

Exploring C-to-G and A-to-Y base editing in rice by using new vector tools

Figure S1. C-to-T, C-to-G and C-to-A substitution without indels efficiency of CGBE-rUNG-TS1~TS5 and CGBE-hUNG-TS1~TS5 during C₃-C₁₂ window.

CGBE-rUNG-TS1											
	G ₃	C ₄	C ₅	C ₆	T ₇	C ₈	C ₉	T ₁₀	C ₁₁	C ₁₂	
C-T		3.7%	7.4%	3.7%		0	0		0	0	
C-G		0	3.7%	0		0	0		0	0	
C-A		0	0	0		0	0		0	0	

CGBE-rUNG-TS2											
	G ₃	T ₄	C ₅	C ₆	C ₇	A ₈	C ₉	G ₁₀	A ₁₁	G ₁₂	
C-T			3.7%	0	3.7%		0				
C-G			0	0	0		0				
C-A			0	0	0		0				

CGBE-rUNG-TS3											
	A ₃	C ₄	C ₅	C ₆	G ₇	C ₈	C ₉	T ₁₀	C ₁₁	G ₁₂	
C-T		0	0	7.4%		0	0		0		
C-G		0	0	0		0	0		0		
C-A		0	0	0		0	0		0		

CGBE-rUNG-TS4											
	A ₃	C ₄	C ₅	C ₆	C ₇	C ₈	G ₉	C ₁₀	T ₁₁	C ₁₂	
C-T		7.4%	29.6%	11.1%	18.5%	3.7%		0		0	
C-G		0	0	3.7%	0	0		0		0	
C-A		3.7%	7.4%	0	3.7%	0		0		0	

CGBE-rUNG-TS6											
	G ₃	C ₄	A ₅	C ₆	C ₇	A ₈	T ₉	G ₁₀	A ₁₁	C ₁₂	
C-T		18.5%		18.5%	18.5%					0	
C-G		3.7%		7.4%	11.1%					0	
C-A		0		3.7%	0					0	

CGBE-hUNG-TS1											
	G ₃	C ₄	C ₅	C ₆	T ₇	C ₈	C ₉	T ₁₀	C ₁₁	C ₁₂	
C-T		4.5%	4.5%	9.1%		0	0		0	0	
C-G		0	0	4.5%		0	0		0	0	
C-A		4.5%	0	0		0	0		0	0	

CGBE-hUNG-TS2											
	G ₃	T ₄	C ₅	C ₆	C ₇	A ₈	C ₉	G ₁₀	A ₁₁	G ₁₂	
C-T			0	4.5%	13.6%		0				
C-G			0	0	0		0				
C-A			4.5%	9.1%	0		0				

CGBE-hUNG-TS3											
	A ₃	C ₄	C ₅	C ₆	G ₇	C ₈	C ₉	T ₁₀	C ₁₁	G ₁₂	
C-T		4.5%	18.1%	18.1%		0	0		0		
C-G		0	0	4.5%		0	0		0		
C-A		0	4.5%	0		0	0		0		

CGBE-hUNG-TS4											
	A ₃	C ₄	C ₅	C ₆	C ₇	C ₈	G ₉	C ₁₀	T ₁₁	C ₁₂	
C-T			9.1%	9.1%	4.5%	9.1%		0		0	
C-G			0	0	0	4.5%		0		0	
C-A			0	0	0	0		0		0	

CGBE-hUNG-TS6											
	G ₃	C ₄	A ₅	C ₆	C ₇	A ₈	T ₉	G ₁₀	A ₁₁	C ₁₂	
C-T		18.2%		13.6%	18.2%					0	
C-G		4.5%		4.5%	18.2%					0	
C-A		0		0	0					0	

Figure S2. A-to-G, A-to-C and A-to-T substitution without indels efficiency of ABE8e-EndoV-TS1~TS5 and ABE8e-hAAG-TS1~TS5 during A₃-A₁₂ window.

ABE8e-Endov-TS1											ABE8e-hAAG-TS1										
	C ₃	T ₄	C ₅	A ₆	A ₇	C ₈	T ₉	T ₁₀	C ₁₁	A ₁₂		C ₃	T ₄	C ₅	A ₆	A ₇	C ₈	T ₉	T ₁₀	C ₁₁	A ₁₂
A-G				36.7%	0					0	A-G				34.8%	0					0
A-C				0	0					0	A-C				0	0					0
A-T				0	0					0	A-T				0	0					0

ABE8e-Endov-TS2											ABE8e-hAAG-TS2										
	G ₃	C ₄	C ₅	G ₆	A ₇	A ₈	G ₉	T ₁₀	C ₁₁	A ₁₂		G ₃	C ₄	C ₅	G ₆	A ₇	A ₈	G ₉	T ₁₀	C ₁₁	A ₁₂
A-G					40.0%	26.7%				0	A-G					47.8%	26.1%				0
A-C					0	0				0	A-C					0	0				0
A-T					0	0				0	A-T					0	0				0

ABE8e-Endov-TS3											ABE8e-hAAG-TS3										
	G ₃	A ₄	A ₅	A ₆	A ₇	A ₈	G ₉	C ₁₀	C ₁₁	G ₁₂		G ₃	A ₄	A ₅	A ₆	A ₇	A ₈	G ₉	C ₁₀	C ₁₁	G ₁₂
A-G		3.3%	26.7%	60.0%	0	0					A-G		8.7%	34.8%	39.1%	8.7%	0				
A-C		0	0	0	0	0					A-C		0	0	0	0	0				
A-T		0	0	0	0	0					A-T		0	0	0	0	0				

ABE8e-Endov-TS4											ABE8e-hAAG-TS4										
	A ₃	A ₄	G ₅	A ₆	A ₇	G ₈	A ₉	C ₁₀	G ₁₁	A ₁₂		A ₃	A ₄	G ₅	A ₆	A ₇	G ₈	A ₉	C ₁₀	G ₁₁	A ₁₂
A-G	10.0%	50.0%		73.3%	20.0%		0			0	A-G	13.0%	60.9%		82.6%	39.1%		0			0
A-C	0	0		0	0		0			0	A-C	0	0		0	0		0			0
A-T	0	0		0	0		0			0	A-T	0	0		0	0		0			0

ABE8e-Endov-TS5											ABE8e-hAAG-TS5										
	C ₃	T ₄	A ₅	A ₆	G ₇	A ₈	C ₉	A ₁₀	C ₁₁	G ₁₂		C ₃	T ₄	A ₅	A ₆	G ₇	A ₈	C ₉	A ₁₀	C ₁₁	G ₁₂
A-G			63.3%	23.3%		6.7%					A-G			65.2%	47.8%		26.1%		0		
A-C			0	0		0		0			A-C			0	0		0		0		
A-T			0	0		0		0			A-T			0	0		0		0		

Figure S3. Off-target analyses of CGBE-rUNG, CGBE-hUNG, ABE8e-EndoV and ABE8e-hAAG.

(a)				(b)			
Target site	Off-target sequence	CGBE-rUNG	CGBE-hUNG	Target site	Off-target sequence	ABE8e-Endov	ABE8e-hAAG
<i>OsSUS6</i> -TS1	CTGCCCTCCTCCATCGGCAA AGG			<i>OsMSP1</i> -TS1	GGCTCAACTTCAGTGGATGT ggg		
TS1-off1	CTGCCCTCCTCC TCG CCAAAGT	0	0	TS1-off1	GGCTCA TC CT TA AGTGGAGGTGGA	0	0
TS1-off2	CTGCCCGCCTCC TTGG CAACGG	0	0	TS1-off2	GGCTCA TC TT GA GTGGAGGTGGA	0	0
TS1-off3	CGGCC G TCCTCCATCGGCAC GGG	0	0	TS1-off3	GGCTCA TC TT GA GTGGAGGTGGA	0	0
<i>OsSUS6</i> -TS2	CTGTCCCAAGAGCTGGTACT TGT			<i>OsMSP1</i> -TS2	AGGCCGAAGTCAGAGACCC TCGG		
TS2-off1	CTGTCCCA TC AGCTGGT TC TTGT	0	0	TS2-off1	AGGCCGAAGTC CG GAGACCC TGGC	3.3%	0
TS2-off2	CT CCA CCACGAGCTGGTACT TGG	0	0	TS2-off2	AGGCCGAAGTC CG GACACCC GCGG	0	0
TS2-off3	CTGTCC CTAG AGCTGG ACTTGG	0	0	TS2-off3	AGGCCGAAGTC CG GAGAC CTTGGC	0	0
<i>OsSPS1</i> -TS3	GCACCCGCCTCGAGAACATG TGC			TS2-off4	AGGCCGAAGTC CG GAGAC CTTGGC	0	0
TS3-off1	GCACCC AACTA GAGAACATGAGC	0	0	<i>Chalk5</i> -TS3	GCGAAAAAGCCGCTACAAAC CGGC		
TS3-off2	GCACCCGCCT GGA TC ACATGCGC	0	0	TS3-off1	G GG AAAAAGCCGCTAC TG AC GGC	0	0
TS3-off3	GCATCCGCCTCGA AG ACATGAGG	0	0	TS3-off2	GCGAAAAAGCC CTC CACAAACT TGA	0	0
<i>OsSPS1</i> -TS4	TGACCCCCGCTCGCCGTCGA TGG			TS3-off3	GCGAAAAAGCCG TG AGAAAC GGT	0	0
TS4-off1	TGACCCC TGGA CGCCGTCGACGG	0	0	<i>Chalk5</i> -TS4	AGAAGAAGACGATGAGCATT AGG		
TS4-off2	TCCCC CGCTCGCCGTCG CCGG	0	4.5%	TS4-off1	AGAAGA TG ACGATGAGCA CTTGG	0	0
TS4-off3	TGCCCCG CGCTCGCCGT GAAAGG	0	0	TS4-off2	AGAAGA TG ACGATGAGCAT AGGT	0	0
<i>Os07g0134700</i> -TS5	TCGCACCATGACGCGCCGCA GGT			TS4-off3	AGAAGAAGAA GAA GA CA ATT TGG	0	0
TS5-off1	TCGCACCATGAC TTA CCGCA CGG	0	0				
TS5-off2	TCGCACCA CGC CGCGCTGCAGGG	0	0				
TS5-off3	TCGCACCATGACGCGCC GAATCA	0	0				

Table S1. The mutation of CGBE-rUNG in T₀ rice.

