

Supplemental Information

Improving adenine base editing efficiency in rice by simplifying base editors

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28 **Supplemental sequence** The DNA sequences of key components in the different
29 adenine base editors.

30 **Wild type *ecTadA*-32aa linker**

31 ATGTCCGAAGTCGAGTTTTCCCATGAGTACTGGATGAGACACGCATTGACT
32 CTCGCAAAGAGGGCTTGGGATGAACGCGAGGTGCCCGTGGGGGCAGTACT
33 CGTGCAACAATCGCGTAATCGGCCAAGGTTGGAATAGGCCGATCGGACG
34 CCACGACCCCACTGCACATGCGGAAATCATGGCCCTTCGACAGGGAGGGC
35 TTGTGATGCAGAATTATCGACTTATCGATGCGACGCTGTACGTCACGCTTGA
36 ACCTTGCGTAATGTGCGCGGGAGCTATGATTCACTCCCGCATTGGACGAGT
37 TGTATTCGGTGCCCGCAGCCAAGACGGGTGCCGCAGGTTCACTGATGG
38 ACGTGCTGCATCACCCAGGCATGAACCACCGGGTAGAAATCACAGAAGGC
39 ATATTGGCGGACGAATGTGCGGCGCTGTTGTCCGACTTTTTTCGCATGCGG
40 AGGCAGGAGATCAAGGCCAGAAAAAAGCACAATCCTCTACTGACTCTGG
41 AGGGTCCTCCGGCGGATCGTCCGGCAGCGAGACGCCAGGCACCTCCGAGA
42 GCGCTACGCCTGAATCCTCTGGAGGGTCCTCCGGCGGATCG

43 ***ecTadA**7.10-32aa linker**

44 ATGTCCGAAGTCGAGTTTTCCCATGAGTACTGGATGAGACACGCATTGACT
45 CTCGCAAAGAGGGCTCGGGATGAACGCGAGGTGCCCGTGGGGGCAGTACT
46 CGTGCTTAACAATCGCGTAATCGGCCAAGGTTGGAATAGGGCGATCGGACT
47 CCACGACCCCACTGCACATGCGGAAATCATGGCCCTTCGACAGGGAGGGC
48 TTGTGATGCAGAATTATCGACTTATCGATGCGACGCTGTACGTCACGTTTGA
49 ACCTTGCGTAATGTGCGCGGGAGCTATGATTCACTCCCGCATTGGACGAGT
50 TGTATTCGGTGTCGCAACGCCAAGACGGGTGCCGCAGGTTCACTGATGGA
51 CGTGCTGCATTACCCAGGCATGAACCACCGGGTAGAAATCACAGAAGGCAT
52 ATTGGCGGACGAATGTGCGGCGCTGTTGTGCTACTTTTTTCGCATGCCGAG
53 GCAAGTGTTCAATGCCAGAAAAAAGCACAATCCTCTACTGACTCTGGAG
54 GGTCCCTCCGGCGGATCGTCCGGCAGCGAGACGCCAGGCACCTCCGAGAGC
55 GCTACGCCTGAATCCTCTGGAGGGTCCTCCGGCGGATCG

56 **nSpCas9 (D10A)-NLS**

57 GACAAGAAGTACAGCATCGGCCTGGCCATCGGCACCAACTCTGTGGGCTGGGCC
58 GTGATCACCGACGAGTACAAGGTGCCAGCAAGAAATTCAAGGTGCTGGGCAAC
59 ACCGACCGGCACAGCATCAAGAAGAACCCTGATCGGAGCCCTGCTGTTTCGACAGC
60 GCGGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACAC
61 CAGACGGAAGAACC GGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGC
62 CAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCCTGGTGGAAAG
63 GGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGACGAGGTGGC
64 CTACCACGAGAAGTACCCACCATCTACCACCTGAGAAAGAACTGGTGGACAG
65 CACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCACATGATCAA
66 GTTCCGGGGCCACTTCCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGT
67 GGACAAGCTGTTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTTCGAGGAAAA
68 CCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAG
69 CAAGAGCAGACGGCTGGAATAATCTGATCGCCAGCTGCCCGGCGAGAAGAAGAA
70 TGGCCTGTTTCGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCAACTTCAA

