1	Supplementary Information for
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3	CRISPR-Cas9 toolkit for genome editing in an autotrophic CO2 fixing
4	methanogenic archaeon
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11	
12	This file contains:
13	Supplementary Figures S1-S5.
14	Supplementary Tables S1-S5.

### 15 Supplementary Figures



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Figure S1. The Cas9 expression in *M. maripaludis*. The optimized SpCas9 was constructed in pMEV4 plasmid and transferred into *M. maripaludis* strain S0001 and its expression was verified by western blot using the commercial antibody of SpCas9. Arrow indicated the protein band of the soluble SpCas9. Lanes 1 to 4 display protein samples from four selected transformants after puromycin selection.



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25 Figure S2. The numbers of puromycin resistant transformants obtained by separately

transferring 1 µg plasmid DNA of pMEV401, 402, and 403 into *M. maripaludis*.



Figure S3. Synchronous deletion of multiple (13) genes located at three different 28 genomic loci using the Cas9-editing system explored in *M. maripaludis* by one-step 29 transformation. (A) The design of simultaneous deletion of the multiple genes 30 including two  $\beta$ -CASP ribonucleases encoding genes, aCPSF2 (MMP0431) and 31 aCPSF1b (MMP1381), and the whole *fla* operon genes of MMP1666 to MMP1676. 32 The pMEV406 plasmid encodes four sgRNAs that respectively match aCPSF2 33 (MMP0431), aCPSF1b (MMP1381), flaB1 (MMP1666) and flaJ (MMP1676), which 34 were expressed by indicated promoters derived from highly expressed genes in M. 35 maripaludis. The sequences upstream (U2, U3, and U4) and downstream (D2, D3, and 36

37	D4) of each target gene were concatenated on pMEV406 to provide the recombinant
38	donor. Distinctly, the Cas9 expressed in pMEV406 plasmid was derived by a promoter
39	of PhmvA, a constitute promoter commonly used in M. maripaludis. (B) Ten puromycin
40	resistance transformants were randomly selected for PCR analysis with primers F2/R2,
41	F2'/R2', F3/R3 F3'/R3', F4/R4, and F4'/R4' to detect the knock out of the <i>aCPSF2</i> and
42	aCPSF1b genes, and the <i>fla</i> operon genes, respectively. Black and red arrows indicate
43	the PCR products amplified from the wild-type (CK) and the mutated genomes,
44	respectively. M, dsDNA size marker.



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Figure S4. Comparison of SpCas9 expression in pMEV406 and pMEV407. Using the commercial antibody of SpCas9, Western blot assayed improved expression of SpCas9 under a stronger promoter P0386 in pMEV407 compared with that under PhmvA in pMEV406. Arrow indicats the soluble SpCas9 protein. By reference to the band intensity (100%) of SpCas9 expressed in pMEV401, the protein percentages expressed in strain S0001 carrying pMEV406 and pMEV407 were calculated.



Figure S5. Curing of the Cas9-based pMEV4 plasmid using the hpt counterselection 53 marker. (A) Growth curves of three puromucin-resistant (Pur<sup>R</sup>) transformants and three 54 8-aza resistant transformants derived from the Pur<sup>R</sup> parent after curing the plasmid were 55 compared in liquid medium with 2.5 µg/ml puromycin. (B) Primers to amplify the hpt 56 gene in the pMEV4 plasmid were used to screen for the completeness of the curing for 57 the Cas9-based pMEV4 plasmid in each of the three Pur<sup>R</sup> parents (lanes Pur resistant) 58 and 8-azahypoxanthine resistant transformants (lanes 8-aza resistant). Plasmid pMEV4 59 and the parental strain S0001 were used as positive and negative controls, respectively 60 (lanes pMEV401 and S0001). 61