CGBE-rUNG-TS1			Allelic variation
CGBE-rUNG	Ref : GACGCCTCACCTCAGC	CTGCCCTCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC
TS1#07	A1 : GACGCCTCACCTCAGC	-TGTT- TCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC C>T, -2bp
	A2 : GACGCCTCACCTCAGC	CTGTTTTCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC C>T
TS1#06	A1 : GACGCCTCACCTCAGC	CTGCCCTCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC WT
	A2 : GACGCCTCACCTCAGC	CTGC- T TCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC C>T, -1bp
TS1#03	A1 : GACGCCTCACCTCAGC	CTGCCCTCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC WT
	A2 : GACGCCTCACCTCAGC	CTG- - CTCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC -2bp
TS1#13	A1 : GACGCCTCACCTCAGC	CTGCCCTCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC WT
	A2 : GACGCCTCACCTCAGC	TTG- - TCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC C>T, -3bp
TS1#26	A1 : GACGCCTCACCTCAGC	CTGCCCTCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC WT
	A2 : GACGCCTCACCTCAGC	- - - - - CCTCCATCGGCAAAGG	CGCGCACTTGGTCTC -7bp
TS1#05	A1 : GACGCCTCACCTCAGC	CTGCCCTCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC WT
	A2 : GACGCCTCACCTCAGC	CTGCCCTC- - - - - GGCAAAGG	CGCGCACTTGGTCTC -7bp
TS1#15	A1 : GACGCCTCACCTCAGC	CTGCCCTCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC WT
	A2 : GACGCCTCACCTCAGC	CT- - - - - ATCGGCAAAGG	CGCGCACTTGGTCTC -10bp
TS1#11	A1 : GACGCCTCACCTCAGC	CTGCC- - - - - CAAAGG	CGCGCACTTGGTCTC -12bp
	A2 : GACGCCTCACCTCAGC	- - - - - CCATCGGCAAAGG	CGCGCACTTGGTCTC -10bp
TS1#17	A1 : GACGCCTCACCTCAGC	CTGTGTTCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC C>T, C>G
	A2 : GACGCCTCACCT- - - - -	- - - - - CAAAGG	CGCGCACTTGGTCTC -21bp
TS1#09	A1 : GACGCCTCACC- - - - -	- - - - - GG	CGCGCACTTGGTCTC -26bp
	A2 : GACGCCTCACC- - - - -	- - - - - GG	CGCGCACTTGGTCTC -26bp
TS1#21	A1 : GACGCCTCACCTCAGC	CTGCCCTCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC WT
	A2 : GACGCCTCACCT- - - - -	- - - - - GG	CGCGCACTTGGTCTC -25bp
TS1#12	A1 : GATTTTGGCGCCCTGGACCTGTCGACGCCTCACCTCAGC	CTGCCCTCCTCCATCGGCAAAGG	CGCGC WT
	A2 : GATTTTGTG- - - - -	- - - - - TCGGCAAAGG	CGCGC -43bp
TS1#02	A1 : GACGCCTCACCTCAGC	CTGCCCTCCTCCATCCTCCATCGGCAAAGG	CGCGCACTTGGTCTC +8bp
	A2 : GACGCCTCACCTCAGC	- - - - - CCTCCA- - - - - TCGGCAAAGG	CGCGCACTTGGTCTC -7bp

Bia, biallelic mutation; Het, heterozygous mutation; Hom, homozygous mutation.

CGBE-rUNG- TS2				
CGBE-rUNG	Ref: TTTTATCCAACGGAT	CTGTCCCACGAGCTGGTACTTGT	TTTATCAGGCTGTGCA	Allelic variation
TS2#28	A1: TTTTATCCAACGGAT	CTGTCCCACGAGCTGGTACTTGT	TTTATCAGGCTGTGCA	WT
	A2: TTTTATCCAACGGAT	CTGTTCACGAGCTGGTACTTGT	TTTATCAGGCTGTGCA	C>T
TS2#21	A1: TTTTATCCAACGGAT	CTGTCCCACGAGCTGGTACTTGT	TTTATCAGGCTGTGCA	WT
	A2: TTTTATCCAACGGAT	CTG--ACACGAGCTGGTACTTGT	TTTATCAGGCTGTGCA	C>A, -2bp
TS2#18	A1: TTTTATCCAACGGAT	CTGTCCCACGAGCTGGTACTTGT	TTTATCAGGCTGTGCA	WT
	A2: TTTTATCCAACGGAT	CTGT--CACGAGCTGGTACTTGT	TTTATCAGGCTGTGCA	-2bp
TS2#09	A1: TTTTATCCAACGGAT	-----CACGAGCTGGTACTTGT	TTTATCAGGCTGTGCA	-6bp
	A2: TTTTATCCAACGGAT	-----CACGAGCTGGTACTTGT	TTTATCAGGCTGTGCA	-6bp
TS2#07	A1: TTTTATCCAACGGAT	-----AGCTGGTACTTGT	TTTATCAGGCTGTGCA	-10bp

	A2: TTTTATCCAACGGATCTGTCCCA--AGCTGGTACTTGT	TTATCAGGCTGTGCA -2bp	
TS2#08	A1: TTTTATCCAACGGATCTGTCCCACGAGCTGGTACTTGT	TTATCAGGCTGTGCA WT	Het
	A2: TTTTATCCAACGGATCTGT-----CCTACTTGT	TTATCAGGCTGTGCA -10bp	
TS2#12	A1: TTTTATCCAACGGATCTGTCCCACGAGCTGGTACTTGT	TTATCAGGCTGTGCA WT	Het
	A2: TTTTATCCAACGGATCTGTC-----TACTTGT	TTATCAGGCTGTGCA -11bp	
TS2#02	A1: TTTTATCCAACGGATCTGT-----TACTTGT	TTATCAGGCTGTGCA -12bp	Het
	A2: TTTTATCCAACGGATCTGTCCCACGAGCTGGTACTTGT	TTATCAGGCTGTGCA WT	
TS2#15	A1: TTTTATCCAACGGATCTGTCCCACGAGCTGGTACTTGT	TTATCAGGCTGTGCA WT	Het
	A2: TTTTATCCAACGGATCTGTC-----ACTTGT	TTATCAGGCTGTGCA -12bp	
TS2#07	A1: TTTTATCCAACGGATCTGTCCCACGAGCTGGTACTTGT	TTATCAGGCTGTGCA WT	Het
	A2: TTTTATCCAACGGATCTGT-----TACTTGT	TTATCAGGCTGTGCA -12bp	
TS2#10	A1: TTTTATCCAACGGATCTGTCCCACGAGCTGGTACTTGT	TTATCAGGCTGTGCA WT	Het
	A2: CTTTATCCAACGGA-----ACTTGT	TTATCAGGCTGTGCA -18bp	
TS2#23	A1: TTTTATCCAACGGATCTGTCCCACGAGCTGGTACTTGT	TTATCAGGCTGTGCA WT	Het
	A2: TTTTATCCAACGGATCT-----TGT	TTATCAGGCTGTGCA -18bp	
TS2#24	A1: TTTTATCCAACGGATCTGTCCCACGAGCTGGTACTTGT	TTATCAGGCTGTGCA WT	Het
	A2: TTTTATCCAACGGATCT-----TGT	TTATCAGGCTGTGCA -18bp	
TS2#10	A1: TTTTATCCAA-----GGCTGTGCA	-34bp	Het
	A2: TTTTATCCAACGGATCTGTCCCACGAGCTGGTACTTGT	TTATCAGGCTGTGCA WT	
TS2#06	A1: CTCGGTCAGTCTGTCTTTTATCCAACGGATCTGTCCCACGAGCTGGTACTTGT	TTATCAGGCTGT WT	Het
	A2: CTCGGT-----ACGAGCTGGTACTTGT	TTATCAGGCTGT -32bp	

CGBE-rUNG- TS3

CGBE-rUNG	Ref : ACGCCCGCAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	Allelic variation
TS3#02	A1: ACGCCCGCAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC WT	Het
	A2: ACGCCCGCAGCGGA	GCACCTGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC C>T	
TS3#06	A1: ACGCCCGCAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC WT	Het
	A2: ACGCCCGCAGCGGA	GCACCCGCCTCGA--CATGTGC	TGGCGCATCTGGCAC -3bp	
TS3#27	A1: ACGCCCGCAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC WT	Het
	A2: ACGCCCGCAGCGGA	GCAC--GCCTCGAGAACATGTGC	TGGCGCATCTGGCAC C>T	
TS3#20	A1: ACGCCCGCAGCGGA	GCACCTGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC C>T	Bia
	A2: ACGCCCGCAGCGGA	GCAC-----CTCGAGAACATGTGC	TGGCGCATCTGGCAC -4bp	
TS3#13	A1: ACGCCCGCAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC WT	Het
	A2: ACGCCCGCGAA-----CGAGAACATGTGC	TGGCGCATCTGGCAC -14bp		
TS3#23	A1: ACGCCCGCAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC WT	Het
	A2: AC-----GCGCATCTGGCAC	-38bp		
TS3#24	A1: ACGCCCGCAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC WT	Het
	A2: AC-----GCGCATCTGGCAC	-38bp		
TS3#09	A1: GTCGTCGCCACCCGCAACGCCCGCAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGT WT	Het
	A2: GTC-----GAGAACATGTGC	TGGCGCATCTGT -39bp		

