華中農業大學 作物遗传改良全国重点实验室
National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University
农业农村部农业基因组学重点实验室（武汉）

基因编辑
操作手册
ABE8e

华中农业大学作物遗传改良全国重点实验室
湖北洪山实验室
棉花遗传改良团队

二〇二五年六月·武汉

华中农业大学

基因编辑平台

GENOME EDITING PLATFORM

目录

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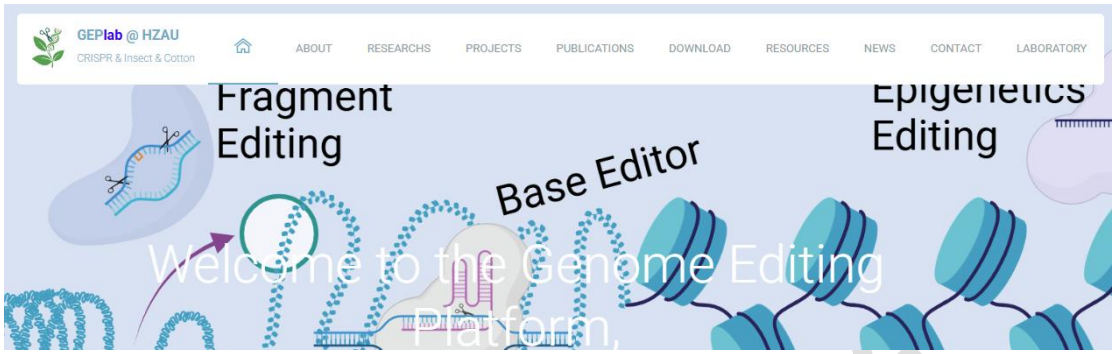
基因编辑平台：http://jinlab.hzau.edu.cn/GenomeEditingPlatform/