# 62 Supplementary Tables

# 63 Table S1. Strains and plasmids used in this study

Strains and plasmids	Characteristics and descriptions	Reference or sources
Strains		
E. coli DH5α	$F^{-}\phi 80d \ lacZ\Delta M15 \ \Delta(lacZYA-arg \ F) \ U169 \ endA1 \ recA1 \ hsdR17(r_{k}^{-},m_{k}^{+}) \ supE44\lambda- \ thi \ -1 \ gyrA96 \ relA1 \ phoA$	TransGen , Beijing
M. maripaludis S0001	S2 Δhpt + ORF1 of pAW42	(1)
Mmp-ΔMMP1197	S0001 with Mmp1197 deletion	This study
$Mmp-\Delta a CPSF1b/a CPSF2$	S0001 with <i>aCPSF1b</i> and <i>aCPSF2</i> deletion	This study
Mmp-Afla	S0001 with <i>fla</i> operon deletion	This study
Mmp-∆aCPSF1b/aCPSF2/∆fla	S0001 with aCPSF1b, aCPSF2 and fla operon deletion	This study
Mmp-mCherry	S0001 with mCherry inserted into the intergenic region of <i>MMP0852/MMP0853</i> ( <i>MMP0852</i> :: Pmcr-sat-Tmcr; <i>MMP0853</i> :: P0386-mCherry-T <sub>mmp1149</sub> )	This study
Mmp-aCPSF1-H2F	S0001 with MMP0694 3'-end His6 and 3Flag tags	This study
Mmp-muaCPSF1-H2F	S0001 with MMP0694 3'-end His <sub>6</sub> and 3Flag tags	This study
Mmp- RpoL-H2F	S0001 with MMP0261 3'-end His6 and 3Flag tags	This study
Mmp- P0386(-3)-mCherry	Mmp-mCherry with -2 point mutagenesis of P0386	This study
Mmp- P0386(-2)-mCherry	Mmp-mCherry with -2 point mutagenesis of P0386	This study
<i>Mmp- P0386(-2、-3)-mCherry</i>	Mmp-mCherry with -2 and -3 point mutagenesis of P0386	This study
Mmp- P0386(1)-mCherry	Mmp-mCherry with 1 point mutagenesis of P0386	This study
Mmp- P0386(3)-mCherry	Mmp-mCherry with 3 point mutagenesis of P0386	This study
Mmp- sg5(-2m)-mCherry	Mmp-mCherry with -2 point mutagenesis of sg5	This study
Mmp- sg8(1m)-mCherry	Mmp-mCherry with 1 point mutagenesis of sg8	This study
Mmp-T0290-mutant	S0001 with multiple mutagenesis of terminator of <i>MMP0290</i> (T1149)	This study
<b>Plasmids</b> pMD19-T	Amp <sup>R</sup>	Takara , Japan
pMD19-T-ORF-1197	pMD19-T with Mmp-1197 donor and its open reading frame (ORF)	This study
pMD19-T-Donor-1197	pMD19-T with Mmp-1197 donor	This study
pMD19-T-ORF-aCPSF1b	pMD19-T with aCPSF1b donor and its open reading frame (ORF)	This study
pMD19-T-Donor-aCPSF1b	pMD19-T with aCPSF1b donor	This study
pMD19-T-ORF-aCPSF2	pMD19-T with aCPSF2 donor and its open reading frame	This study
pMD19-T-Donor-aCPSF2	(ORF) pMD19-T with aCPSF2 donor	This study
pMEV4	<i>E.</i> coli/ <i>M.</i> maripaludis shuttle vector, only replicates in <i>M.</i>	This study
pMEV4-Cas9 (pMEV401)	pMEV4 containing the Cas9 ORF. Amp <sup>R</sup> , Pur <sup>R</sup>	This study
pMEV4-sgRNA-Cas9 (pMEV402)	pMEV4 containing the Cas9 ORF and a guide sequence 5'- TGATTTATTTGATACAACAG targeting to <i>Mmp1197</i> , Amp <sup>R</sup> , Pur <sup>R</sup>	This study