CGBE-rUNG-TS4

CGBE-rUNG	Ref : CGCGTCGTTTCATGGA	TGACCCCCGCTCGCCGTCGATGAG	ACAGGCGCAGCGAGA	Allelic variation
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TS4#02	A1: CGCGTCGTTTCATGGA TGAATTCTGCTCGCCGTCGATGG ACAGGCGCAGCGAGA C>T, C>A A2: CGCGTCGTTTCATGGA TGACTGCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA C>T, C>G	Bia
TS4#18	A1: CGCGTCGTTTCATGGA TGACCCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA WT A2: CGCGTCGTTTCATGGA TGACTCTCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA C>T	Het
TS4#23	A1: CGCGTCGTTTCATGGA TGACATCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA C>T, C>A A2: CGCGTCGTTTCATGGA TGATTCTCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA C>T	Bia
TS4#24	A1: CGCGTCGTTTCATGGA TGACATCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA C>T, C>A A2: CGCGTCGTTTCATGGA TGATTCTCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA C>T	Bia
TS4#28	A1: CGCGTCGTTTCATGGA TGACCCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA WT A2: CGCGTCGTTTCATGGA TGACCCACGCTCGCCGTCGATGG ACAGGCGCAGCGAGA C>A	Het
TS4#01	A1: CGCGTCGTTTCATGGA TGACCCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA WT A2: CGCGTCGTTTCATGGA TGACTCCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA C>T	Het
TS4#26	A1: CGCGTCGTTTCATGGA TGACCCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA WT A2: CGCGTCGTTTCATGGA TGACTCCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA C>T	Het
TS4#05	A1: CGCGTCGTTTCATGGA TGACCCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA WT A2: CGCGTCGTTTCATGGA TGA---CCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA -3bp	Het
TS4#14	A1: CGCGTCGTTTCATGGA TGACCC---CGCCGTCGATGG ACAGGCGCAGCGAGA -3bp A2: CGCGTCGTTTCATGGA TGACCCCTCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA C>T	Bia
TS4#06	A1: CGCGTCGTTTCATGGA TG-----CTCGCCGTCGATGG ACAGGCGCAGCGAGA -7bp A2: CGCGTCGTTTCATGGA TGACCCCGC--GTCGTTTCATGG ACAGGCGCAGCGAGA -2bp, C>T	Bia
TS4#09	A1: CGCGTCGTTTCATGGA TGACCCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA WT A2: CGCGTCGTTTCATGGA TGACC-----GCCGTCGATGG ACAGGCGCAGCGAGA -7bp	Het
TS4#12	A1: CGCGTCGTTTCATGGA TGACCCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA WT A2: CGCGTCGTTTCATGGA TGA-----TCGCCGTCGATGG ACAGGCGCAGCGAGA -7bp	Het
TS4#17	A1: CGCGTCGTTTCATGGA TGAC-----GCTCGCCGTCGATGG ACAGGCGCAGCGAGA -4bp A2: CGCGTCGTTTCATGGA -----GCCGTCGATGG ACAGGCGCAGCGAGA -12bp	Bia
TS4#16	A1: CGCGTCGTTTCATGGA TGA-----TGCGATGG ACAGGCGCAGCGAGA -12bp A2: CGCGTCGTTTCATGGA TGA-CCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA -1bp	Bia
TS4#15	A1: CGCGTCGTTTCATGGA TGACCCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA WT A2: CGCGTCGTTTCATGGA TGACCCCGCTCG-----GGCGCAGCGAGA -13bp	Het
TS4#20	A1: CGCGTCGTTTCATGGA -----CGTCGATGG ACAGGCGCAGCGAGA -19bp A2: CGCGTCGTTTCATGG -----CTCGCCGTCGATGG ACAGGCGCAGCGAGA -10bp	Bia
TS4#27	A1: CGCGTCGTTTCATGGA TGACCCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA WT A2: C -----GCGCAGCGAGA -41bp	Het
TS4#10	A1: AGTCCTGCGGGTCCGACGATGGCGCTCGTTTCATGGA TGACCCCGCTCGCCGTCGATGG ACAGG WT A2: AGTC -----CCGCTCGCCGTCGATGG ACAGG -39bp	Het
TS4#13	A1: CTGCGGGT -----CGTCGATGG ACAGGCGCA -38bp A2: CTGCGGGTCCGACGATGGCGCTCGTTTCATGGA TG-----CTCGCCGTCGATGG ACAGGCGCA -7bp	Bia
TS4#22	A1: GTCCGACGAT -----CGAGA -50bp A2: GTCCGACGATGGCGCTCGTTTCATGGA TGA-----TGCGATGG ACAGGCGCAGCGAGA -12bp	Bia
TS4#21	A1: TGGATGA -----AG -55bp A2: TGGAT TGACTCTCGCTCGCCGTCGATGG ACAGGCGCAGCGAGAGGTCTGGACGTCATGAGCGAG WT	Het
TS4#07	A1: CGCGTCGTTTCATGGA TGACCCCG-----ATGG ACAGGCGCAGCGAGA -10bp	Bia

A2: CGCGTCGTTTCATGGATGACCCCGCTCGCCGTCTCGCCGTGATGGACAGGCGCAGCGAGA +8bp

CGBE-rUNG-TS5

CGBE-rUNG	Ref: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC	Allelic variation
TS5#06	A1: GAGATCAATCAGCGGTCGTACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC C>T, C>G	Bia
	A2: GAGATCAATCAGCGGTCGCACATATGACGCGCCGCAAGGTACTGGTATTTTGGCC C>T	
TS5#18	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC WT	Het
	A2: GAGATCAATCAGCGGTCGTAGCATGACGCGCCGCAAGGTACTGGTATTTTGGCC C>T, C>G	
TS5#03	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC WT	Het
	A2: GAGATCAATCAGCGGTCGTATCATGACGCGCCGCAAGGTACTGGTATTTTGGCC C>T	
TS5#04	A1: GAGATCAATCAGCGGTCGCATCATGACGCGCCGCAAGGTACTGGTATTTTGGCC WT	Bia
	A2: GAGATCAATCAGCGGTCGTAGTATGACGCGCCGCAAGGTACTGGTATTTTGGCC C>T, C>G	
TS5#08	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC WT	Het
	A2: GAGATCAATCAGCGGTCGCATTATGACGCGCCGCAAGGTACTGGTATTTTGGCC C>T	
TS5#11	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC WT	Het
	A2: GAGATCAATCAGCGGTCGCATCATGACGCGCCGCAAGGTACTGGTATTTTGGCC C>T	
TS5#26	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC WT	Het
	A2: GAGATCAATCAGCGGTCGCA-CATGACGCGCCGCAAGGTACTGGTATTTTGGCC -1bp	
TS5#07	A1: GAGATCAATCAGCGGTCG-AATATGACGCGCCGCAAGGTACTGGTATTTTGGCC -1bp, C>T	Bia
	A2: GAGATCAATCAGCGGTCGCACGATGACGCGCTGCAGGTACTGGTATTTTGGCC C>T, C>G	
TS5#22	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC WT	Het
	A2: GAGATCAATCAGCGGTCGCA--ATGACGCGCCGCAAGGTACTGGTATTTTGGCC -2bp	
TS5#27	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC WT	Het
	A2: GAGATCAATCAGCGGTCGCAC--TGACGCGCCGCAAGGTACTGGTATTTTGGCC -2bp	
TS5#21	A1: GAGATCAATCAGCGGTCG---TATGACGCGCCGCAAGGTACTGGTATTTTGGCC C>T, -3bp	Bia
	A2: GAGATCAATCAGCGGTCGCAACATGACGCGCCGCAAGGTACTGGTATTTTGGCC C>A	
TS5#28	A1: GAGATCAATCAGCGGTCGTACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC C>T, C>G	Bia
	A2: GAGATCAATCAGCGGTCGC-----TGACGCGCCGCAAGGTACTGGTATTTTGGCC -4bp	
TS5#14	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC WT	Het
	A2: GAGATCAATCAGCGGTCGC---ATGACGCGCCGCAAGGTACTGGTATTTTGGCC -3bp	
TS5#09	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC WT	Het
	A2: GAGATCAATCAGCGGTC-----GCGCCGCAAGGTACTGGTATTTTGGCC -10bp	
TS5#15	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC WT	Het
	A2: GAGATCAATCAGCGGTCGCACC-----GCAAGGTACTGGTATTTTGGCC -10bp	
TS5#13	A1: GAGATCAATCAGCGGT-----CGCAGGTACTGGTATTTTGGCC -15bp	Bia
	A2: GAGATCAAT-----CATGACGCGCCGCAAGGTACTGGTATTTTGGCC -12bp	
TS5#19	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC WT	Het
	A2: GAGATCAATCAGCGGTC-----CAGGTACTGGTATTTTGGCC -16bp	
TS5#20	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC WT	Het
	A2: GAG-----ACGCGCCGCAAGGTACTGGTATTTTGGCC -22bp	
TS5#10	A1: GAGATCAATCAG-----GTACTGGTATTTTGGCC -24bp	Bia
	A2: GAGATCAATCAGCGGTCGACATATGACGCGCCGCAAGGTACTGGTATTTTGGCC C>T, C>G	
TS5#16	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAAGGTACTGGTATTTTGGCC WT	Het

	A2: GAGATCAA-----TGTTATTTTGGCC -32bp	
TS5#01	A1: GAGATCAATCAGCGGTCTGC-----CGCAGGTACTGGTATTTTGGCC -12bp	Bia
	A2: GAGATCAATCA-----GCC -39bp	
TS5#02	A1: GAGATCAATCAGCGGTCTGCACCTATGACG---CGCCGCAGGTACTGGTATTTTG C>T	Bia
	A2: GAGATCAATCAGCGGTCTGCACCATGACGCGCCGCCGCAGGTACTGGTATTTTG +3bp	
TS5#24	A1: GAGATCAATCAGCGGTCTGCACCATGACG---CGCCGCAGGTACTGGTATTTTG WT	Het
	A2: GAGATCAATCAGCGGTCTGCACCATGACGCGCCGCCGCAGGTACTGGTATTTTG +3bp	
TS5#23	A1: GAGATCAATCAGCGGTCTGCACCATGA----CGCGCCGCCGCAGGTACTGGTA +3bp	Bia
	A2: GAGATCAATCAGCGGTCTGCACCATGACGCGCCG---CGCCGCAGGTACTGGTA +5bp	

Table S2. The mutation of CGBE-hUNG in T₀ rice.