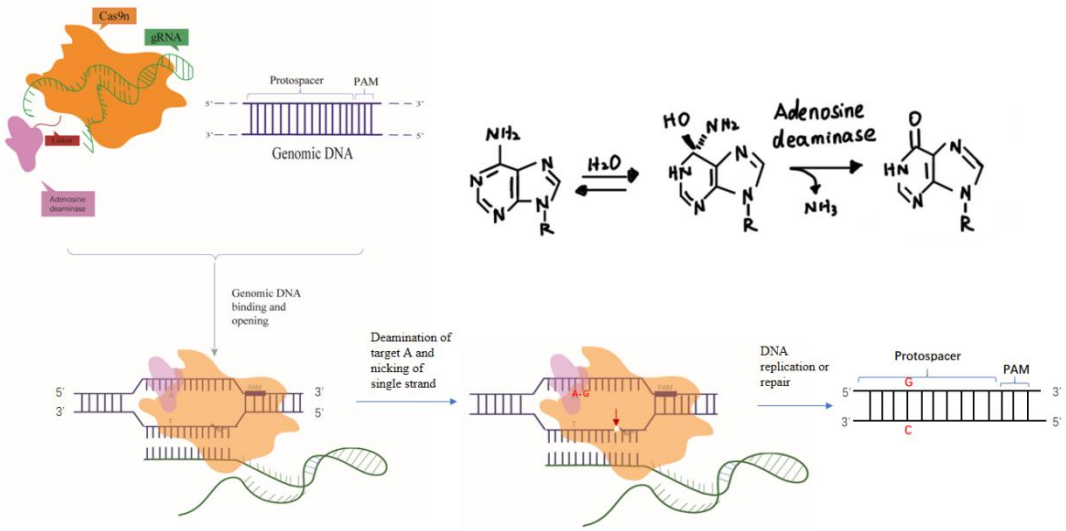


CRISPR/ABE8e protocol（中文版）

——以 CLA 为例

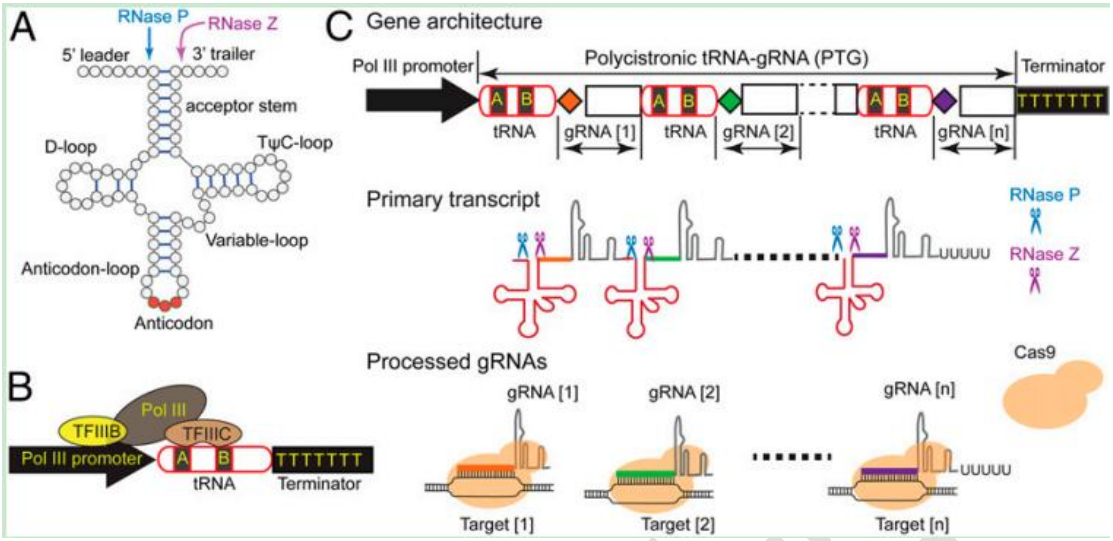
1.基本原理

ABE8e 是一种经过优化的腺嘌呤碱基编辑系统，能够在不造成 DNA 双链断裂（DSB）的情况下，将 DNA 中的 A•T 碱基对精准地转换为 G•C 碱基对。ABE8e 主要由以下三个功能模块组成：(1)TadA8e：将靶点 DNA 链上的腺嘌呤（A）脱氨，转化为次黄嘌呤（I），后者在复制时可被识别为鸟嘌呤（G）；(2)Cas9 nickase（D10A）：一个只在非编辑链上产生单链裂口的 Cas9 酶突变体，配合 sgRNA 实现靶向；(3)sgRNA：指导 Cas9 准确识别靶点序列，使脱氨酶作用于目标 A 碱基所在窗口。

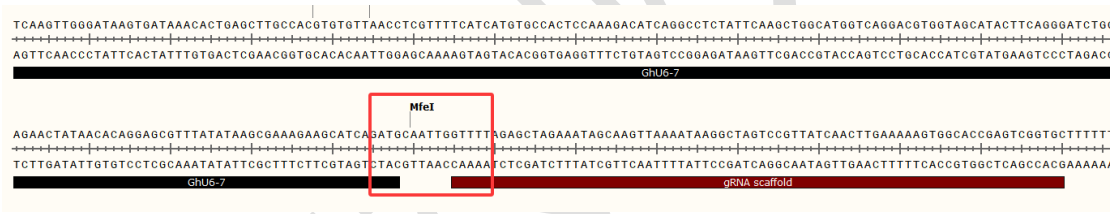


我们采用的载体可以串联多个 tRNA+靶标+gRNA（下图 C），从而提高突变效率，植物体自身的 RNase P 和 RNase Z 分别切割 tRNA 的 5’端和 3’端（如下图 A），可以将多个靶标（引导序列）的 gRNA 释放，与目标序列互补后，Cas9/gRNA

会在 PAM 前 3bp 左右的位置精确的切割靶 DNA 双链。



目前我们实验室 ABE8e 为卡纳抗性，以及引导 gRNA 转录的棉花内源 U6 启动子（编号为 U6-7），但驱动 Cas9 表达的依然是水稻 Ubiquitin2 启动子，原核中的抗性均为 kan。以下主要以 U6-7 启动子载体连接两个靶标位点，针对同一基因为例介绍载体构建过程。



ABE8e

2.设计靶标以及设计引物

CLA 序列及靶标：可以进行手动搜索， Blast 后，具有特异性的序列可以作为靶标。最好在 PAM 前 3bp 左右的位置有唯一的酶切位点，方便后续的验证。负链为 T-C 突变，正链为 A-G 突变。突变的碱基最好在远离 PAM 的第 4-8 的窗口内。

CTCGACGGACCTATACCACCTGTGGGAGCTTTGAGCAGTGCTCTCAGCAGGCTGCAAT
CAAACAGGCCTCTTAGAGAACTGAGAGAGGTTGCAAAGGTAAGTAGAAATGAATAGA
ACCCAGAAAACTAATATAATTTTTACTAGAAACTAAAACTTACTAAGACTGGATGTGGT
TTGATTGCAGGGAGTTACCAAGCAAATCGGTGGGCCTATGCATGAACTGGCTG

CAAAAGTTGATGAGTATGCTCGTGGAATGATCAGTGGTTCTGGATCTACACTTTTCGAA
GAACTTGGACTATATTATATTGGACCTGTTGATGGCCACAACATCGATGATTTAGTTTCT
ATTCTCAAAGAGGTTAAGACTACTAAAACAACGGGTCCGGTCTTGATCCATGTTGTCAC
TGAGAAAGGCCGAGGTTATCCATATGCAGAGAGAGCTGCTGACAAGTATCACGGTAAC

ATACAGAATAAGCCTTTTTAGAAGAGAGATCATTTCATATGATTTAATTTACTGGTGCCT
CGATATCTGACCTTAGTTTAGGGAATAAAAGAATAAACTGTACCTGGATTTCTTTTCTCA
GGAGTG**GTGAAGTTCGATCCGGCAACTGG**AAAGCAATTCAAAGGCAA