pMEV4-Cas9-△ <i>Mmp1197</i> (pMEV403)	pMEV4 containing donor, Cas9 ORF and a guide sequence 5'-	This study
	TGATTTATTTGATACAACAG targeting to Mmp1197,	
	Amp <sup>R,</sup> Pur <sup>R</sup>	
pMEV4-Cas9-△ <i>aCPSF1b/aCPSF2</i>	pMEV4 containing donor, Cas9 ORF and guide sequence 5'-	This study
(pMEV404)	ATAATTATTGAATCTACTTA and 5'- TCCCTGTATTTGCAGTTGAT targeting to <i>aCPSF1b</i> and <i>aCPSF1</i> areas. Durk	
pMEV4-Cas9- <i>∆fla</i> (pMEV405)	pMEV4 containing donor, Cas9 ORF and a guide sequence 5'- CCGAAGAGGTAAAAATCTCA and 5'- GTAATGACTGGAAGCCTCCT targeting to <i>flaB1</i> and <i>flaJ</i> , Amp <sup>R</sup> . Pur <sup>R</sup> .	This study
pMEV4-Cas9-∆ <i>aCPSF1b/aCPSF2/fla</i> (pMEV406 and pMEV407)	pMEV4 containing donor, Cas9 ORF and the guide sequences that pMEV4-Cas9- $\triangle aCPSF1b/aCPSF2$ and pMEV4-Cas9- $\triangle fla$ contians, Amp <sup>R</sup> , Pur <sup>R</sup>	This study
pMD19-T- aCPSF1	pMD19-T with S0001 MMP0694-MMP0693 fragment	This study
pMD19-T- aCPSF1-H2F	pMD19-T with S0001 MMP0694-His6-3Flag-MMP0693 fragment	This study
pMEV4- <i>Cas9-sg2- aCPSF1-</i> <i>H2F</i> (pMEV409)	pMEV4- Cas9 with sg2 targeting aCPSF1 and donor (MMP0694-His6-3Flag-MMP0693)	This study
pMD19-T- <i>RpoL</i>	pMD19-T with S0001 MMP0261-MMP0260 fragment	This study
pMD19-T- <i>RpoL-H2F</i>	pMD19-T with S0001 MMP0261-His6-3Flag-MMP0260 fragment	This study
pMEV4- <i>Cas9-sg3- RpoL-H2F</i> (pMEV408)	pMEV4- Cas9 with sg3 targeting RpoL and donor (MMP0261-His <sub>6</sub> -3Flag-MMP0260)	This study
pMEV4-Cas9-mu0290-sg (pMEV410)	pMEV4- <i>Cas9</i> with sg targeting T1149 and <i>donor</i> ( <i>MMP0290-MMP0291</i> with point mutagenesis of T1149 sequence)	This study
pMEV4- <i>Cas9-sgP0386-</i> <i>P0386(-3) -mcherry</i> (pMEV411)	pMEV4- Cas9 with sgP0386 targeting P0386 and donor (P0386-mCherry with -3 point mutagenesis of sgP0386 targting sequence)	This study
pMEV4- Cas9- sgP0386- P0386(-2) -mcherry	pMEV4- Cas9 with sgP0386 targeting P0386 and donor (P0386-mCherry with -2 point mutagenesis of sgP0386 targeting sequence)	This study
pMEV4- <i>Cas9- sgP0386-</i> <i>P0386(-2 and -3) -mcherry</i> (pMEV413)	pMEV4- <i>Cas9</i> with sg <i>P0386</i> targeting <i>P0386</i> and donor ( <i>P0386-mCherry</i> with -2 and -3 point mutagenesis of <i>sgP0386</i> targeting sequence)	This study
pMEV4- Cas9- sgP0386- P0386(1) -mcherry (pMEV414)	pMEV4- Cas9 with sgP0386 targeting P0386 and donor (P0386-mCherry with 1 point mutagenesis of sgP0386 targting sequence)	This study
pMEV4- <i>Cas9- sgP0386-</i> <i>P0386(3) -mcherry</i> (pMEV415)	pMEV4- <i>Cas9</i> with sg <i>P0386</i> targeting <i>P0386</i> and donor ( <i>P0386-mCherry</i> with 3 point mutagenesis of <i>sgP0386</i> targting sequence)	This study
pMEV4- Cas9-sg1- (- 2)mcherry (pMEV416)	pMEV4- <i>Cas9</i> with sg1 targeting <i>mCherry</i> and <i>donor</i> ( <i>P0386-mCherry</i> with -2 point mutagenesis of <i>sg1</i> targting sequence)	This study
pMEV4- Cas9-sg2- (1m)mcherry (pMEV417)	pMEV4- <i>Cas9</i> with sg2 targeting <i>mCherry</i> and <i>donor</i> ( <i>P0386-mCherry</i> with 1 point mutagenesis of <i>sg2</i> targting sequence)	This study