CGBE-hUNG-TS1

CGBE-hUNG	Ref : ACGCCTCACCTCACGCTGCCCCCTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC	Allelic variation
TS1#20	A1 : ACGCCTCACCTCACGCTGCCCCCTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC WT	Het
	A2 : ACGCCTCACCTCACGCTGTCTCTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC C>T	
TS1#19	A1 : ACGCCTCACCTCACGCTGCCCCCTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC WT	Het
	A2 : ACGCCTCACCTCACGCTGATCTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC C>T, C>A	
TS1#03	A1 : ACGCCTCACCTCACGCTGCCCCCTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC WT	Het
	A2 : ACGCCTCACCTCACGCTGCCCCTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC C>G	
TS1#14	A1 : ACGCCTCACCTCACGCTGCCCCCTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC WT	Het
	A2 : ACGCCTCACCTCACGCTGCC-----ATCGGCAAAGGCGCGCACTTGGTCTC -7bp	
TS1#01	A1 : ACGCCTCACCTCACGCTGCCCCGA-----GGCAAAGGCGCGCACTTGGTCTC -7bp	Bia
	A2 : ACGCCTCACCTCACGCTGCCCTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC C>T	
TS1#06	A1 : ACGCCTCACCTCACGCTGCCCCCTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC WT	Het
	A2 : ACGCCTCACCT-----CTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC -9bp	
TS1#15	A1 : ACGCCTCACCTCACGCTGCCGAT-----GGCGCGCACTTGGTCTC -13bp	Bia
	A2 : ACGCCTCACCTCACGCTGCC-----CGCACTTGGTCTC -20bp	
TS1#09	A1 : ACGCCTCACCTCACGCTGCCCCCTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC WT	Het
	A2 : ACGCCTCACCTCAC-----GCAAAGGCGCGCACTTGGTCTC -17bp	
TS1#17	A1 : ACGC-----CTCCATCGGCAAAGGCGCGCACTTGGTCTC -19bp	Het
	A2 : ACGCCTCACCTCACGCTGCCCCCTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC WT	
TS1#21	A1 : ACGCCTCACCTCACGCTGCCCCCTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC WT	Het
	A2 : ACGCCTCACCT-----CAAAGGCGCGCACTTGGTCTC -21bp	
TS1#16	A1 : TGTACGCTCACCTCACGCTGCCCCCTCCTCCATCGGCAAAGGCGCGCACTTGGTCTC WT	Het
	A2 : TGT-----CGGCAAAGGCGCGCACTTGGTCTC -30bp	
TS1#05	A1 : CGCCTCACCTCACGCTGCCCTCCGACCTCCATCGGCAAAGGCGCGCACTTGGTCTC +5bp	Bia
	A2 : CGCCTCACCTCACG-----TCCATCGGCAAAGGCGCGCACTTGGTCTC -9bp	
TS1#08	A1 : TTG-----TT -62bp	Bia
	A2 : TTGGCGCCCTGGACCTGTCG-----CTCCATCGGCAAAGGCGCGCACTT -22bp	
TS1#12	A1 : CCTCACCTCACGCTGGCGATTAAATCGGAGTAGTTTGTGCTTCCATCGGCAAAGGCGCGCACTTGG +21bp	Bia
	A2 : CCT-----CGCGCACTTGG -32bp	

Bia, biallelic mutation; Het, heterozygous mutation; Hom, homozygous mutation.

CGBE-hUNG-TS2

CGBE-hUNG	Ref : CTTTTATCCAACGGATCTGTCCACAGAGCTGGTACTTGTTTATCAGGCTGTG	Allelic variation
TS2#19	A1 : CTTTTATCCAACGGATCTGTCCACAGAGCTGGTACTTGTTTATCAGGCTGTG WT	Het
	A2 : CTTTTATCCAACGGATCTGTCTATACAGAGCTGGTACTTGTTTATCAGGCTGTG C>T, C>A	
TS2#17	A1 : CTTTTATCCAACGGATCTGTCCACAGAGCTGGTACTTGTTTATCAGGCTGTG WT	Het
	A2 : CTTTTATCCAACGGATCTGT-----ACGAGCTGGTACTTGTTTATCAGGCTGTG -3bp	
TS2#08	A1 : CTTTTATCCAACGGATCTGTCCACAGAGCTGGTACTTGTTTATCAGGCTGTG WT	Het
	A2 : CTTTTATCCAACGGAT-----ACGAGCTGGTACTTGTTTATCAGGCTGTG -7bp	
TS2#15	A1 : CTTTTATCCAACGGATCTGTC-----ACTTGTTTATCAGGCTGTG -12bp	Bia
	A2 : CTTTTATCCAACGGATCTGTAATACAGAGCTGGTACTTGTTTATCAGGCTGTG C>T, C>A	

TS2#05	A1: CTTTATCCAACGGATCTGTCCCACGAGCTGGTACTTGTTTATCAGGCTGTG WT	Het
	A2: CTTTATCCAACGGATCT-----GTACTTGTTTATCAGGCTGTG -13bp	
TS2#01	A1: CTTTATCCAACGGATCTGT-----TACTTGTTTATCAGGCTGTG -12bp	Bia
	A2: CTTTATCCAACGGATC-----ACTTGTTTATCAGGCTGTG -15bp	
TS2#06	A1: CTTTATCCAACGGATCT-----TTTGTTTATCAGGCTGTG -16bp	Bia
	A2: CTTTATCCAACGGATCT-----GTACTTGTTTATCAGGCTGTG -13bp	
TS2#16	A1: TATCCAACGGATCTGTCC-----TCTATC -37bp	Bia
	A2: TATCCAACGGATCTGTCTTACGAGCTGGTACTTGTTTATCAGGCTGTGCATCTGTTTATC C>T	
TS2#04	A1: CAGTCTGTCCTTTATCCAACGGATCTGTCCCACGAGCTGGTACTTGTTTATCAGGCTGTG WT	Het
	A2: CAGTCTGTC-----TTATCAGGCTGTG -39bp	

CGBE-hUNG-TS3

CGBE-hUNG	Ref : ACGCCCGCGAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	Allelic variation	
TS3#12	A1 : ACGCCCGCGAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	WT	Het
	A2 : ACGCCCGCGAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	C>G	
TS3#16	A1 : ACGCCCGCGAGCGGA	GCACCTTGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	C>T	Hom
	A2 : ACGCCCGCGAGCGGA	GCACCTTGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	C>T	
TS3#01	A1 : ACGCCCGCGAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	WT	Het
	A2 : ACGCCCGCGAGCGGA	GCATTTGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	C>T	
TS3#21	A1 : ACGCCCGCGAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	WT	Het
	A2 : ACGCCCGCGAGCGGA	GCACACGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	C>A	
TS3#18	A1 : ACGCCCGCGAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	WT	Het
	A2 : ACGCCCGCGAGCGGA	GCACCTTGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	C>T	
TS3#17	A1 : ACGCCCGCGAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	WT	Het
	A2 : ACGCCCGCGAGCGGA	GCACC-----GAGAACATGTGC	TGGCGCATCTGGCAC	-6bp	
TS3#08	A1 : ACGCCCGCGAGCGGA	GCAC-----ATGTGC	TGGCGCATCTGGCAC	-13bp	Bia
	A2 : ACGCCCGCGA-----CCTCGAGAACATGTGC	TGGCGCATCTGGCAC	-12bp		
TS3#5	A1 : ACGCCCGCGAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	WT	Het
	A2 : ACGCCCGCGAGCGGA	GCAA-----ATGTGC	TGGCGCATCTGGCAC	-13bp	
TS3#15	A1 : CCCGCGAGCGGA	GCACC-----ATGTGC	TGGCGCATCTGGCAC	-12bp	Bia
	A2 : CCCGCGAGCGGA	GCACCCGCCGCTCGAGAACATGTGC	TGGCGCATCTGGCAC	+3bp	
TS3#19	A1 : CGTCGCCACCCGCAACGCCGCGAGCGGA	GCACCCGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC	WT	Het
	A2 : CGT-----TGCTCGAGAACATGTGC	TGGCGCATCTGGCAC	-31bp		
TS3#04	A1 : CG-----TCGAGAACATGTGC	TGGCGCATCTGGCAC	-49bp	Bia	
	A2 : CGTGGATCAAGTTCGTCGCCACCCGCAACGCCGCGAGCGGA	GCACCTTGCCTCGAGAACATGTGC	TGGCGCATCTGGCAC		C>T

CGBE-hUNG-TS4

CGBE-hUNG	Ref : CGCGTCGTT	CATGGA	TGACCCCGCTCGCCGTCGA	TGGACAGGCGCAGCGAGA	Allelic variation	
TS4#6	A1 :	CGCGTCGTT	CATGGA	TGA - - - CCGCTCGCCGTCGA	TGGACAGGCGCAGCGAGA -3bp	Bia
	A2 :	CGCGTCGTT	CATGGA	TGACCCCGCTCGCCGTCGA	TGGACAGGCGCAGCGAGA C>G	
TS4#18	A1 :	CGCGTCGTT	CATGGA	TGACCCCGCTCGCCGTCGA	TGGACAGGCGCAGCGAGA WT	Het
	A2 :	CGCGTCGTT	CATGGA	TGA - CCGCTCGCCGTCGA	TGGACAGGCGCAGCGAGA -1bp	