TTCTGCTACCCAGTCTTACACTACATATTTTGCTGAGGCTTTGATTGCGGAAGCTGAGG
CAGACAAAAATATTGTTGCCATCCATGCTGCAATGGGAGGTGGAACCGGATTAAACCT
CTTCCTCCGCCGGTTCCCACAAAGATGTTTCGATGTGGGGATAGCTGAACAACATGCTG
TCACCTTTGCTGCAGGCTTGGCCTGTGAAGGCTTGAAACCTTTTTGTGCAATCTACTCA
TCATTCATGCAAAGGGCTTATGACCAG

插入目标序列连接在载体图方框所示 MfeI 酶切位点之间，最终连接方法为一步克隆法。

*aagcatcagatgggca**AACAAA***GCACCAGTGGTCTAGTGGTAGAATAGTACCCTGC
CACGGTACAGACCCGGGTTCGATTCCCGGCTGGTGCA*CATAGGCCCACCGA*
*TTTGCT***GTTTTAGAGCTAGAAATA**GCAAGTTAAAATAAGGCTAGTCCGTTA
TCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACAAAGCACCAGTGGT
CTAGTGGTAGAATAGTACCCTGCCACGGTACAGACCCGGGTTCGATTCCCG
GCTGGTGCA*GTGAAGTTCGATCCGGCAAC**gttttagagctagaa**……（载体 gRNA）*

注：小写部分是载体序列；下划线部分是 tRNA;加粗部分是 gRNA；斜体部分是靶标位置。

需要用到的引物：

CLA1 as: 5’ AGCAAATCGGTGGGCCTATGtgcaccagccgggaat3’（靶标 1 互补序列）
CLA 2 s:5’ CATAGGCCCACCGATTTGCTgttttagagctagaaata 3’（靶标 1 序列）
CLA 2 as: 5’ GTTGCCGGATCGAACTTCACtgcaccagccgggaat3’（靶标 2 互补序列）
inf CLA as: 5’ ttctagctctaaaacGTTGCCGGATCGAACTTCAC3’（靶标 2 互补序列）
pRGEB32-7 s: 5’ AAGCATCAGATGGGCAAACAAAGCACCAGTGGTCTAG3’
inf pRGEB32-7 s: 5’ AAGCATCAGATGGGCAAACAAA 3’

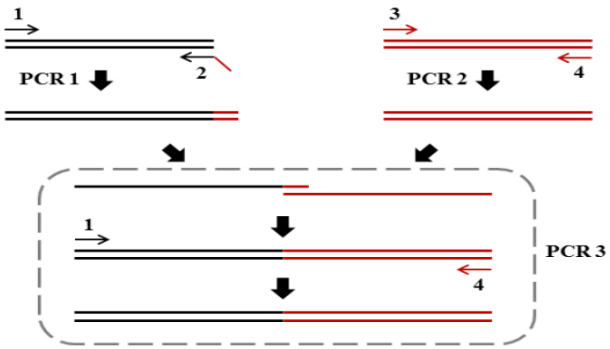
小写部分是固定序列，引物设计只需修改引物中的下划线标示的靶标序列即可。

其中，**inf pRGEB32-7 s、pRGEB32-7 s、u6-7 s** 为通用引物无须更改。pRGEB32-7 s 含有载体一部分序列，方便 In-fusion 连接。因插入序列中有多个 tRNA，inf pRGEB32-7 s 为增强扩增特异性，序列长度比 pRGEB32-7 s 短。Inf CLA as 含有载体序列接头，方便后续 In-fusion 连接。