71 GAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTA
72 CGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCT
73 GTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAG
74 AGTGAACACCGAGATCACCAAGGCCCCCTGAGCGCCTCTATGATCAAGAGATAC
75 GACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTG
76 CCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGC
77 TACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCC
78 TGAAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGAC
79 CTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCACCAGATCCAC
80 CTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTACCCATTCTTG
81 AAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTAC
82 GTGGGCCCTCTGGCCAGGGGAAAACAGCAGATTTCGCTGGATGACCAGAAAAGAGC
83 GAGGAAACCATCACCCCTGGAACCTTCGAGGAAAGTGGTGGACAAGGGCGCTTCC
84 GCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAG
85 AAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGC
86 TGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAAGCCCGCCTTCTGAGCG
87 GCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAAGTGA
88 CCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCG
89 TGAAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATAACCAG
90 ATCTGCTGAAAATTATCAAGGACAAGGACTTCTGGACAATGAGGAAAACGAGG
91 ACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGAT
92 CGAGGAACGGCTGAAAACCTATGCCACCTGTTTCGACGACAAAAGTGATGAAGCA
93 GCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCA
94 ACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCTGAAAGTCCG
95 ACGGCTTCGCCAACAGAACTTCATGCAGCTGATCCACGACGACAGCCTGACCT
96 TTAAAGAGGACATCCAGAAAAGCCAGGTGTCCGGCCAGGGCGATAGCCTGCACG
97 AGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGA
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99 AACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCAGAAGGGACAGAAG
100 AACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAG
101 CCAGATCCTGAAAGAACACCCCGTGGA AAAACACCCAGCTGCAGAACGAGAAGCT
102 GTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGAC
103 ATCAACCGGCTGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGA
104 AGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGC
105 AAGAGCGACAACGTGCCCTCCGAAGAGGTCTGTAAGAAGATGAAGA ACTACTGG
106 CGGCAGCTGCTGAACGCCAAGCTGATTACCAGAGAAAAGTTCGACAATCTGACC
107 AAGGCCGAGAGAGGCGGCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAG
108 ACAGCTGGTGGAAAACCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTC
109 CCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGT
110 GATCACCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTAC
111 AAAGTGCGCGAGATCAACA ACTACCACCGCCACGACGCCTACCTGAACGCC
112 GTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAAGCGAGTTCGTG
113 TACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAG
114 GAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTT

115 TCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCG
116 AGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCA
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118 TGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCAAGAGGAACAGCGATA
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120 GCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAAGTGGAAAAGGGCAAGT
121 CCAAGAAACTGAAGAGTGTGAAAAGAGCTGCTGGGGATCACCATCATGGAAAGAA
122 GCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAAGAAG
123 TGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTTCGAGCTGGAAAA
124 CGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAAC
125 TGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAA
126 GCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCA
127 CAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCCTCCAAGAGAGT
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133 TCCGGCGGCAGCGCTTCTCCAAAGCGTCCGCGTGACCGTCACGATGGAGAATTGGGTG
134 GACGCAAACGTGCAAGAGGTTAA

