAGCCCGGCCATCAAGAAGGGCATCCTGCAGACCGTGAAGGTGGTGGACGAGCTGGTGAAGGTGATGGGCCGCCACAAGCCGGAAAACATCGTGATCGAGATGGCCCGCGAAAACCAGACCACCCAGAAGGGCCAGAAGAACAGCCGCGAGCGCATGAAGCGCATCGAGGAAGGCATCAAGGAACTGGGCAGCCAGATCCTGAAGGAGCACCCGGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAACGGCCGCGACATGTACGTGGACCAGGAACTGGACATCAACCGCCTGAGCGACTACGACGTGGACCACATCGTGCCGCAGAGCTTCCTGGCCGACGACAGCATCGACAACAAGGTGCTGACCCGCAGCGACAAGAACCGCGGCAAGAGCGACAACGTGCCGAGCGAGGAAGTGGTGAAGAAGATGAAGAACTACTGGCGCCAGCTGCTGAACGCCAAGCTGATCACCCAGCGCAAGTTCGACAACCTGACCAAGGCCGAGCGCGGCGGCCTGAGCGAACTGGACAAGGCCGGCTTCATCAAGCGCCAGCTGGTCGAGACCCGCCAGATCACCAAGCACGTGGCCCAGATCCTGGACAGCCGCATGAACACCAAGTA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**DNA sequence of plasmid pSEVA6BE-PobA-TrpE**