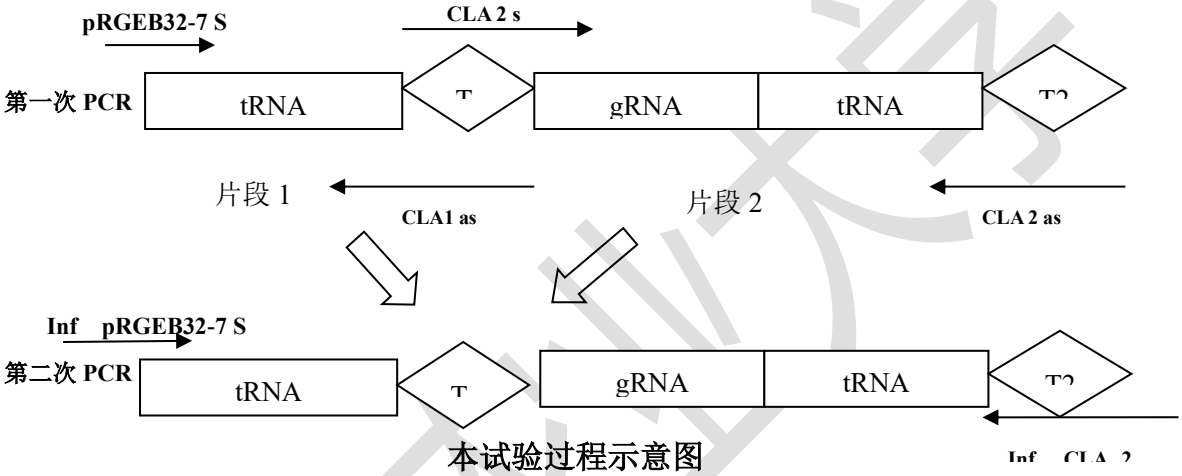
3. 第一次 PCR 扩增

重叠延伸 PCR：

PCR 循环中，扩增产生的新链是引物和延伸产物共同组成的，而且新链可以作为下一循环的模版。如果在引物的 5‘端加入接头，下一轮循环过后产生的链便会带有接头互补的序列。如此循环，最后的产物中，几乎所有的产物都含有接头序列。如果将接头序列设计得和待融合片段的引物互补，那么两个独立 PCR 的产物便可以借助这一区域产生配对，经 Taq 酶延伸成为融合片段。



重叠延伸示意图



本试验过程示意图

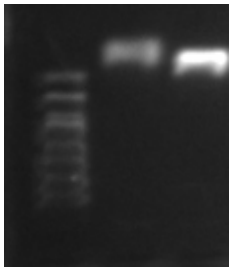
gRNA+tRNA 组合序列可自行合成序列连接到公共载体（如用 T 载体），第一次 PCR:1、2 两个片段分别从含 gRNA+tRNA 载体的菌液或者质粒中扩增。（相关序列可见附件）

20μl 体系：

	1	2
ddH_2O	**16.1**	**16.1**
Buffer	**2**	**2**
dNTP	**0.3**	**0.3**
S primer	**pRGEB32-7 s 0.2**	**CLA 2 s 0.2**
AS primer	**CLA1 as 0.2**	**CLA 2 as 0.2**
Taq	**0.2**	**0.2**
模板	**1**	**1**

PCR 条件：

预变性：95℃ 4min
变性：95℃ 30S
退火：55℃ 30S
延伸：72℃ 20S
循环：3C
变性：95℃ 30S
退火：60℃ 30S
延伸：72℃ 20S
循环：27C
最后延伸 72℃ 5min
电泳检测



5K 1

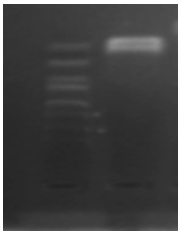
4.第二次 PCR 及纯化:

使用重叠延伸 PCR 将两个小片段进行连接，

		100μl 体系
ddH_2O		**83.5μl**
Buffer		**10μl**
dNTP		**1.5μl**
S primer	**Inf pRGEB32-7 s**	**1μl**
AS primer	**Inf CLA as**	**1μl**
Taq		**1μl**
片段 1		**1μl**
片段 2		**1μl**

PCR 条件：

预变性：95℃ 4min
变性：95℃ 30S
退火：59℃ 30S
延伸：72℃ 20S
循环：28C
最后延伸 72℃ 5min
电泳检测



5k 拼接

使用凝胶回收的试剂盒对 PCR 产物进行纯化、测浓度

5.载体 酶切：

	100μl 体系：
ABE8e	10μg
10X cut smart Buffer	10μl
MfeI	4μl
ddH_2O	up to 100μl

37℃ 酶切 5.5h

可**与第四步同时做**，电泳检测酶切效果、使用凝胶回收的试剂盒对酶切产物进行纯化、测浓度。

6.In-fusion 连接:

目的片段	100ng
线性化表达载体	100ng
Exnase	0.5μl
CE Buffer	1μl

37℃水浴 30min，冰上放置 5min，可-20℃保存备用

7.转化感受态

连接产物与感受态混合，冰上放置 30min，42℃热激 90S，冰上静置 5min。取 300μlSOC 加入新的 2ml 离心管，将热激产物加入 SOC 中，37℃震荡 45min，涂于 KAN 皿，37℃培养过夜，挑单克隆于 500μl kan 抗性液体 LB,37℃震荡 3h,使用 Inf pRGEB32-7 s Inf CLA as 引物阳性检测，电泳跑胶，挑阳性送测序（**GC rich**）.