#### Primer Sequence (5'-3')Purpose Mmp1197- geno GTGACTTTGGCAGTACGCTT Construction of strain $\triangle Mmp1197$ me-F Mmp1197- geno CAGTCTGCCATATTTTTAAG Construction of strain $\triangle Mmp1197$ me-R Del-1197-ORF-F TCCTGGAAGTGATGCTGGAC Construction of strain $\triangle Mmp1197$ Del-1197-ORF-R TCCTGTTCCAAGGATTCCAA Construction of strain $\triangle Mmp1197$ pMEV4-(1197)-F GAGAATAGAAAGTACATTATATTGC Construction of strain $\triangle Mmp1197$ Construction of strain $\triangle Mmp1197$ pMEV4-(1197)-R ATAACTTAAAAAAACCTTGGATTTTTG *Mmp1197-*(pME TCCAAGGTTTTTTAAGTTATGTGACTTTGGCAG Construction of strain $\triangle Mmp1197$ V4)-F TACGC *Mmp1197-*(pME ATAATGTACTTTCTATTCTCCAGTCTGCCATATT Construction of strain $\triangle Mmp1197$ V4)-R TTTAAGAGG △ - *Mmp1197*out-GCACAGCATGCAACAGCAAC Verification of knockout- Mmp1197 F (F1) $\Delta$ - *Mmp1197* out CTTGAGTCTCAGGCTCTTCG Verification of knockout- Mmp1197 -R (R1) △ - *MMP1197* in-AGCATGGGAAGCTCTTGCAA Verification of knockout-Mmp1197 F (F1) △ -*MMP1197* in-Verification of knockout- Mmp1197 CCAGCATCACTTCCAGGAAG R(R1`) aCPSF2up-dn-Deletion of *Mmp* (aCPSF2) CTTTCAAAACATCGTAATCTATTTTGG (T)F: aCPSF2up-dn-Deletion of *Mmp* (aCPSF2) AAAATAAATCGGAGAGTCCTTGAAA (T)R: aCPSF2del-(T)-CGTCGCACGCAGAAGTTGTAAAAATATTTAAA Deletion of *Mmp* (aCPSF2) GATTG E: aCPSF2del-(T)-Deletion of *Mmp* (*aCPSF2*) TACAACTTCTGCGTGCGACGCAAAGACAC R: aCPSF1b up-dn-CCAGATTTTCTTATCCATGCGAC Deletion of *Mmp* (*aCPSF1b*) (T)F: aCPSF1b up-dn-CTGCTGTTTTTCCTTGCAG Deletion of *Mmp* (*aCPSF1b*) (T)R: aCPSF1b del-(T)-Deletion of *Mmp* (aCPSF1b) AGATAAACACGAGCGATTCCGGTAAATG F٠ aCPSF1b del-(T)-GGAATCGCTCGTGTTTATCTCTACGCAAG Deletion of *Mmp* (aCPSF1b) R: Sg aCPSF1b/aCP Construction of strain $\triangle Mmp$ (*aCPSF1b/aCP* TAAAAATATGGCAGACTGGATCAAATGGTAAG SF2-(pMEV4)-F: GTATATATAGTG SF2) flaJ dn-(pMEV4)-ATATACCTTACCATTTGATCGCGGGTTTGGAAA Construction of strain $\triangle Mmp \ fla$