TS4#17	A1: CGTCGTTTCATGGA TGACCCCCGCTCGCGCCGTCGATGG ACAGGCGCAGCGAGA +2bp	Bia
	A2: CGTCGTTTCATGGA TGACTCCCGCT--CGCCGTCGATGG ACAGGCGCAGCGAGA C>T	
TS4#16	A1: CGCGTCGTTTCATGGA TGACCCCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA WT	Het
	A2: CGCGTCGTTTCATGGA TGA--CCCCTCGCCGTCGATGG ACAGGCGCAGCGAGA -2bp	
TS4#05	A1: GTCGTTTCATGGA TGACCCCCGCTGCTCGCCGTCGATGG ACAGGCGCAGCGAGA +3bp	Bia
	A2: GTCGTTTCATGGA TGACCTCC--GCTCGCCGTCGATGG ACAGGCGCAGCGAGA C>T	
TS4#14	A1: TCGTTTCATGGA TGACCCCCGCTCG---CCGTCGATGG ACAGGCGCAGCGAGA WT	Het
	A2: TCGTTTCATGGA TGACCCCCGCTCGCCGTCCGTCGATGG ACAGGCGCAGCGAGA +3bp	
TS4#20	A1: CGCGTCGTTTCATGGA TGACCCCCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA WT	Het
	A2: CGCGTCGTTTCATGGA -----ACGCTCGCCGTCGATGG ACAGGCGCAGCGAGA -6bp, C>A	
TS4#21	A1: CGCGTCGTTTCATGGA -----ACGCTCGCCGTCGATGG ACAGGCGCAGCGAGA -6bp, C>A	Bia
	A2: CGCGTCGTTTCATGGA TGACC-----GCCGTCGATGG ACAGGCGCAGCGAGA -7bp	
TS4#15	A1: CGCGTCGTTTCATGGA TG-----CTCGCCGTCGATGG ACAGGCGCAGCGAGA -7bp	Bia
	A2: CGCGTCGTTTCATGGA TGA-----GTCGATGG ACAGGCGCAGCGAGA -12bp	
TS4#19	A1: CGCGTCGTTTCATGGA TGAC-----GATGG ACAGGCGCAGCGAGA -14bp	Bia
	A2: CGCGTCGTTTCATGGA TGAC---TGCTCGCCGTCGATGG ACAGGCGCAGCGAGA -3bp, C>T	
TS4#01	A1: CGCGTCGTTTCATGGA -----GATGG ACAGGCGCAGCGAGA -18bp	Bia
	A2: CGCGTCGTTTCATGGA TGA---CCGCTCGCCGTCGATGG ACAGGCGCAGCGAGA -3bp	
TS4#10	A1: CGCGTCGTTTCATGGA TGACCCTTGCTCGCCGTCGATGG ACAGGCGCAGCGAGA CC>TT	Bia
	A2: CGCGTCGTTTC -----CGTCGATGG ACAGGCGCAGCGAGA -19bp	
TS4#09	A1: CGCGTCG -----CGTCGATGG ACAGGCGCAGCGAGA -22bp	Bia
	A2: CGCGTCGTTTCATGGA TGACC-----GTCGATGG ACAGGCGCAGCGAGA -10bp	
TS4#11	A1: CGCGTCGTTTCATGG -----ACAGGCGCAGCGAGA -24bp	Bia
	A2: CGCGTCGTTTCATGGA TGACCCCCGCTC-----CGATGG ACAGGCGCAGCGAGA -5bp	
TS4#12	A1: CGCGTCGTTTCATGG -----ACAGGCGCAGCGAGA -24bp	Bia
	A2: CGCGTCGTTTCATGGA TGACCCC-----GATGG ACAGGCGCAGCGAGA -11bp	
TS4#08	A1: CGACGATGGCGCTCGTTTCATGGA TGAC-----TCGATGG ACAGGCGCAGCGAGA -12bp	Bia
	A2: CGACGATG -----GACAGGCGCAGCGAGA -38bp	
TS4#04	A1: CTCTGCACCGAGTCTGCGGGTCCGACGATGGCGCTCGTTTCATGGA TGACTTCTGCTCGCCGTCGA C>T	Bia
	A2: CTCTGC -----TCGCCGTCGA -51bp	

CGBE-hUNG-TS5

CGBE-hUNG	Ref : GAGATCAATCAGCGG	TCGCACCATGACGCGCCGCAGGT	ACTGGTATTTTGGCC		Allelic variation
TS6#13	A1 : GAGATCAATCAGCGG	TCGCACCATGACGCGCCGCAGGT	ACTGGTATTTTGGCC	WT	Het
	A2 : GAGATCAATCAGCGG	TCGTACGATGACGCGCCGCAGGT	ACTGGTATTTTGGCC	C>T , C>G	
TS6#08	A1 : GAGATCAATCAGCGG	TCGCACATGACGCGCCGCAGGT	ACTGGTATTTTGGCC	C>T	Bia
	A2 : GAGATCAATCAGCGG	TCGCAGCATGACGCGCCGCAGGT	ACTGGTATTTTGGCC	C>G	
TS6#09	A1 : GAGATCAATCAGCGG	TCGTATGATGACGCGCCGCAGGT	ACTGGTATTTTGGCC	C>T , C>G	Bia
	A2 : GAGATCAATCAGCGG	TCGCACGATGACGCGCCGCAGGT	ACTGGTATTTTGGCC	C>G	
TS6#11	A1 : GAGATCAATCAGCGG	TCGCACCATGACGCGCCGCAGGT	ACTGGTATTTTGGCC	WT	Het
	A2 : GAGATCAATCAGCGG	TCGCATCATGACGCGCCGCAGGT	ACTGGTATTTTGGCC	C>T	
TS6#19	A1 : GAGATCAATCAGCGG	TCGTACCATGACGCGCCGCAGGT	ACTGGTATTTTGGCC	C>T	Het
	A2 : GAGATCAATCAGCGG	TCGCACCATGACGCGCCGCAGGT	ACTGGTATTTTGGCC	WT	

TS6#16	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAGGTACTGGTATTTTGGCC +1bp	Bia
	A2: GAGATCAATCAGCGGTCGGACTATGACGCG-CCGCAGGTACTGGTATTTTGGCC C>G, C>T	
TS6#06	A1: GAGATCAATCAGCGGTGCTATCATGACGCGCCGCAGGTACTGGTATTTTGGCC C>T	Bia
	A2: GAGATCAATCAGCGGTC---TATGACGCGCCGCAGGTACTGGTATTTTGGCC -4bp	
TS6#14	A1: GAGATCAATCAGCGGTCGCACCATGACG---CGCAGGTACTGGTATTTTGGCC -3bp	Hom
	A2: GAGATCAATCAGCGGTCGCACCATGACG---CGCAGGTACTGGTATTTTGGCC -3bp	
TS6#21	A1: GAGATCAATCAGCGGTCGCAC-----GCGCCGCAGGTACTGGTATTTTGGCC -6bp	Bia
	A2: GAGATCAATCAGCGGTCGCACCATGA-----CGCAGGTACTGGTATTTTGGCC -5bp	
TS6#04	A1: GAGATCAATCAGCGGTCGCACCA-----CAGGTACTGGTATTTTGGCC -10bp	Bia
	A2: GAGATCAATCAGCGGTCGCACGATGACGCGCCGCAGGTACTGGTATTTTGGCC C>G	
TS6#15	A1: GAGATCAATCAGCGGTCGCACC-----GCAGGTACTGGTATTTTGGCC -10bp	Bia
	A2: GAGATCAATCAGCGGTCGCACGATGACGCGCCGCAGGTACTGGTATTTTGGCC C>G	
TS6#05	A1: GAGATCAATCAGCGGT-----CGCAGGTACTGGTATTTTGGCC -15bp	Bia
	A2: GAGATCAATCAGCGGTCGCACTATGACGCGCCGCAGGTACTGGTATTTTGGCC C>T	
TS6#17	A1: GAGATCAATCAGCGGTCGCACTATGACGCGCCGCAGGTACTGGTATTTTGGCC C>T	Bia
	A2: GAGATCAATCAGCGG-----GTACTGGTATTTTGGCC -21bp	
TS6#10	A1: GAGATCAATCAGCGGTCGCACCATGACGCGCCGCAGGTACTGGTATTTTGGCC WT	Het
	A2: GAGATCAAT-----GTGCAGGTACTGGTATTTTGGCC -21bp	
TS6#01	A1: GAG-----GTACTGGTATTTTGGCC -33bp	Bia
	A2: GAGATCAATCAGCGGTCG---CATGACGCGCCGCAGGTACTGGTATTTTGGCC -3bp	
TS6#12	A1: CAATCAGCGGT-----CGCAGGTACTGGTATTTTGGCC -15bp	Bia
	A2: CAATCAGCGGTCGCACCATGACGCGCCGCAGGTACTGGTATTTTGGCC +5bp	
TS6#20	A1: TCAATCAGCGGTCGCACCA-----GCCGCAGGTACTGGTATTTTGGCCTTAGAACA -6bp	Bia
	A2: TCAATCAGCGGTCGCACCATGACGC-----AACA -28bp	

Table S3. The mutation of ABE8e-EndoV in T₀ rice.**ABE8e-EndoV-TS1**

ABE8e-Endov	Ref : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT	Allelic variation
TS1#7	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#15	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#10	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#11	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#16	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#18	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#19	A1 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	Hom
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#21	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#22	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#26	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCAAC---AGTGGATGTGGGTTTTCGGAGAGCTT -3bp	
TS1#08	A1 : TCCAGTCACTTGTTCCGGCTCAAC-----AGTGGGTTTTCGGAGAGCTT -9bp	Bia
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#05	A1 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	Bia
	A2 : T-----TTCAGTGGATGTGGGTTTTCGGAGAGCTT -23bp	

Bia, biallelic mutation; Het, heterozygous mutation; Hom, homozygous mutation.

ABE8e-EndoV-TS2

ABE8e-Endov	Ref : CTGATGATCCTTGCAAGGCCGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC	Allelic variation
TS2#02	A1 : CTGATGATCCTTGCAAGGCCGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	Bia
	A2 : CTGATGATCCTTGCAAGGCCGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#05	A1 : CTGATGATCCTTGCAAGGCCGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	Bia
	A2 : CTGATGATCCTTGCAAGGCCGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#06	A1 : CTGATGATCCTTGCAAGGCCGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	Bia
	A2 : CTGATGATCCTTGCAAGGCCGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#09	A1 : CTGATGATCCTTGCAAGGCCGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	Bia
	A2 : CTGATGATCCTTGCAAGGCCGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#10	A1 : CTGATGATCCTTGCAAGGCCGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC WT	Het
	A2 : CTGATGATCCTTGCAAGGCCGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#12	A1 : CTGATGATCCTTGCAAGGCCGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC WT	Het
	A2 : CTGATGATCCTTGCAAGGCCGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	