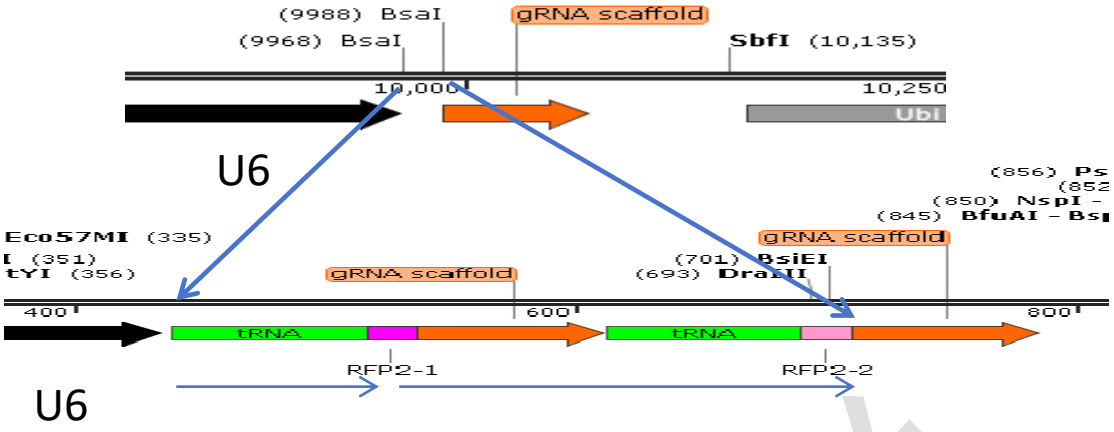
阳性检测引物/测序引物

u6-7 s: TGTGCCACTCCAAAGACATCAG + Inf XX AS

阳性检测电泳图：

5K 阴 阳

构建成功载体图：



8. 电转

测序成功后，电转农杆菌
阳性检测引物
u6-7 s: TGTGCCACTCCAAAGACATCAG + Inf XX AS

9.效果验证

（1）提取愈伤/单株 DNA，PCR 扩增含有靶标位置的一段序列，TA 克隆测序或 barcode 高通量测序。

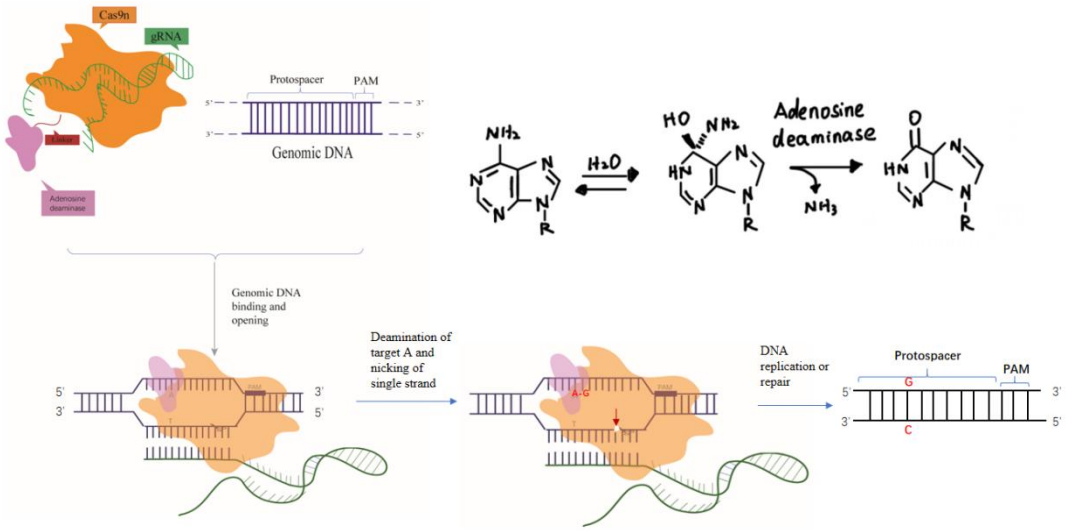
华中农业大学

CRISPR/ABE8e protocol（英文版）

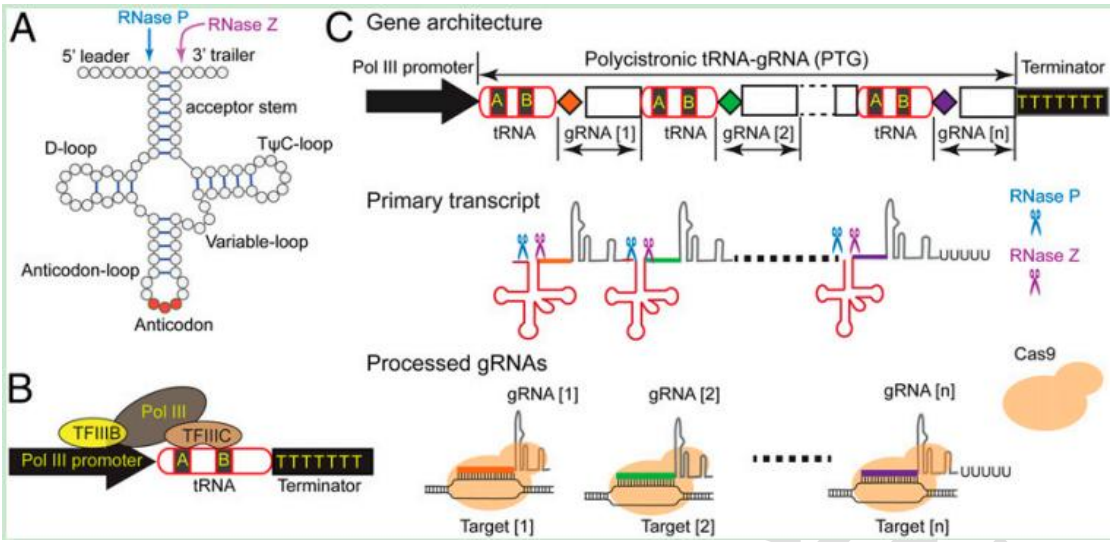
——Using CLA as an Example

1. Basic Principles

ABE8e is an optimized adenine base editing system that enables the precise conversion of A•T base pairs to G•C base pairs without inducing double-strand breaks (DSBs) in DNA. ABE8e mainly consists of the following three functional modules: **(1)** TadA8e: An evolved adenine deaminase that deaminates adenine (A) on the target DNA strand, converting it into inosine (I), which is interpreted as guanine (G) during DNA replication. **(2)** Cas9 nickase (D10A): A mutated version of Cas9 that introduces a single-strand nick on the non-edited DNA strand, working in conjunction with sgRNA to ensure site-specific targeting. **(3)** sgRNA: A single-guide RNA that directs Cas9 to the target DNA sequence, enabling the deaminase to act on the desired adenine base within a defined editing window.



Our vector system allows tandem integration of multiple **tRNA** + **target** + **gRNA** units (Fig. C), enhancing mutation efficiency. Plant endonucleases RNase P and RNase Z cleave the 5' and 3' ends of tRNA (Fig. A), releasing gRNAs that guide Cas9/gRNA to cleave the target DNA at the specified site.



In our lab, we modified the ABE8e vector by replacing the kanamycin resistance marker with hygromycin and incorporating the cotton endogenous U6 promoters (U6-7) for gRNA transcription. The protocol below focuses on constructing a vector with two target sites under the U6-7 promoter using rice Ubiquitin2 as the Cas9 promtor.

2. Target Search and Primer Design