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TTAATTAATGACACCATGAATTCTTGACAGCTAGCTCAGTCCTAGGTATAATGCTAGCAAAACTCAGGTTGCAATTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTTGAGGAGCTCGGTCACCGTTACATATCAAAGGGAAAACTGTCCATACCCATGGGGCATGGCGAATTATGACAACTTGACGGCTACATCATTCACTTTTTCTTCACAACCGGCACGGAACTCGCTCGGGCTGGCCCCGGTGCATTTTTTAAATACCCGCGAGAAGTAGAGTTGATCGTCAAAACCAACATTGCGACCGACGGTGGCGATAGGCATCCGGGTGGTGCTCAAAAGCAGCTTCGCCTGGCTGATACGTTGGTCCTCGCGCCAGCTTAAGACGCTAATCCCTAACTGCTGGCGGAAAAGATGTGACAGACGCGACGGCGACAAGCAAACATGCTGTGCGACGCTGGCGATATCAAAATTGCTGTCTGCCAGGTGATCGCTGATGTACTGACAAGCCTCGCGTACCCGATTATCCATCGGTGGATGGAGCGACTCGTTAATCGCTTCCATGCGCCGCAGTAACAATTGCTCAAGCAGATTTATCGCCAGCAGCTCCGAATAGCGCCCTTCCCCTTGCCCGGCGTTAATGATTTGCCCAAACAGGTCGCTGAAATGCGGCTGGTGCGCTTCATCCGGGCGAAAGAACCCCGTATTGGCAAATATTGACGGCCAGTTAAGCCATTCATGCCAGTAGGCGCGCGGACGAAAGTAAACCCACTGGTGATACCATTCGCGAGCCTCCGGATGACGACCGTAGTGATGAATCTCTCCTGGCGGGAACAGCAAAATATCACCCGGTCGGCAAACAAATTCTCGTCCCTGATTTTTCACCACCCCCTGACCGCGAATGGTGAGATTGAGAATATAACCTTTCATTCCCAGCGGTCGGTCGATAAAAAAATCGAGATAACCGTTGGCCTCAATCGGCGTTAAACCCGCCACCAGATGGGCATTAAACGAGTATCCCGGCAGCAGGGGATCATTTTGCGCTTCAGCCATACTTTTCATACTCCCGCCATTCAGAGAAGAAACCAATTGTCCATATTGCATCAGACATTGCCGTCACTGCGTCTTTTACTGGCTCTTCTCGCTAACCAAACCGGTAACCCCGCTTATTAAAAGCATTCTGTAACAAAGCGGGACCAAAGCCATGACAAAAACGCGTAACAAAAGTGTCTATAATCACGGCAGAAAAGTCCACATTGATTATTTGCACGGCGTCACACTTTGCTATGCCATAGCATTTTTATCCATAAGATTAGCGGATCCTACCTGACGCTTTTTATCGCAACTCTCTACTGTTTCTCCATCTTAAGGGCGATAGGAGGAATATACCATGAGCAGCGAAACCGGCCCGGTGGCCGTGGACCCGACCCTGCGTCGCCGCATCGAGCCGCACGAGTTCGAAGTGTTCTTCGACCCGCGCGAGCTGCGCAAGGAAACCTGCCTGCTGTACGAAATCAACTGGGGCGGCCGCCACAGCATCTGGCGCCACACCAGCCAGAACACCAACAAGCACGTGGAGGTGAACTTCATCGAAAAGTTCACCACCGAGCGCTACTTCTGCCCGAACACCCGCTGCAGCATCACCTGGTTCCTGAGCTGGAGCCCGTGCGGCGAATGCAGCCGCGCCATCACCGAGTTCCTGAGCCGCTACCCGCACGTGACCCTGTTCATCTACATCGCCCGCCTGTACCACCACGCCGACCCGCGCAACCGCCAGGGCCTGCGCGACCTGATCAGCAGCGGCGTGACCATCCAGATCATGACCGAGCAGGAAAGCGGCTACTGCTGGCGCAACTTCGTGAACTACAGCCCGAGCAACGAAGCCCACTGGCCGCGCTACCCGCACCTGTGGGTGCGCCTGTACGTGCTGGAGCTGTACTGCATCATCCTGGGCCTGCCGCCGTGCCTGAACATCCTGCGTCGCAAGCAGCCGCAGCTGACCTTCTTCACCATCGCCCTGCAGAGCTGCCACTACCAGCGCCTGCCGCCGCACATCCTGTGGGCCACCGGCCTGAAGAGCGGCAGCGAGACTCCCGGGACCTCAGAGTCCGCCACACCCGAAAGTGACAAGAAGTACAGCATCGGCCTGGCTATCGGCACCAACAGCGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCGAGCAAGAAGTTCAAGGTGCTGGGCAACACCGACCGCCACAGCATCAAGAAGAACCTGATCGGCGCCCTGCTGTTCGACAGCGGCGAGACCGCCGAAGCCACCCGCCTGAAGCGCACCGCCCGCCGCCGCTACACCCGTCGCAAGAACCGCATCTGCTACCTGCAGGAGATCTTCAGCAACGAAATGGCCAAGGTGGACGACAGCTTCTTCCACCGCCTGGAGGAAAGCTTCCTGGTGGAGGAAGACAAGAAGCACGAGCGCCACCCGATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAAAAGTACCCGACCATCTACCACCTGCGCAAGAAGCTGGTCGACAGCACCGACAAGGCCGACCTGCGCCTGATCTACCTGGCCCTGGCCCACATGATCAAGTTCCGCGGCCACTTCCTGATCGAAGGCGACCTGAACCCGGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCGATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGAGCGCCCGCCTGAGCAAGAGCCGCCGCCTGGAGAACCTGATCGCCCAGCTGCCGGGCGAAAAGAAGAACGGCCTGTTCGGCAACCTGATCGCCCTGAGCCTGGGCCTGACCCCGAACTTCAAGAGCAACTTCGACCTGGCCGAGGACGCCAAGCTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTCCTGGCCGCCAAGAACCTGAGCGACGCCATCCTGCTGAGCGACATCCTGCGCGTGAACACCGAGATCACCAAGGCCCCGCTGAGCGCCAGCATGATCAAGCGCTACGACGAACACCACCAGGACCTGACCCTGCTGAAGGCCCTGGTGCGCCAGCAGCTGCCGGAGAAGTACAAGGAAATCTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATCGACGGTGGCGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCGATCCTGGAGAAGATGGACGGCACCGAGGAACTGCTGGTGAAGCTGAACCGCGAAGACCTGCTGCGCAAGCAGCGCACCTTCGACAACGGCAGCATCCCGCACCAGATCCACCTGGGCGAGCTGCACGCCATCCTGCGTCGCCAGGAAGACTTCTACCCGTTCCTGAAGGACAACCGCGAGAAGATCGAAAAGATCCTGACCTTCCGCATCCCGTACTACGTGGGCCCGCTGGCCCGCGGCAACAGCCGCTTCGCCTGGATGACCCGCAAGAGCGAGGAAACCATCACCCCGTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCCAGCGCCCAGAGCTTCATCGAGCGCATGACCAACTTCGACAAGAACCTGCCGAACGAAAAGGTGCTGCCGAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTACAACGAACTGACCAAGGTGAAGTACGTGACCGAGGGCATGCGCAAGCCGGCCTTCCTGAGCGGCGAACAGAAGAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGCAAGGTGACCGTGAAGCAGCTGAAGGAAGACTACTTCAAGAAGATCGAATGCTTCGACAGCGTGGAGATCAGCGGCGTGGAAGACCGCTTCAACGCCAGCCTGGGCACCTACCACGACCTGCTGAAGATCATCAAGGACAAGGACTTCCTGGACAACGAGGAAAACGAGGACATCCTGGAAGACATCGTGCTGACCCTGACCCTGTTCGAGGACCGCGAAATGATCGAGGAACGCCTGAAGACCTACGCCCACCTGTTCGACGACAAGGTGATGAAGCAGCTGAAGCGCCGCCGCTACACCGGCTGGGGCCGCCTGAGCCGCAAGCTGATCAACGGCATCCGCGACAAGCAGAGCGGCAAGACCATCCTGGACTTCCTGAAGAGCGACGGCTTCGCCAACCGCAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTCAAGGAAGACATCCAGAAGGCCCAAGTGAGCGGCCAGGGCGACAGCCTGCACGAACACATCGCCAACCTGGCCGGCAGCCCGGCCATCAAGAAGGGCATCCTGCAGACCGTGAAGGTGGTGGACGAGCTGGTGAAGGTGATGGGCCGCCACAAGCCGGAAAACATCGTGATCGAGATGGCCCGCGAAAACCAGACCACCCAGAAGGGCCAGAAGAACAGCCGCGAGCGCATGAAGCGCATCGAGGAAGGCATCAAGGAACTGGGCAGCCAGATCCTGAAGGAGCACCCGGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAACGGCCGCGACATGTACGTGGACCAGGAACTGGACATCAACCGCCTGAGCGACTACGACGTGGACCACATCGTGCCGCAGAGCTTCCTGGCCGACGACAGCATCGACAACAAGGTGCTGACCCGCAGCGACAAGAACCGCGGCAAGAGCGACAACGTGCCGAGCGAGGAAGTGGTGAAGAAGATGAAGAACTACTGGCGCCAGCTGCTGAACGCCAAGCTGATCACCCAGCGCAAGTTCGACAACCTGACCAAGGCCGAGCGCGGCGGCCTGAGCGAACTGGACAAGGCCGGCTTCATCAAGCGCCAGCTGGTCGAGACCCGCCAGATCACCAAGCACGTGGCCCAGATCCTGGACAGCCGCATGAACACCAAGTA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**DNA sequence of UGI**