135 nSaCas9 (D10A)-NLS

136 AAGCGAACTACATCCTGGGCCTGGCCATCGGCATCACCAGCGTGGGCTACGGC
137 ATCATCGACTACGAGACACGGGACGTGATCGATGCCGGCGTGCGGCTGTTCAA
138 GAGGCCAACGTGGAAAACAACGAGGGCAGGCGGAGCAAGAGAGGCGCCAGAAG
139 GCTGAAGCGGCGGAGGGCGGCATAGAATCCAGAGAGTGAAGAAGCTGCTGTTTCA
140 CTACAACCTGCTGACCGACCACAGCGAGCTGAGCGGCATCAACCCCTACGAGGC
141 CAGAGTGAAGGGCCTGAGCCAGAAGCTGAGCGAGGAAGAGTTCTCTGCCGCC
142 TGCTGCACCTGGCCAAGAGAAGAGGCGTGCAACAGTGAACGAGGTGGAAGAG
143 GACACCGGCAACGAGCTGTCCACCAAAGAGCAGATCAGCCGGAACAGCAAGGC
144 CCTGGAAGAGAAATACGTGGCCGAACTGCAGCTGGAACGGCTGAAGAAAGACG
145 GCGAAGTGCGGGGCAGCATCAACAGATTCAAGACCAGCGACTACGTGAAAGAAG
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148 GCGAGGGCAGCCCCTTCGGCTGGAAGGACATCAAAGAATGGTACGAGATGCTGA
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150 ACGCCGACCTGTACAACGCCCTGAACGACCTGAAACAATCTCGTGATCACCAGGG
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153 CGAAGAGGATATTAAGGGCTACAGAGTGACCAGCACCGGCAAGCCCAGTTTAC
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155 GAGAACGCCGAGCTGCTGGATCAGATTGCCAAGATCCTGACCATCTACCAGAGC
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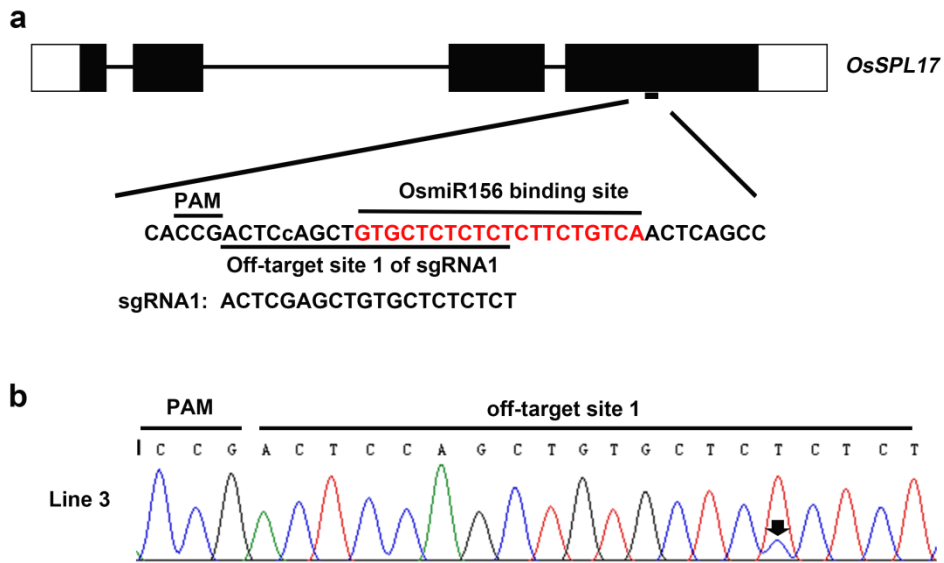
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160 AGAAAGAGATCCCCACCACCCTGGTGGACGACTTCATCCTGAGCCCCGTCGTGA
161 AGAGAAGCTTCATCCAGAGCATCAAAGTGATCAACGCCATCATCAAGAAGTACGG
162 CCTGCCCAACGACATCATTATCGAGCTGGCCCGCGAGAAGAACTCCAAGGACGC
163 CCAGAAAATGATCAACGAGATGCAGAAGCGGAACCGGCAGACCAACGAGCGGAT
164 CGAGGAAATCATCCGGACCACCGGCAAAGAGAACGCCAAGTACCTGATCGAGAA
165 GATCAAGCTGCACGACATGCAGGAAGGCAAGTGCCTGTACAGCCTGGAAGCCAT
166 CCCTCTGGAAGATCTGCTGAACAACCCCTTCAACTATGAGGTGGACCACATCATC
167 CCCAGAAGCGTGTCTTCGACAACAGCTTCAACAACAAGGTGCTCGTGAAGCAG
168 GAAGAAAACAGCAAGAAGGGCAACCGGACCCCATTCCAGTACCTGAGCAGCAGC
169 GACAGCAAGATCAGCTACGAAACCTTCAAGAAGCACATCCTGAATCTGGCCAAG
170 GGCAAGGGCAGAATCAGCAAGACCAAGAAAGAGTATCTGCTGGAAGAACGGGAC
171 ATCAACAGGTTCTCCGTGCAGAAAAGACTTCATCAACCGGAACCTGGTGGATACCA
172 GATACGCCACCAGAGGCCTGATGAACCTGCTGCGGAGCTACTTCAGAGTGAACA
173 ACCTGGACGTGAAAGTGAAGTCCATCAATGGCGGCTTCACCAGCTTTCTGCGGC
174 GGAAGTGGAAAGTTAAGAAAAGAGCGGAACAAGGGGTACAAGCACCACGCCGAG
175 GACGCCCTGATCATTGCCAACGCCGATTTTCATCTTCAAAGAGTGGAAGAACTGG
176 ACAAGGCCAAAAAAGTGATGGAAAACCAGATGTTTCGAGGAAAAGCAGGCCGAGA
177 GCATGCCCCGAGATCGAAACCGAGCAGGAGTACAAAGAGATCTTCATCACCCCC
178 ACCAGATCAAGCACATTAAGGACTTCAAGGACTACAAGTACAGCCACCGGGTGG
179 ACAAGAAGCCTAATAGAGAGCTGATTAACGACACCCTGTACTCCACCCGGAAGGA
180 CGACAAGGGCAACACCCTGATCGTGAACAATCTGAACGGCCTGTACGACAAGGA
181 CAATGACAAGCTGAAAAAGCTGATCAACAAGAGCCCCGAAAAGCTGCTGATGTA
182 CCACCACGACCCCCAGACCTACCAGAACTGAAGCTGATTATGGAACAGTACGG
183 CGACGAGAAGAATCCCCTGTACAAGTACTACGAGGAAACCGGGAACCTACCTGAC
184 CAAGTACTCCAAAAAGGACAACGGCCCCGTGATCAAGAAGATTAAGTATTACGGC
185 AACAACTGAACGCCATCTGGACATCACCGACGACTACCCCAACAGCAGAAAC
186 AAGGTCGTGAAGCTGTCCCTGAAGCCCTACAGATTCGACGTGTACCTGGACAAT
187 GGCGTGTACAAGTTCGTGACCGTGAAGAATCTGGATGTGATCAAAAAAGAAAAC
188 ACTACGAAGTGAATAGCAAGTGCTATGAGGAAGCTAAGAAGCTGAAGAAGATCA
189 GCAACCAGGCCGAGTTTATCGCCTCCTTCTACAACAACGATCTGATCAAGATCAA
190 CGGCGAGCTGTATAGAGTGATCGGCGTGAACAACGACCTGCTGAACCGGATCGA
191 AGTGAACATGATCGACATCACCTACCGCGAGTACCTGGAAAACATGAACGACAAG
192 AGGCCCCCCAGGATCATTAAAGACAATCGCCTCCAAGACCCAGAGCATTAAAGAAGT
193 ACAGCACAGACATTCTGGGCAACCTGTATGAAGTGAAATCTAAGAAGCACCCCTCA
194 GATCATCAAAAAGGGACTAGTTCCGGCGGCAGCGCTTCTCCAAAGCGTCCGCGTGAC
195 CGTCACGATGGAGAATTGGGTGGACGCAAACGTGCAAGAGGTTAA