CLA Sequence and Targets: Use the CRISPR-P website (http://cbi.hzau.edu.cn/crispr/) to search for targets (limited to *Gossypium raimondii* data). Alternatively, manually BLAST sequences for specificity. Prefer targets with unique restriction sites near the PAM (3 bp upstream) for downstream validation. T-to-C mutation on the negative strand corresponds to an A-to-G mutation on the positive strand. The target base is ideally located within positions 4 to 8 distal from the PAM site.

CTCGACGGACCTATACCACCTGTGGGAGCTTTGAGCAGTGCTCTCAGCAGGCTGCAAT
CAAACAGGCCTCTTAGAGAACTGAGAGAGGTTGCAAAGGTAAGTAGAAATGAATAGA
ACCCAGAAAACTAATATAATTTTTACTAGAAACTAAAACTTACTAAGACTGGATGTGGT
TTGATTGCAGGGAGTTACCA**AGCAAATCGGTGGGCCTATG**CATGAACTGGCTG

CAAAAGTTGATGAGTATGCTCGTGGAATGATCAGTGGTTCTGGATCTACACTTTTCGAA

GAACTTGGACTATATTATATTGGACCTGTTGATGGCCACAACATCGATGATTTAGTTTCT
ATTCTCAAAGAGGTTAAGACTACTAAAACAACGGGTCCGGTCTTGATCCATGTTGTCAC
TGAGAAAGGCCGAGGTTATCCATATGCAGAGAGAGCTGCTGACAAGTATCACGGTAAC
ATACAGAATAAGCCTTTTTAGAAGAGAGATCATTTCATATGATTTAATTTACTGGTGCCT
CGATATCTGACCTTAGTTTAGGGAATAAAAGAATAAACTGTACCTGGATTTCTTTTCTCA
GGAGTG**GTGAAGTTCGATCCGGCAACTGG**AAAGCAATTCAAAGGCAA

TTCTGCTACCCAGTCTTACACTACATATTTTGCTGAGGCTTTGATTGCGGAAGCTGAGG
CAGACAAAAATATTGTTGCCATCCATGCTGCAATGGGAGGTGGAACCGGATTAAACCT
CTTCCTCCGCCGGTTCCCACAAAGATGTTTCGATGTGGGGATAGCTGAACAACATGCTG
TCACCTTTGCTGCAGGCTTGGCCTGTGAAGGCTTGAAACCTTTTTGTGCAATCTACTCA
TCATTCATGCAAAGGGCTTATGACCAG

Insert the target sequence and ligate between the MfeI digestion sites shown in the box of the vector diagram. The final ligation method is the one-step cloning method.

*aagcatcagatgggca**AACAAA***GCACCAGTGGTCTAGTGGTAGAATAGTACCCTGC
CACGGTACAGACCCGGGTTCGATTCCCGGCTGGTGCA*CATAGGCCCACCGA*
*TTTGCT***GTTTTAGAGCTAGAAATA**GCAAGTTAAAATAAGGCTAGTCCGTTA
TCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACAAAGCACCAGTGGT
CTAGTGGTAGAATAGTACCCTGCCACGGTACAGACCCGGGTTCGATTCCCG
GCTGGTGCA*GTGAAGTTCGATCCGGCAAC**gttttagagctagaa**……（载体 gRNA）*

notes：Note: Lowercase = vector backbone; underscores = tRNA; bold = gRNA; italics = target site.