ATGTCTGGTGGTTCTACTAATCTGTCAGATATTATTGAAAAGGAAACCGGTAAGCAACTGGTTATCCAGGAATCCATCCTCATGCTCCCAGAGGAGGTGGAAGAAGTCATTGGGAACAAGCCGGAAAGCGATATACTCGTGCACACCGCCTACGACGAGAGCACCGACGAGAATGTCATGCTTCTGACTAGCGACGCCCCTGAATACAAGCCTTGGGCTCTGGTCATACAGGATAGCAACGGTGAGAACAAGATTAAGATGCTCTCTGGTGGTTCTTGA

**DNA sequence of XTEN linker**

GATAGCGGCGGCTCGAGCGGCGGCAGTAGCGGCAGCGAAACCCCGGGCACCTCGGAGTCGGCCACCCCGGAGAGCTCGGGTGGAAGCTCGGGTGGCTCC

**DNA sequence of SacB**

ATGAACATCAAAAAGTTTGCAAAACAAGCAACAGTATTAACCTTTACTACCGCACTGCTGGCAGGAGGCGCAACTCAAGCGTTTGCGAAAGAAACGAACCAAAAGCCATATAAGGAAACATACGGCATTTCCCATATTACACGCCATGATATGCTGCAAATCCCTGAACAGCAAAAAAATGAAAAATATCAAGTTCCTGAATTCGATTCGTCCACAATTAAAAATATCTCTTCTGCAAAAGGCCTGGACGTTTGGGACAGCTGGCCATTACAAAACGCTGACGGCACTGTCGCAAACTATCACGGCTACCACATCGTCTTTGCATTAGCCGGAGATCCTAAAAATGCGGATGACACATCGATTTACATGTTCTATCAAAAAGTCGGCGAAACTTCTATTGACAGCTGGAAAAACGCTGGCCGCGTCTTTAAAGACAGCGACAAATTCGATGCAAATGATTCTATCCTAAAAGACCAAACACAAGAATGGTCAGGTTCAGCCACATTTACATCTGACGGAAAAATCCGTTTATTCTACACTGATTTCTCCGGTAAACATTACGGCAAACAAACACTGACAACTGCACAAGTTAACGTATCAGCATCAGACAGCTCTTTGAACATCAACGGTGTAGAGGATTATAAATCAATCTTTGACGGTGACGGAAAAACGTATCAAAATGTACAGCAGTTCATCGATGAAGGCAACTACAGCTCAGGCGACAACCATACGCTGAGAGATCCTCACTACGTAGAAGATAAAGGCCACAAATACTTAGTATTTGAAGCAAACACTGGAACTGAAGATGGCTACCAAGGCGAAGAATCTTTATTTAACAAAGCATACTATGGCAAAAGCACATCATTCTTCCGTCAAGAAAGTCAAAAACTTCTGCAAAGCGATAAAAAACGCACGGCTGAGTTAGCAAACGGCGCTCTCGGTATGATTGAGCTAAACGATGATTACACACTGAAAAAAGTGATGAAACCGCTGATTGCATCTAACACAGTAACAGATGAAATTGAACGCGCGAACGTCTTTAAAATGAACGGCAAATGGTACCTGTTCACTGACTCCCGCGGATCAAAAATGACGATTGACGGCATTACGTCTAACGATATTTACATGCTTGGTTATGTTTCTAATTCTTTAACTGGCCCATACAAGCCGCTGAACAAAACTGGCCTTGTGTTAAAAATGGATCTTGATCCTAACGATGTAACCTTTACTTACTCACACTTCGCTGTACCTCAAGCGAAAGGAAACAATGTCGTGATTACAAGCTATATGACAAACAGAGGATTCTACGCAGACAAACAATCAACGTTTGCGCCAAGCTTCCTGCTGAACATCAAAGGCAAGAAAACATCTGTTGTCAAAGACAGCATCCTTGAACAAGGACAATTAACAGTTAACAAATAA