TS2#13	A1: CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC WT	Het
	A2: CTGATGATCCTTGCAAGGCCGGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#14	A1: CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC WT	Het
	A2: CTGATGATCCTTGCAAGGCCGGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#20	A1: CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC WT	Het
	A2: CTGATGATCCTTGCAAGGCCGGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#24	A1: CTGATGATCCTTGCAAGGCCGGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	Bia
	A2: CTGATGATCCTTGCAAGGCCGGGGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#25	A1: CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC WT	Het
	A2: CTGATGATCCTTGCAAGGCCGGGGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#28	A1: CTGATGATCCTTGCAAGGCCGGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	Bia
	A2: CTGATGATCCTTGCAAGGCCGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#17	A1: CTGATGATCCTTGCAAGGCCGG-GTCAGAGACCCTCGGCTCGAAGTTCTCATC -1bp, A>G	Het
	A2: CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC WT	
TS2#23	A1: CTGATGATCCTTGCAAGGCCGG-GTCAGAGACCCTCGGCTCGAAGTTCTCATC -1bp, A>G	Bia
	A2: CTGATGATCCTTGCAAGGCCGAGGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#29	A1: CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC WT	Het
	A2: CTGATGATCCTTGCAAGGCCGG-GTCAGAGACCCTCGGCTCGAAGTTCTCATC -1bp, A>G	
TS2#30	A1: CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC WT	Het
	A2: CTGATGATCCTTGCAAGGCCGG-GTCAGAGACCCTCGGCTCGAAGTTCTCATC -1bp, A>G	
TS2#08	A1: CTGATGATCCTTGCAAGGCTGAGGGTCAGAGACCCTCGGCTCGAAGTTCTCAT +1bp, A>G	Bia
	A2: CTGATGATCCTTGCAAGGC-CGAGGTCAGAGACCCTCGGCTCGAAGTTCTCAT A>G	
TS2#16	A1: ATGATCCTTGCAAGGCCGAG-----GTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	Bia
	A2: ATGATCCTTGCAAGGCCGAAGTCTCTTGTGTCAGAGACCCTCGGCTCGAAGTTCTCATC +7bp	

ABE8e-EndoV-TS3

ABE8e-Endov	Ref: TCACCAAGAAAAGTAGCGAAAAAGCCGCTACAAACGGCACCGTCTAGAATCCT	Allelic variation
TS3#01	A1: TCACCAAGAAAAGTAGCGAGGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	Hom
	A2: TCACCAAGAAAAGTAGCGAGGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#04	A1: TCACCAAGAAAAGTAGCGAAAAAGCCGCTACAAACGGCACCGTCTAGAATCCT WT	Het
	A2: TCACCAAGAAAAGTAGCGAAGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#07	A1: TCACCAAGAAAAGTAGCGAAAAAGCCGCTACAAACGGCACCGTCTAGAATCCT WT	Het
	A2: TCACCAAGAAAAGTAGCGAAGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#08	A1: TCACCAAGAAAAGTAGCGAGGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	Bia
	A2: TCACCAAGAAAAGTAGCGAAGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#10	A1: TCACCAAGAAAAGTAGCGAAAAAGCCGCTACAAACGGCACCGTCTAGAATCCT WT	Het
	A2: TCACCAAGAAAAGTAGCGAAGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#12	A1: TCACCAAGAAAAGTAGCGAAAAAGCCGCTACAAACGGCACCGTCTAGAATCCT WT	Het
	A2: TCACCAAGAAAAGTAGCGAGGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#15	A1: TCACCAAGAAAAGTAGCGAAAAAGCCGCTACAAACGGCACCGTCTAGAATCCT WT	Het
	A2: TCACCAAGAAAAGTAGCGGAGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#16	A1: TCACCAAGAAAAGTAGCGAAAAAGCCGCTACAAACGGCACCGTCTAGAATCCT WT	Het
	A2: TCACCAAGAAAAGTAGCGAAGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	

TS3#13	A1: TCACCAAGAAAAGTA GCGAAAAAGCCGCTACAAACGGC ACCGTCTAGAATCCT WT	Het
	A2: TCACCAAGAAAAGTA GCGAAG AAGCCGCTACAAACGGC ACCGTCTAGAATCCT A>G	
TS3#17	A1: TCACCAAGAAAAGTA GCGAAAAAGCCGCTACAAACGGC ACCGTCTAGAATCCT WT	Het
	A2: TCACCAAGAAAAGTA GCGAGG AAGCCGCTACAAACGGC ACCGTCTAGAATCCT A>G	
TS3#11	A1: TCACCAAGAAAAGTA GCGAGG AAGCCGCTACAAACGGC ACCGTCTAGAATCCT A>G	Het
	A2: TCACCAAGAAAAGTA GCGAAAAAGCCGCTACAAACGGC ACCGTCTAGAATCCT WT	
TS3#24	A1: TCACCAAGAAAAGTA GCGAAAAAGCCGCTACAAACGGC ACCGTCTAGAATCCT WT	Het
	A2: TCACCAAGAAAAGTA GCGAAG AAGCCGCTACAAACGGC ACCGTCTAGAATCCT A>G	
TS3#28	A1: TCACCAAGAAAAGTA GCGAAAAAGCCGCTACAAACGGC ACCGTCTAGAATCCT WT	Het
	A2: TCACCAAGAAAAGTA GCGAAG AAGCCGCTACAAACGGC ACCGTCTAGAATCCT A>G	
TS3#29	A1: TCACCAAGAAAAGTA GCGAAAAAGCCGCTACAAACGGC ACCGTCTAGAATCCT WT	Het
	A2: TCACCAAGAAAAGTA GCGAGG AAGCCGCTACAAACGGC ACCGTCTAGAATCCT A>G	
TS3#30	A1: TCACCAAGAAAAGTA GCGAAAAAGCCGCTACAAACGGC ACCGTCTAGAATCCT WT	Het
	A2: TCACCAAGAAAAGTA GCGAGG AAGCCGCTACAAACGGC ACCGTCTAGAATCCT A>G	
TS3#05	A1: TCACCAAGAAAAGTA GCGAAAAAGCCGCTACAAACGGC ACCGTCTAGAATCCT WT	Het
	A2: TCACCAAGAAAAGTA GCGA - GG AAGCCGCTACAAACGGC ACCGTCTAGAATCCT -1bp	
TS3#03	A1: TCACCAAGAAAAGTA GCGAGG - - - - - TTTGGACGC ACCGTCTAGAATCCT -8bp	Bia
	A2: TCACCAAGAAAAGTA GCGAAG AAGCCGCTACAAACGGC ACCGTCTAGAATCCT A>G	
TS3#23	A1: TCACCAAGAAAAGTA GCGAGG AAGCCGCTACAAACGGC ACCGTCTAGAATCCT A>G	Bia
	A2: TCACCAAGAAAAGTA GCGA - - - - - - GGAACGGC ACCGTCTAGAATCCT -11bp	

ABE8e-EndoV-TS4

ABE8e-Endov	Ref: ACGCATGGATAAACA AGAAGAAGACGATGAGCATTAGG GTTCCTTAACCAAGTT	Allelic variation
TS4#01	A1: ACGCATGGATAAACA AGAAGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	Bia
	A2: ACGCATGGATAAACA AGAGGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	
TS4#03	A1: ACGCATGGATAAACA AGAAGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	Bia
	A2: ACGCATGGATAAACA AGAGGGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	
TS4#05	A1: ACGCATGGATAAACA AGAAGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	Hom
	A2: ACGCATGGATAAACA AGAAGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	
TS4#06	A1: ACGCATGGATAAACA AGAAGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	Bia
	A2: ACGCATGGATAAACA AGAGGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	
TS4#08	A1: ACGCATGGATAAACA AGAGGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	Bia
	A2: ACGCATGGATAAACA AGGAGAAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	
TS4#10	A1: ACGCATGGATAAACA AGAGGAAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	Bia
	A2: ACGCATGGATAAACA AGAAGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	
TS4#13	A1: ACGCATGGATAAACA AGAAGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	Bia
	A2: ACGCATGGATAAACA AGGAGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	
TS4#14	A1: ACGCATGGATAAACA AGAAGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	Bia
	A2: ACGCATGGATAAACA AGAGGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	
TS4#15	A1: ACGCATGGATAAACA AGAAGAAGACGATGAGCATTAGG GTTCCTTAACCAAGTT WT	Het
	A2: ACGCATGGATAAACA AGAGGAAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	
TS4#17	A1: ACGCATGGATAAACA AGAGGAAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	Bia
	A2: ACGCATGGATAAACA AGAGGGAGACGATGAGCATTAGG GTTCCTTAACCAAGTT A>G	

TS4#18	A1: ACGCATGGATAAAACAAGAAGAAGACGATGAGCATTAGGGTTTCCTTAACCAGTT WT	Het
	A2: ACGCATGGATAAAACAAGAGGAAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#11	A1: ACGCATGGATAAAACAAGGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
	A2: ACGCATGGATAAAACAAGAAGAGGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#20	A1: ACGCATGGATAAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
	A2: ACGCATGGATAAAACAAGAGGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#23	A1: ACGCATGGATAAAACAAGAGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
	A2: ACGCATGGATAAAACAAGAGGGGGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#24	A1: ACGCATGGATAAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
	A2: ACGCATGGATAAAACAAGAGGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#25	A1: ACGCATGGATAAAACAAGAAGAAGACGATGAGCATTAGGGTTTCCTTAACCAGTT WT	Het
	A2: ACGCATGGATAAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#27	A1: ACGCATGGATAAAACAAGAAGAA--CGATGAGCATTAGGGTTTCCTTAACCAGTT -2bp	Bia
	A2: ACGCATGGATAAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#29	A1: ACGCATGGATAAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
	A2: ACGCATGGATAAAACAAGAGG---ACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G, -3bp	
TS4#28	A1: ACGCATGGATAAAACAAGAGGGGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
	A2: ACGCATGGATAAAACAAGAAA---ACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G, -3bp	
TS4#04	A1: ACGCATGGATAAAACAAGAAGA-----ATTAGGGTTTCCTTAACCAGTT -11bp	Bia
	A2: ACGCATGGATAAAACAAGAGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#07	A1: ACGCATGGATAAAACAAGAAGA-----ATTAGGGTTTCCTTAACCAGTT -11bp	Bia
	A2: ACGCATGGATAAAACAAGAAGGGGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#09	A1: ACGCATGGATAAAACAAGAAGA-----ATTAGGGTTTCCTTAACCAGTT -11bp	Bia
	A2: ACGCATGGATAAAACAAGAAGAAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#12	A1: ACGCATGGATAAAACAAGAAGG-----ATTAGGGTTTCCTTAACCAGTT A>G, -11bp	Bia
	A2: ACGCATGGATAAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#16	A1: ACGCATGGATAAAACAAGAAGA-----ATTAGGGTTTCCTTAACCAGTT -11bp	Bia
	A2: ACGCATGGATAAAACAAGAAGGGGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#02	A1: ACGCATGGATAAAACAAGAAGG-----ATTAGGGTTTCCTTAACCAGTT -11bp	Bia
	A2: ACGCATGGATAAAACAAGGG---GACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G, -3bp	