Primers:：

CLA1 as: 5’ AGCAAATCGGTGGGCCTATGtgcaccagccgggaat3’（靶标 1 互补序列）
CLA 2 s:5’ CATAGGCCCACCGATTTGCTgttttagagctagaaata 3’（靶标 1 序列）
CLA 2 as: 5’ GTTGCCGGATCGAACTTCACtgcaccagccgggaat3’（靶标 2 互补序列）
inf CLA as: 5’ ttctagctctaaaacGTTGCCGGATCGAACTTCAC3’（靶标 2 互补序列）
pRGEB32-7 s: 5’ AAGCATCAGATGGGCAAACAAAGCACCAGTGGTCTAG3’
inf pRGEB32-7 s: 5’ AAGCATCAGATGGGCAAACAAA 3’

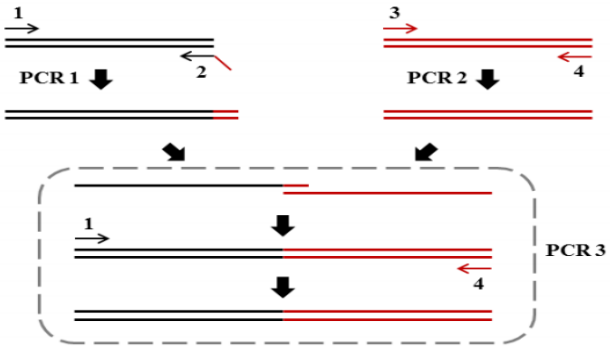
The lowercase part is a fixed sequence. Primer design only requires modifying the target sequence indicated by the underline in the primer.

Among them, inf pRGEB32-7 s, pRGEB32-7 s, u6-7 s are universal primers and do not need to be changed. pRGEB32-7s contain a part of the vector sequence, facilitating In-fusion ligation. Because there are multiple trnas in the inserted sequence, inf pRGEB32-7 s, in order to enhance amplification specificity, have shorter sequence lengths than pRGEB32-7 s. Inf CLA as contains carrier sequence connectors for convenient subsequent In-fusion connections.

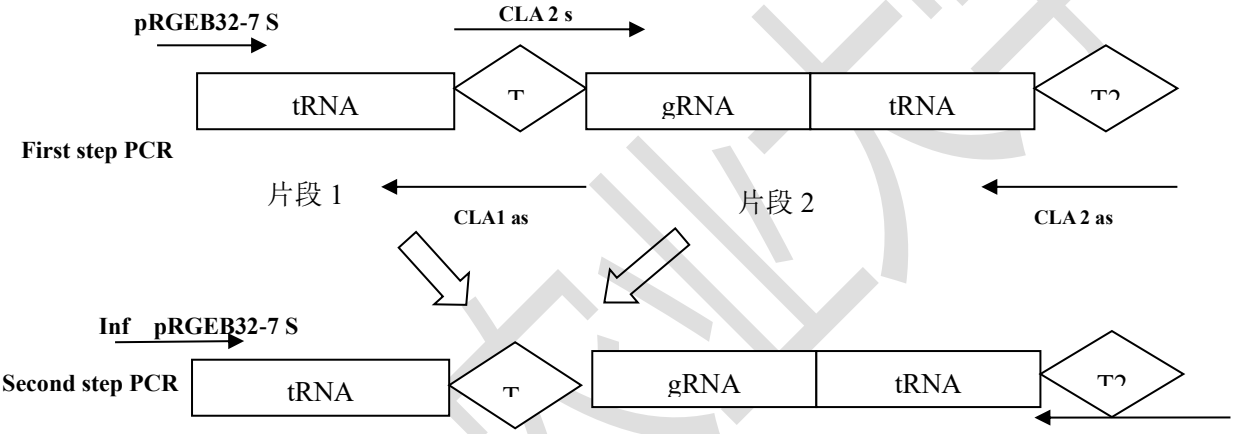
3. First PCR Amplification

Overlap Extension PCR:

This method generates fusion fragments by designing primers with complementary overhangs. Two overlapping PCR products are combined and extended to form a single construct.



Overlapping extension schematic diagram



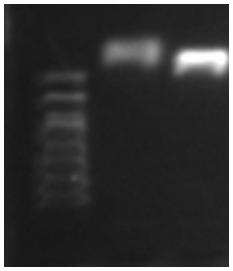
This is a schematic diagram of the test process

The gRNA+tRNA combination sequence can be synthesized by itself and ligated to a common vector (such as using the T vector). In the first PCR: Fragments 1 and 2 were amplified respectively from the bacterial liquid or plasmid containing the gRNA+tRNA vector. (The relevant sequence can be found in the attachment.)