**DNA sequence of the pykA gene in *P.putida* KT2440**

ATGAGCATCCGCCGCACCAAAATCGTCGCCACCCTTGGCCCCGCCAGCAACTCGCCGGAAGTGATCGAACAACTGATCCTCGCCGGCCTGGACGTGGCACGTCTGAACTTCTCCCACGGCACGCCGGACGAGCACAAGGCCCGCGCGCGCCTGATCCGTGACATCGCCGCCAAGAATGGCCGCCATGTTGCACTGCTGGGCGACCTGCAGGGTCCGAAGATCCGCATCGCCAAGTTCGCCAACAAGCGCATCGAACTGAAGATCGGTGACAAGTTCACCTTCTCCACCGCCCACCCGCTGACCGAAGGCAACCAGGACATCGTCGGTATCGACTACCCCGACCTGGTCAAGGACTGCGGCGTTGGTGACGAACTGCTGCTCGACGATGGCCGCGTGGTCATGCGCGTCGAAACCGCCACTGCAGATGCCCTGCACTGCGTGGTGATCATCGGTGGCCCACTGTCGGACCACAAAGGCATCAACCGTAAAGGTGGCGGCCTGACCGCACCGGCCCTGACCGAAAAAGACAAGGCCGACATCAAACTGGCTGCGGAAATGGACCTGGACTACCTGGCCGTATCCTTCCCGCGTGACGCCAGCGATATGGAATACGCGCGCAAGCTGCGTGACGAAGCCGGCGGCAGCGCCTGGCTGGTAGCCAAGATCGAACGCGCCGAAGCGGTGGCCGATGACGAGACCCTCGACAAGCTGATCGCCGCCTCCGACGCTGTGATGGTTGCCCGTGGTGACCTGGGCGTGGAAATCGGCGACGCCGAGCTGATCGCTATCCAGAAGAAGATCATCCAGCACGCCCGCCGCAACAACAAGGCCGTGATCGTGGCGACCCAGATGATGGAGTCGATGATCCAGAACCCGATGCCGACCCGCGCGGAAGTGTCCGACGTGGCCAACGCCGTGCTGGACAACACCGATGCGGTGATGCTGTCGGCCGAAAGCGCCGCCGGTTCCTACCCGATCGAAGCTGTCCAGGCCATGGCACGCATCTGCCTGGGTGCCGAAAAGCACCCGACCAGCCAGAAGTCCAGCCATCGCCTGCACACCACCTTCCAGCGCTGCGACGAAAGCATCGCCTTGGCGGCCATGTACACTGCCAACCACTTCCCGGGCGTAAAGGCGATCATCGCCCTGACCGAAAGCGGCTACACCCCGCTGATCATGTCGCGCCTGCGTTCGCATGTACCGATCTTCGCCCTGTCGCCGCACCGCGCCACCCAGGCGCGCGCCTCGATGTTCCGTGGCGTGTACCCGATTGCCTTCGACCCGGCCGCGCTGCCGGCCGATAAGGTGAGCCAGGCGGCGGTCGACGAACTGCTCAAACGTGGCCTGGTGGAGCAAGGTGACTGGGTGATCCTGACCAAGGGTGACAGCTACCACACCATCGGTGGCACCAATGGCATGAAGATCCTGCACGTCGGTGATCCGCTGGTCGGTTGA