ABE8e-EndoV-TS5

ABE8e-Endov	Ref: TAGATCCATCACATCTACTAAGACACGCGCCGCCATGATCGAGGTAATTAAGG	Allelic variation
TS5#01	A1: TAGATCCATCACATCTACTAAGGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	Bia
	A2: TAGATCCATCACATCTACTGAGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	
TS5#04	A1: TAGATCCATCACATCTACTAAGACACGCGCCGCCATGATCGAGGTAATTAAGG WT	Het
	A2: TAGATCCATCACATCTACTGAGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	
TS5#06	A1: TAGATCCATCACATCTGCTAAGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	Bia
	A2: TAGATCCATCACATCTACTGAGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	
TS5#07	A1: TAGATCCATCACATCTACTAAGACACGCGCCGCCATGATCGAGGTAATTAAGG WT	Het
	A2: TAGATCCATCACATCTACTGAGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	
TS5#08	A1: TAGATCCATCACATCTACTGGGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	Hom

	A2: TAGATCCATCACATC	TACTGGGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#12	A1: TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	Bia
	A2: TAGATCCATCACATC	TACTGGGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#15	A1: TAGATCCATCACATC	TACTAAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG WT	Het
	A2: TAGATCCATCACATC	TACTGGGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#16	A1: TAGATCCATCACATC	TACTAAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG WT	Het
	A2: TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#05	A1: TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG	Bia
	A2: TAGATCCATCACATC	TACTGGGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#17	A1: TAGATCCATCACATC	TACTAAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG WT	Het
	A2: TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#18	A1: TAGATCCATCACATC	TACTAAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG WT	Het
	A2: TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#11	A1: TAGATCCATCACATC	TACTAAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG WT	Het
	A2: TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#20	A1: TAGATCCATCACATC	TACTAAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG WT	Het
	A2: TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#24	A1: TAGATCCATCACATC	TACTAAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG WT	Het
	A2: TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#29	A1: TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	Bia
	A2: TAGATCCATCACATC	TACTGAGGCACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#23	A1: TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	Bia
	A2: TAGATCCATCACATC	TACTGGGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#10	A1: TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	Bia
	A2: TAGATCCATCACATC	TACT----CACGCGCCGCCATGA	TCGAGGTAATTAAGG -4bp	
TS5#19	A1: TAGATCCATCACATC	TACT-----CGCGCCGCCATGA	TCGAGGTAATTAAGG -6bp	Bia
	A2: TAGATCCATCACATC	TACTGGGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#13	A1: TAGATCCATCACATC	TACTGGGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	Bia
	A2: TAGATCCATCACATC	TACT-----CCATGA	TCGAGGTAATTAAGG -13bp	
TS5#09	A1: TAGATCCATCACATC	TACTAAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG WT	Het
	A2: TAGATCCATCACATC	TA-----CCATGA	TCGAGGTAATTAAGG -15bp	
TS5#30	A1: TAGATCCATCACATC	TACT-----GAGGTAATTAAGG	-21bp	Bia
	A2: TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	

Table S4. The mutation of ABE8e-hAAG in T₀ rice.**ABE8e-hAAG-TS1**

ABE8e-hAAG	Ref : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT	Allelic variation
TS1#01	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#10	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#13	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#14	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#18	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#19	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#21	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	
TS1#23	A1 : TCCAGTCACTTGTTCCGGCTCAACTTCAGTGGATGTGGGTTTTCGGAGAGCTT WT	Het
	A2 : TCCAGTCACTTGTTCCGGCTCGACTTCAGTGGATGTGGGTTTTCGGAGAGCTT A>G	

Bia, biallelic mutation; Het, heterozygous mutation; Hom, homozygous mutation.

ABE8e-hAAG-TS2

ABE8e-hAAG	Ref : CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC	Allelic variation
TS2#01	A1 : CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC WT	Het
	A2 : CTGATGATCCTTGCAAGGCCGGGTTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#05	A1 : CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC WT	Het
	A2 : CTGATGATCCTTGCAAGGCCGGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#08	A1 : CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC WT	Het
	A2 : CTGATGATCCTTGCAAGGCCGGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#10	A1 : CTGATGATCCTTGCAAGGCCGGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	Bia
	A2 : CTGATGATCCTTGCAAGGCCGGGTTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#13	A1 : CTGATGATCCTTGCAAGGCCGGGTTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	Bia
	A2 : CTGATGATCCTTGCAAGGCCGGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#14	A1 : CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	Bia
	A2 : CTGATGATCCTTGCAAGGCCGGGTTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#16	A1 : CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC WT	Het
	A2 : CTGATGATCCTTGCAAGGCCGGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#18	A1 : CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC WT	Het
	A2 : CTGATGATCCTTGCAAGGCCGGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#19	A1 : CTGATGATCCTTGCAAGGCCGGGTTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	Bia
	A2 : CTGATGATCCTTGCAAGGCCGGAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	
TS2#20	A1 : CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	Bia
	A2 : CTGATGATCCTTGCAAGGCCGGGTTCAGAGACCCTCGGCTCGAAGTTCTCATC A>G	

TS2#23	A1: CTGATGATCCTTGCAAGGCCGAAGTCAGAGACCCCTCGGCTCGAAGTTCTCATC	WT	Het
	A2: CTGATGATCCTTGCAAGGCCGGAGTCAGAGACCCCTCGGCTCGAAGTTCTCATC	A>G	

ABE8e-hAAG-TS3

ABE8e-hAAG	Ref : TCACCAAGAAAAGTAGCGAAAAAGCCGCTACAAACGGCACCGTCTAGAATCCT	Allelic variation
TS3#1	A1 : TCACCAAGAAAAGTAGCGAAAAAGCCGCTACAAACGGCACCGTCTAGAATCCT WT	Het
	A2 : TCACCAAGAAAAGTAGCGGGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#10	A1 : TCACCAAGAAAAGTAGCGAAAAAGCCGCTACAAACGGCACCGTCTAGAATCCT WT	Het
	A2 : TCACCAAGAAAAGTAGCGAGGAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#13	A1 : TCACCAAGAAAAGTAGCGAAAAAGCCGCTACAAACGGCACCGTCTAGAATCCT WT	Het
	A2 : TCACCAAGAAAAGTAGCGAGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#14	A1 : TCACCAAGAAAAGTAGCGAAGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	Bia
	A2 : TCACCAAGAAAAGTAGCGAGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#16	A1 : TCACCAAGAAAAGTAGCGAAGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	Bia
	A2 : TCACCAAGAAAAGTAGCGAGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#18	A1 : TCACCAAGAAAAGTAGCGAAAAAGCCGCTACAAACGGCACCGTCTAGAATCCT WT	Het
	A2 : TCACCAAGAAAAGTAGCGAAGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#19	A1 : TCACCAAGAAAAGTAGCGAGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	Bia
	A2 : TCACCAAGAAAAGTAGCGAAGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#21	A1 : TCACCAAGAAAAGTAGCGAGGGAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	Bia
	A2 : TCACCAAGAAAAGTAGCGGGGAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	
TS3#23	A1 : TCACCAAGAAAAGTAGCGAAAAAGCCGCTACAAACGGCACCGTCTAGAATCCT WT	Het
	A2 : TCACCAAGAAAAGTAGCGAGGAAGCCGCTACAAACGGCACCGTCTAGAATCCT A>G	

ABE8e-hAAG-TS4

ABE8e-hAAG	Ref : ACGCATGGATAAACAAGAAGAAGACGATGAGCATTAGGGTTTCCTTAACCAGTT	Allelic variation
TS4#01	A1 : ACGCATGGATAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Hom
	A2 : ACGCATGGATAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#04	A1 : ACGCATGGATAAACAAGAAGAAGACGATGAGCATTAGGGTTTCCTTAACCAGTT WT	Het
	A2 : ACGCATGGATAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#05	A1 : ACGCATGGATAAACAAGAAGGGGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
	A2 : ACGCATGGATAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#07	A1 : ACGCATGGATAAACAAGAAGAAGACGATGAGCATTAGGGTTTCCTTAACCAGTT WT	Het
	A2 : ACGCATGGATAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#08	A1 : ACGCATGGATAAACAAGAAGGAAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
	A2 : ACGCATGGATAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#10	A1 : ACGCATGGATAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
	A2 : ACGCATGGATAAACAAGAAGGAAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#11	A1 : ACGCATGGATAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
	A2 : ACGCATGGATAAACAAGAAGGGGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#12	A1 : ACGCATGGATAAACAAGAAGAAGACGATGAGCATTAGGGTTTCCTTAACCAGTT WT	Het
	A2 : ACGCATGGATAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#13	A1 : ACGCATGGATAAACAAGAAGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia

	A2 : ACGCATGGATAAAACAAGAGGGGGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	
TS4#14	A1 : ACGCATGGATAAAACAAGGGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G A2 : ACGCATGGATAAAACAAGGGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Hom
TS4#15	A1 : ACGCATGGATAAAACAAGAAGGGGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G A2 : ACGCATGGATAAAACAAGAAGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
TS4#16	A1 : ACGCATGGATAAAACAAGAGGGGGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G A2 : ACGCATGGATAAAACAAGAAGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
TS4#17	A1 : ACGCATGGATAAAACAAGAGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G A2 : ACGCATGGATAAAACAAGAAGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
TS4#19	A1 : ACGCATGGATAAAACAAGAGGGGGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G A2 : ACGCATGGATAAAACAAGAAGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
TS4#20	A1 : ACGCATGGATAAAACAAGAAGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G A2 : ACGCATGGATAAAACAAGAGGAAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
TS4#21	A1 : ACGCATGGATAAAACAAGAGGGGGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G A2 : ACGCATGGATAAAACAAGAAGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
TS4#22	A1 : ACGCATGGATAAAACAAGAGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G A2 : ACGCATGGATAAAACAAGGGGGGGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
TS4#23	A1 : ACGCATGGATAAAACAAGGGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G A2 : ACGCATGGATAAAACAAGAGGGGGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia
TS4#02	A1 : ACGCATGGATAA - - - - - AAGACGATGAGCATTAGGGTTTCCTTAACCAGTT -8bp A2 : ACGCATGGATAAAACAAGAGGGAGACGATGAGCATTAGGGTTTCCTTAACCAGTT A>G	Bia