Reaction Mixture (20 μL):

	1	2
ddH_2O	**16.1**	**16.1**
Buffer	**2**	**2**
dNTP	**0.3**	**0.3**
S primer	**pRGEB32-7 s 0.2**	**CLA 2 s 0.2**
AS primer	**CLA1 as 0.2**	**CLA 2 as 0.2**
Taq	**0.2**	**0.2**
Template DNA	**1**	**1**

PCR Conditions:



1. Initial denaturation: 95° C for 4 min
2. Denaturation: 95° C for 30 s
3. Annealing: 55° C for 30 s
4. Extension: 72° C for 20 s
    - Repeat steps 2 – 4 for 3 cycles
5. Denaturation: 95° C for 30 s
6. Annealing: 60° C for 30 s
7. Extension: 72° C for 20 s
    - Repeat steps 5 – 7 for 27 cycles
8. Final extension: 72° C for 5 min

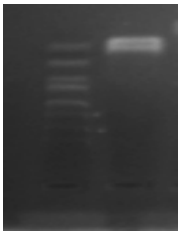
Electrophoresis: Verify amplification.

4. Second PCR and Purification

Combine the two PCR products from Step 3 using overlap extension，

		Reaction Mixture (100 μL)
ddH_2O		**83.5μl**
Buffer		**10μl**
dNTP		**1.5μl**
S primer	**Inf pRGEB32-7 s**	**1μl**
AS primer	**Inf CLA as**	**1μl**
Taq		**1μl**
Fragment 1		**1μl**
Fragment 2		**1μl**

PCR Conditions:



1. Initial denaturation: 95° C for 4 min
2. Denaturation: 95° C for 30 s

3. Annealing: 59° C for 30 s
4. Extension: 72° C for 20 s
    - Repeat steps 2 – 4 for 28 cycles
5. Final extension: 72° C for 5 min

Purification: Use a gel extraction kit to purify the product and measure concentration.

5. Vector Digestion

Digest the vector with BsaI.

Reaction Mixture (100 µL):

	Volume (µL):
ABE8e	10 µg
CutSmart Buffer	10 µL
MfeI	1 µL
ddH_2O	Up to 100 µL

Digestion: 37°C for 5.5 h.

6. In-Fusion Cloning

Assemble the digested vector and insert using In-Fusion technology.

Components:

- **Insert (100 ng)**
- **Linearized vector (100 ng)**
- **Exnase (0.5 µL)**
- **CE Buffer (1 µL)**

Incubation: 37°C for 30 min, then ice for 5 min. Store at -20°C.

7. Transformation
Transform competent cells with the ligation product.

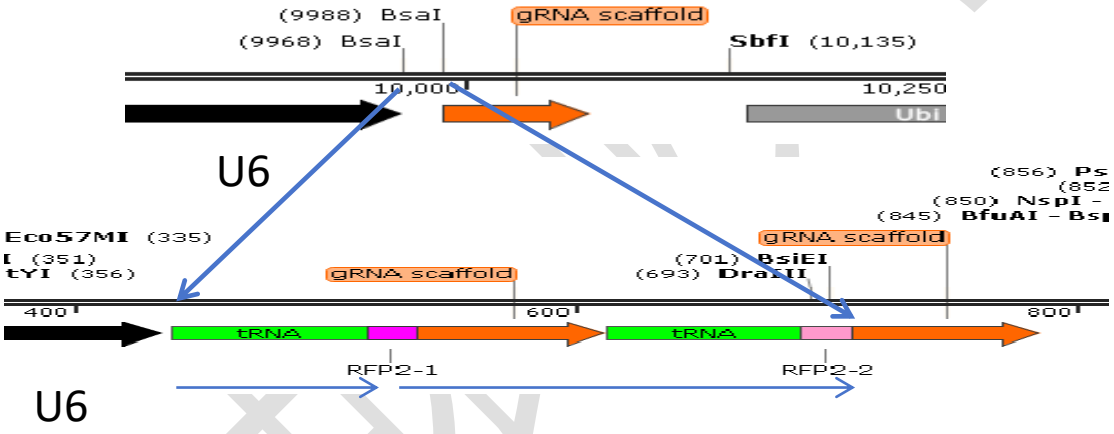
Steps:

Mix with SOC medium and incubate at 37°C for 45 min.
Plate on kanamycin agar plates and incubate overnight.
Pick colonies for PCR validation using primers:
u6-7s: TGTGCCACTCCAAAGACATCAG + Inf XX AS

Positive clones are sequenced (GC-rich regions).
Electrophoresis: Confirm positive clones.

Positive detection electrophoresis pattern：

Construct a successful carrier diagram：



8. Agrobacterium Electroporation
Electroporate the verified construct into *Agrobacterium*.

u6-7 s: TGTGCCACTCCAAAGACATCAG + Inf XX AS

9. Validation

Genomic DNA Extraction: PCR amplify the target region, clone, and sequence.