### 64 **Table S2. Primers used in this study.**

R:	TGCTTTAAATG	
<i>aCPSF1b</i> in-F (F2`)	TGCGGTGCAATACCTTACTT	Verification of knockout- <i>aCPSF1b</i>
aCPSF1b in-R(R 2`)	CCTTCAGCTTGATATCCGGT	Verification of knockout- <i>aCPSF1b</i>
<i>aCPSF1b</i> out-F(F 2)	TGGAAGACCCACTCAAAGAG	Verification of knockout- <i>aCPSF1b</i>
<i>aCPSF1b</i> out-R (R2)	AGGGTGAATTCCTTCTCCAC	Verification of knockout- <i>aCPSF1b</i>
aCPSF2 in-F(F3	GAAGGGCAGGATATCCCCTA	Verification of knockout- <i>aCPSF2</i>
aCPSF2 in-R(R3 `)	AATTCGTCCATTTCGCCATG	Verification of knockout- <i>aCPSF2</i>
<i>aCPSF2</i> out-F(F 3)	GTGAACTACTGCTGGAAGGT	Verification of knockout- <i>aCPSF2</i>
aCPSF2 out-R(R 3)	GACGGTAGCGTTGCAGTTCA	Verification of knockout- <i>aCPSF2</i>
flaB1-in F(F4`)	CTGGAAGCGTTGGAACATCA	Verification of knockout- fla
<i>flaB1</i> -in R(R4`)	ACCTGGAGCACCAAATTCTG	Verification of knockout- fla
flaJ-in-F (F4``)	CAGGCTACACTCGGTTGGTC	Verification of knockout- fla
flaJ-in-R (R4``)	CACCGTAGTCTTCCATCACG	Verification of knockout- <i>fla</i>
Fla-out-F (F4)	CAACGAGTGTATCAGTTGCA	Verification of knockout- <i>fla</i>
Fla-out-R (R4)	AATTCTCGCATCAATAGTCG	Verification of knockout- <i>fla</i>
P0386-newRBS- Cas9-F	TTTTAAACGATTTTTCCGAAAGATTTATATATTTA GTTTTCCAAAATTAAACTGGATAACTAATACTAG AGAGGAGGTGAAATAATGGATAAAAAATATAGT ATTGGTTTAGATATAGG	Construction of strain $\triangle Mmp \ aCPSF1b/aCPS$ F2/fla
P0386-newRBS- Cas9-R	ATTTTTTATCCATTATTTCACCTCCTCTCTAGTATT AGTTATCCAGTTTTAATTTTGGAAAACTAAATAT ATAAATCTTTCGGAAAAATCGTTTAAAAATAAA AAAAAGTAGTATATTTATATATTTCGCACCGACTC G	Construction of strain $\triangle Mmp \ aCPSF1b/aCPS$ F2/fla
P0386-oldRBS-F	TATTTTTAAACGATTTTTCCGAAAGATTTATATAT TTAGTTTTCCAAAATTAAAACTGACTAGAGTGC AGGTAGCGCTATGG	Construction of strain $\triangle Mmp \ aCPSF1b/aCPS$ F2/fla
P0386-oldRBS-R	CCTGCACTCTAGTCAGTTTTAATTTTGGAAAACT AAATATATAAATCTTTCGGAAAAATCGTTTAAAA ATAAAAAAAGTAGTATATTTATATATTTC	Construction of strain $\triangle Mmp \ aCPSF1b/aCPS$ F2/fla
<i>H2F-</i> F	GAGATCTCACCACCACCACCACGAAAATGA TTATAAAGATGACGATGACAAAGATTATAAAGAT GACGATGACAAAGATTATAAAGATGACGATGAC AAATAAGTATTCTTTTTTTTTT	Construction of in situ tagging of <i>aCPSF1</i>
H2F-R	AAAGAATACTTATTTGTCATCGTCATCTTTATAAT CTTTGTCATCGTCATCTTTATAATCTTTGTCATCG TCATCTTTATAATCATTTTCGTGGTGGTGGTGGT GGTGAGATCTCAATCTTATTGAATCG	Construction of in situ tagging of <i>aCPSF1</i>
Sg2-anti0694tem- (Cas9-pMEV4)-F	ATTATACTTGCTTATTGAATCGAGATTCATGTTTT AGAGCTAGAAATAGCAAG	Construction of in situ tagging of <i>aCPSF1</i>
Sg2-anti0694tem- (Cas9-pMEV4)-R	GCTCTAAAACATGAATCTCGATTCAATAAGCAA GTATAATTACTAATCAGCAATATAATG	Construction of in situ tagging of <i>aCPSF1</i>
CI-HF-F	AGAAAAAC	Construction of in situ tagging of <i>aCPSF1</i>
C1-HF-R	ATAATGTACTTTCTATTCTCCCTGCTTCTTCTAAT	Construction of in situ tagging of aCPSF1