ABE8e-hAAG-TS5

ABE8e-hAAG	Ref : TAGATCCATCACATCTACTAAGACACGCGCCGCCATGATCGAGGTAATTAAGG	Allelic variation
TS5#01	A1 : TAGATCCATCACATCTACTGAGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G A2 : TAGATCCATCACATCTACTGAGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	Hom
TS5#05	A1 : TAGATCCATCACATCTACTAAGACACGCGCCGCCATGATCGAGGTAATTAAGG WT A2 : TAGATCCATCACATCTACTGAGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	Het
TS5#07	A1 : TAGATCCATCACATCTACTAAGACACGCGCCGCCATGATCGAGGTAATTAAGG WT A2 : TAGATCCATCACATCTACTGGGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	Het
TS5#08	A1 : TAGATCCATCACATCTACTGGGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G A2 : TAGATCCATCACATCTACTGGGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	Hom
TS5#10	A1 : TAGATCCATCACATCTACTGAGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G A2 : TAGATCCATCACATCTACTGGGGACGCGCCGCCATGATCGAGGTAATTAAGG A>G	Bia
TS5#11	A1 : TAGATCCATCACATCTACTAAGACACGCGCCGCCATGATCGAGGTAATTAAGG WT A2 : TAGATCCATCACATCTACTGGGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	Het
TS5#13	A1 : TAGATCCATCACATCTACTGGGGACGCGCCGCCATGATCGAGGTAATTAAGG A>G A2 : TAGATCCATCACATCTACTGAGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	Bia
TS5#14	A1 : TAGATCCATCACATCTACTGAGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G A2 : TAGATCCATCACATCTACTGGGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	Bia
TS5#15	A1 : TAGATCCATCACATCTACTGGGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G A2 : TAGATCCATCACATCTACTGAGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	Bia
TS5#16	A1 : TAGATCCATCACATCTACTGAGACACGCGCCGCCATGATCGAGGTAATTAAGG A>G	Bia

	A2 : TAGATCCATCACATC	TACTGAGGCACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#17	A1 : TAGATCCATCACATC	TACTAAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG WT	Het
	A2 : TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#18	A1 : TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	Bia
	A2 : TAGATCCATCACATC	TACTAGGGCACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#19	A1 : TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	Hom
	A2 : TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#20	A1 : TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	Bia
	A2 : TAGATCCATCACATC	TACTGGGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#21	A1 : TAGATCCATCACATC	TACTAAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG WT	Het
	A2 : TAGATCCATCACATC	TACTAGGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#22	A1 : TAGATCCATCACATC	TACTAGGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	Bia
	A2 : TAGATCCATCACATC	TACTAAGGCACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	
TS5#23	A1 : TAGATCCATCACATC	TACTGAGACACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	Bia
	A2 : TAGATCCATCACATC	TACTGAGGCACGCGCCGCCATGA	TCGAGGTAATTAAGG A>G	

Sequence S1. The sequence of rUNG and hUNG.

>rUNG

ATGGCTCCACCACTTCCACCAACAGCTCCAAAGACGATCGCCGACTACCTCATCAGGCCGTCCAAGAGGCT
TAGGCCAACATCTCCAGCTCCAGCCGCTGCTGCCTCTGCTCCACTCTTCTAGTTGCTCTCCCCGGAACA
AAGGCGCAGGGCCGATACAAATCTCGCCCTCGCCAGAGCTAGACGCCATCTCAGACTTGCCGAGTCTAAG
GCTTCTGGCGGCACAGCCAAGCTCGAGGAACTCCTCGTTGAGGAAACCTGGCTCGAAGCGTTGCCAGGC
GAGCTGCATAAGCCATACGCTCTCGAGCTTTGCCGCTTCGTGGCCCATGAGAGGCTTCATTCTCCGGTGCC
AGTGTACCCACCACCGCACCTCGTTTTTCATGCGCTCCATGCCACACCGTTCGATCGCGTGAAGGCCGTGA
TCATCGGACAGGACCCATATCATGGCCAGGCCAAGCTATGGGCCTCAGCTTTTCTGTGCCAGAGGGCAT
CAAGATCCCGTCCAGCCTCGCGAACATCTTCAAAGAGCTTCAGAAGGACCTCGGCTGCACCGTGCCATCTC
ATGGCAATCTTGAGAGGTGGGCCGTGCAGGGCGTGCTCATGCTCAATACTGTGCTCACCGTGCGCGAGC
ACCAGGCCAATAGCCATGCTAAGAAAGGCTGGGAGCAGTTCACCGACGCCGTCAAGACCATCAGCCT
CAAGAAGTCCGGCATCGTTTTTCATCCTCTGGGGCAACAGCGCCCAGGCTAAGACCAGGCTCATCGACGAG
ACAAAGCACCATCCTCAAGAGCGCCATCCATCTGGCCTTTCTGCTTCCAGAGGCTTCTTCGGCTGCCG
CCACTTCTCCAAGACCAACCAGATTCTCGAGCGCCTCGGCCTCTCTGCCATTGATTGGCAGCTC

>hUNG

ATGTTTGGCGAGTCCTGGAAGAAGCACCTCTCCGGCGAATTCGGCAAGCCGTACTTCATCAAGCTCATGGG
CTTCGTGGCCGAGGAACGCAAGCACTACACAGTGTACCCACCGCCGCACCAGGTGTTACCTGGACACAGA
TGTGCGACATCAAGGACGTGAAGGTGGTGATCCTCGGACAGGACCCATACCACGGACCAAATCAAGCCCAC
GGCCTCTGCTTCTCTGTGCAGAGGCCAGTTCACCAACCACCGAGCCTCGAGAACATCTACAAAGAGCTGTC
CACCGACATCGAGGACTTCGTGCATCCAGGCCATGGCGATCTTTCTGGCTGGGCCAAACAAGGCGTGCTCC
TCCTCAATGCCGTGCTCACAGTTAGGGCCCATCAGGCCAACAGCCACAAAGAAAGAGGCTGGGAGCAGTT
CACCGACGCCGTTGTGTCTTGGCTCAACCAGAACTCCAACGGCCTCGTGTCTTGCTCTGGGGCTCTTACGC
CCAGAAGAAGGGCTCTGCCATCGACCGCAAGAGGCACCATGTGCTCCAAACAGCTCATCCGTCACCGCTCT
CAGTGACAGGGGCTTCTTCGGCTGTGCCACTTCTCCAAGACCAACGAGCTGCTCCAGAAGTCCGGCAAG
AAGCCGATCGACTGGAAAGAGCTT

Sequence S2. The sequence of hAAG and EndoV.

>hAAG

ATGAAGGGCCATCTCACAAGGCTCGGCCTCGAGTTCTTCGATCAACCAGCTGTTTCCTCTCGCCAGGGCCTTCCTCGGCC
AAGTGCTCGTTAGAAGGCTCCCGAATGGCACCGAACTCCGCGGCAGAATCGTTGAGACAGAGGCCTATCTCGGCCCAGA
GGATGAGGCCGCTCATTCTAGAGGCGGCAGACAGACACCTCGCAACCGCGGCATGTTTATGAAGCCGGGCACGCTCTAC
GTGTACATTATCTACGGCATGTATTTCTGCATGAACATCTCCAGCCAAGGCGACGGCGCTTGCGTTCTCCTTAGAGCCC
TTGAGCCACTCGAGGGCCTCGAAACCATGAGGCATGTGAGGTCCCAGCTGAGGAAGGGCACAGCTTCTAGGGTGCTCAA
GGATCGCGAGTTGTGCAGCGGACCGTCCAAGCTCTGTCAAGCCCTCGCCATCAACAAGTCCTTCGACCAGAGAGATCTC
GCCCAGGACGAGGCTGTTTGGCTTGAAAGAGGCCCCACTCGAGCCATCTGAGCCAGCCGTTGTTGCTGCTGCTAGAGTTG
GCGTTGGCCATGCTGGCGAATGGGCTAGAAAGCCGCTCCGCTTCTATGTGAGAGGCTCCCCATGGGTGTCAGTGGTGGA
TAGAGTGGCCGAGCAAGA

> EndoV

ATGGATCTCGCTTCTCTCAGGGCCCAGCAGATCGAGCTTGCCCTTCTGTGATCCGCGAGGACAGGCTCGATAAGGACC
CGCCGGATCTTATTGCCGGCGCTGATGTTGGCTTTGAGCAAGGCGGCGAGGTTACAAGAGCCGCCATGGTGCTCCTCAA
GTACCCATCTCTCGAGCTGGTCGAGTACAAGGTGGCCAGGATCGCCACCACCATGCCGTATATTCAGGCTTCCTCAGC
TTCCGCGAGTACCCTGCACTTCTCGCTGCTTGGGAGATGCTCAGCCAAAAGCCGGACCTCGTGTTCTGTTGATGGCCACG
GCATTTCTCATCCAAGAAGGCTCGGCGTCGCCAGCCATTTCCGGCCTTCTCGTGATGTTCCAACCATCGGCGTGGCCAA
GAAGAGGCTCTGCGGCAAGTTTGAGCCACTCTCTTCAGAGCCAGGCGCTCTCGCTCCGCTTATGGATAAGGGCGAGCAA
CTCGCCTGGGTGTGGCGTTCTAAGGCCAGGTGCAACCCGCTCTTTATCGCCACAGGCCATAGGGTGTCAGTGGATTCTG
CCCTCGCTTGGGTGCAGAGATGCATGAAGGGCTACAGACTCCCAGAGCCAACCATGGGCCGATGCTGTTGCTTCTGA
GAGGCCAGCCTTCGTGAGGTACACCGCCAATCAGCCA