	TGGG	
pMEV-sg-Cas9-F	GAGAATAGAAAGTACATTATATTGC	Construction of in situ tagging of aCPSF1
pMEV-sg-Cas9-R	ATAACTTAAAAAACCTTGGATTTTTG	Construction of in situ tagging of <i>aCPSF1</i>
<i>mutant-0694tem -</i> F	CGAAAGCTCCAATGAATTTAGATTCAATAAGATT GAGATCTCACCAC	Construction of in situ tagging of <i>aCPSF1</i>
mutant-0694tem - R	TGAGATCTCAATCTTATTGAATCTAAATTCATTG GAGCTTTCGTTTC	Construction of in situ tagging of <i>aCPSF1</i>
<i>vz-C1-</i> F (F6)	GGACACATTTTAGGTTCAGC	Validation of in situ tagging of <i>aCPSF1</i>
<i>yz-0693-</i> R (R	CCTTTCAAGAACTAGTTCTCCCG	Validation of in situ tagging of <i>aCPSF1</i>
<i>RpoLC- (S000</i> 1) -F	ATTCTTGACATTTATTCTGAAC	Construction of in situ tagging of <i>RpoL</i>
<i>RpoLC- (S000</i> 1) -R	CGATAAAGAAGCCGTGTG	Construction of in situ tagging of <i>RpoL</i>
H2F-RpoLC-F	TTTACACCACCACCACCACGAAAATGATTA TAAAGATGACGATGACAAAGATTATAAAGATGA CGATGACAAAGATTATAAAGATGACGATGACAA ATAATTGATATTTTATATCGGCATAATTTAT	Construction of in situ tagging of <i>RpoL</i>
H2F-RpoLC-R	TATCAATTATTTGTCATCGTCATCTTTATAATCTTT GTCATCGTCATCTTTATAATCTTTGTCATCGTCAT CTTTATAATCATTTTCGTGGTGGTGGTGGTGGTGGTG TAAATCTTCAAGGGTTTTGTTAC	Construction of in situ tagging of <i>RpoL</i>
SgRpoLCtem-3- (Cas9-pMEV4)-F	ATTATACTTGTATCAATTATAAATCTTCAAGTTTT AGAGCTAGAAATAGCAAG	Construction of in situ tagging of <i>RpoL</i>
SgRpoLCtem-3- (Cas9-pMEV4)-R	GCTCTAAAACTTGAAGATTTATAATTGATACAAG TATAATTACTAATCAGCAATATAAT	Construction of in situ tagging of <i>RpoL</i>
<i>RpoLC-( pMEV4- Cas9)-</i> F	TCCAAGGTTTTTTAAGTTATATTCTTGACATTTAT TCTGAACTCAAC	Construction of in situ tagging of <i>RpoL</i>
RpoLC-( pMEV4- Cas9)-R	ATAATGTACTTTCTATTCTCCGATAAAGAAGCCG TGTGCG	Construction of in situ tagging of <i>RpoL</i>
<i>yz-RpoL-</i> F (F 5)	GGCGATGAAAAGTACAAACTCGTAGAAGACC	Validation of in situ tagging of <i>RpoL</i>
<i>yz-2060-</i> R (R 5)	GTTTGCATTTGCAGGCACTGGTTGTGGC	Validation of in situ tagging of <i>RpoL</i>
<i>Sg0386tem-(Cas9</i> <i>-pMEV4)-</i> F	ATTATACTTGAACTAAATATATAAATCTTTGTTTT AGAGCTAGAAATAGCAAG	Construction of in situ point mutagenesis of <i>P0</i> 386
Sg0386tem-(Cas9 -pMEV4)-R	GCTCTAAAACAAAGATTTATATATTTAGTTCAAG TATAATTACTAATCAGCAATATAAT	Construction of in situ point mutagenesis of <i>P0</i> 386
Sat-P0386-mCher ry-(Cas9-pMEV4) -F	TCCAAGGTTTTTTAAGTTATCTTTAGTTAATGGT GGATCAACTGG	Construction of in situ point mutagenesis of <i>P0</i> 386
<i>Sat</i> -P0386-mCher ry- <i>(Cas9-pMEV4)</i> -R	ATAATGTACTTTCTATTCTC TGATGCTTCCCAAC CCATTG	Construction of in situ point mutagenesis of <i>P0</i> 386
<i>P0386</i> -negative3- F	TTTATTAACCTATTTTTTTTTTTCGAAAGATTTATAT ATTTAG	Construction of in situ point mutagenesis of <i>P0</i> 386
P0386-negative3- R	CTAAATATATAAATCTTTCGAAAAAAAAAAAAGG TTAATAAA	Construction of in situ point mutagenesis of <i>P0</i> 386
P0386-negative2- F	TTTATTAACCTATTTTTTTTTTTTTCTGAAAGATTTATA TATTTAG	Construction of in situ point mutagenesis of <i>P0</i> 386
P0386-negative2- R	CTAAATATATAAATCTTTCAGAAAAAAAAAAAGG TTAATAAA	Construction of in situ point mutagenesis of <i>P0</i> 386
<i>P0386</i> -negative 2、3-F	TTTATTAACCTATTTTTTTTTTTTTTTTGAAAGATTTATA TATTTAG	Construction of in situ point mutagenesis of <i>P0</i> 386
<i>P0386</i> -negative 2、3-R	CTAAATATATAAATCTTTCAAAAAAAAAAAAAAAAAAGG TTAATAAA	Construction of in situ point mutagenesis of <i>P0</i> 386
<i>P0386</i> -1-F	TAACCTATTTTTTTTTTCCGGAAGATTTATATATTT AGTTTTCC	Construction of in situ point mutagenesis of <i>P0</i> 386
<i>P0386</i> -1-R	GGAAAACTAAATATATAAATCTTCCGGAAAAAA AAATAGGTTA	Construction of in situ point mutagenesis of <i>P0</i> 386
<i>P0386</i> -3-F	CCTATTTTTTTTTTCCGAAGGATTTATATATTTAGT TTTCC	Construction of in situ point mutagenesis of <i>P0</i> 386
<i>P0386</i> -3-R	GGAAAACTAAATATATAAATCCTTCGGAAAAAA	Construction of in situ point mutagenesis of P0

	AAATAGG	386	
SAT-F	GTGTCCTGCTCCTCTTTCTCTAGC	Validation of in situ point mutagenesis of <i>P038</i> 6	
MCH-R	AACGTTGTATGCACCTGGTAACTGAACTG	Validation of in situ point mutagenesis of <i>P038</i> 6	
Sg5-mCherry -F	ATTATACTTGGTGGTCCATTACCATTCGCAGTTTT	Construction of in situ point mutagenesis of $m$	
-	AGAGCTAGAAATAGCAAG	Cherry	
Sg5-mCherry -R	GCTCTAAAACTGCGAATGGTAATGGACCAC CAA	Construction of in situ point mutagenesis of $m$	
	GTATAATTACTAATCAGCAATATAAT	Cherry	
temsg8-mCherry -	ATTATACTTG TTTGAACCGTACATAAACTGGTTT	Construction of in situ point mutagenesis of $m$	
F	TAGAGCTAGAAATAGCAAG	Cherry	
temsg8-mCherry -	GCTCTAAAACCAGTTTATGTACGGTTCAAA CAA	Construction of in situ point mutagenesis of $m$	
R	GTATAATTACTAATCAGCAATATAAT	Cherry	
mCherry sg1-pam	CCATTCGCATAGGATATATTATCACCACAGTTTAT	Construction of in situ point mutagenesis of $m$	
<i>(-2) TAG</i> -F2	GTACGGTTC	Cherry	
mCherry sg1-pam	CTGTGGTGATAATATATCCTATGCGAATGGTAATG	Construction of in situ point mutagenesis of m	
(-2) TAG -R2	GACCACC	Cherry	
mCherry temsg2-	GCATGGGATATATTATCACCATAGTTTATGTACGG	Construction of in situ point mutagenesis of $m$	
1TAG -F2	TTCAAAAGCATACG	Cherry	
mCherry temsg2-	GCTTTTGAACCGTACATAAACTATGGTGATAATA	Construction of in situ point mutagenesis of m	
<i>1TAG</i> -R2	TATCCCATGCG	Cherry	
Mmp0290- geno	TTGGAATCCTTGGAACAGGACGAAGATTTAAAG	Construction of strain Mrsn T0200 mutant	
me-F	GCTGTC	Construction of strain <i>mmp-10290-matani</i>	
Mmp0291- geno	ATAATGTACTTTCTATTCTCATGGAAAATCACTTA	Construction of strain Mmn T0200 mutant	
me-R	ATCTTGAG	Construction of strain <i>imp-10290-matani</i>	
	TTTTTTAATTAAAGAATACACTACATACACCAA		
<i>mutant-</i> T1149 -F	TAAGAAATACTCATCTAAGGCCGGTGAGAGAAT	Construction of strain Mmp-T0290-mutant	
	G		
	CGGCCTTAGATGAGTATTTCTTATTGGTGTATGTA		
<i>mutant-</i> T1149 -R	GTGTATTCTTTAATTAAAAAAAATTAAAAAATTAGT	Construction of strain Mmp-T0290-mutant	
	TTCCGAG		
<i>S9-T1149-</i> F	ATTATACTTGGTGAGAGAATGGATATCGAAGTTT	Construction of strain Mmn-T0290-mutant	
~8 **** **	TAGAGCTAGAAATAGCAAG	construction of strain map 10250 mature	
S9-T1149-R	GCTCTAAAACTTCGATATCCATTCTCTCACCAAG	Construction of strain Mmn-T0290-mutant	
~8 11177 10	TATAATTACTAATCAGCAATATAATG	construction of Strain Minip 10290 matura	

## 67 Table S3. Sequences of promoters and terminators used to express sgRNAs in this study.

Plasmid	sgRNA	Promoters(5'-3')	Terminators(5'-3')
pMEV402 pMEV403	ssuC(1197)	Pmcr: GAATAGAAAGTACATTATATTGCTGATTAGTAATTATACTTG	T1149: TTATTTTTTTACTTTTTTAAATTTTAAA
pMEV404	aCPSF1b(1381)	P0383: TCAAATGGTAAGGTATATATAGTGATGGCGACAAGGCTATTCTTG	T1249: AAAACTTAATCTAATACTTTTTTTTTTTTTTTGAAAT
	aCPSF2(0431)	P1555: TTTAATGAAAACTTGAATATATATTCTTTCAGTAATGTTATGATG	T1274: TTAAAAGAATAATTCTTTTTTTTTTTTTTTTTTTAACTG
pMEV405	flaB1(1666)	P0383 TCAAATGGTAAGGTATATATAGTGATGGCGACAAGGCTATTCTTG	T1249: AAAACTTAATCTAATACTTTTTTTAATTTTTGAAAT
	flaJ(1676)	P1555: TTTAATGAAAACTTGAATATATATATTCTTTCAGTAATGTTATGATG	T1274: TTAAAAGAATAATTCTTTTTTTTTTTTTTTTTTTAACTG
pMEV406 pMEV407	flaB1(1666)	P0076: ATGAACTCAGATACTTATATATACTAGCAAATGAAGTGTAATATA	T1149: TTATTTTTTACTTTTTTAAATTTTAAA
	flaJ(1676)	P0386: TTTTTCCGAAAGATTTATATATATTTAGTTTTCCAAAATTAAAACTG	T1274: TTAAAAGAATAATTCTTTTTTTTTTTTTTTTTTTAACTG
	aCPSF1b(1381)	P0383: TCAAATGGTAAGGTATATATAGTGATGGCGACAAGGCTATTCTTG	T1249: ААААСТТААТСТААТАСТТТТТТТААТТТТТБАААТ
	aCPSF2(0431)	P0260: TTTAACTCAGTAACTTATATAATAGTAAGTGATAGTATGTCTG	T0204: TATATAAATATACTACTTTTTTTTTTTTTTTTTAAACGA
pMEV408	RpoL(0261)	Pmcr: GAATAGAAAGTACATTATATTGCTGATTAGTAATTATACTTG	T1149: TTATTTTTTACTTTTTTAAATTTTAAA
pMEV409	aCPSF1(0694)	Pmcr: GAATAGAAAGTACATTATATTGCTGATTAGTAATTATACTTG	T1149: TTATTTTTTACTTTTTTAAATTTTAAA
pMEV410	MMP0290 terminator(T1149)	Pmcr: GAATAGAAAGTACATTATATTGCTGATTAGTAATTATACTTG	T1149: TTATTTTTTTACTTTTTTAAATTTTAAA

pMEV411~	w Ch away	Pmcr:	T1149:
pMEV417	mCherry	GAATAGAAAGTACATTATATTGCTGATTAGTAATTATACTTG	TTATTTTTTACTTTTTTAAATTTTAAA

### 69 **Table S4. Probes used in northern blot assy.**

MMP0290- mid-probe	GCTTTTCCAGTAATCGAATAAGTTTTATTTCCAAGCATGTCCATTACCTGAACTTTTGG
MMP0291-5'- probe	CCACTGCTTCGACAAATCTTCTTGCCCATCCTTCATCAGTGTCTTTAACTTCAATCACT

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## 72 Table S5. Summary of the genome editing efficiency and precision achieved in this study.

Table 55. Summ	Table 55. Summary of the genome eutring efficiency and precision achieved in this study.			
Target	Plasmid	Selected transformants	Positive transformants	Editing efficiency* (Precision)
suuC	pMEV403	18	18	100%
aCPSF1b、 aCPSF2	pMEV404	16	12	75%
fla	pMEV405	10	10	100%
aCPSF1b、 aCPSF2、fla	pMEV407	9	9	100%
RpoL	pMEV408	5	5	100%
aCPSF1	pMEV409			100%
<i>T1149</i>	pMEV410	5	5	100%
-3 point mutagenesis of <i>P0386</i>	pMEV411	5	4	80%
-2 point mutagenesis of <i>P0386</i>	pMEV412	5	5	100%
-3 and -2 point mutagenesis of <i>P0386</i>	pMEV413	5	5	100%
1 point mutagenesis of <i>P0386</i>	pMEV414	5	5	100%
3 point mutagenesis of <i>P0386</i>	pMEV415	5	3	60%
mCherry	pMEV416~ pMEV417	5	5	100%

\* The editing efficiency was calculated as the positive transformant numbers divided by the selected transformant

74 numbers, and the editing precision was determined by the accuracy of the positive transformants by PCR product

75 sequencing.

# **Reference**

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