196 nSaKKH-Cas9 (D10A)-NLS

197 AAGCGGAACATACCTGGGCCTGGCCATCGGCATCACCGCGTGGGCTACGGC
198 ATCATCGACTACGAGACACGGGACGTGATCGATGCCGGCGTGCGGCTGTTCAA
199 GAGGCCAACGTGGAAAACAACGAGGGCAGGCGGAGCAAGAGAGGCGCCAGAAG
200 GCTGAAGCGGCGGAGGCGGCATAGAATCCAGAGAGTGAAGAAGCTGCTGTTTCA
201 CTACAACCTGCTGACCGACCACAGCGAGCTGAGCGGCATCAACCCTACGAGGC
202 CAGAGTGAAGGGCCTGAGCCAGAAGCTGAGCGAGGAAGAGTTCTCTGCCGCC

203 TGCTGCACCTGGCCAAGAGAAGAGGCGTGCACAACGTGAACGAGGTGGAAGAG
204 GACACCGGCAACGAGCTGTCCACCAAAGAGCAGATCAGCCGGAACAGCAAGGC
205 CCTGGAAGAGAAATACGTGGCCGAACCTGCAGCTGGAACGGCTGAAGAAAGACG
206 GCGAAGTGCGGGGCAGCATCAACAGATTCAAGACCAGCGACTACGTGAAAGAAG
207 CCAAACAGCTGCTGAAGGTGCAGAAGGCCTACCACCAGCTGGACCAGAGCTTCA
208 TCGACACCTACATCGACCTGCTGGAAAACCCGGCGGACCTACTATGAGGGACCTG
209 GCGAGGGCAGCCCCTTCGGCTGGAAGGACATCAAAGAATGGTACGAGATGCTGA
210 TGGGCCACTGCACCTACTTCCCCGAGGAACTGCGGAGCGTGAAGTACGCCTACA
211 ACGCCGACCTGTACAACGCCCTGAACGACCTGAACAATCTCGTGATCACCAGGG
212 ACGAGAACGAGAAGCTGGAATATTACGAGAAGTTCCAGATCATCGAGAACGTGTT
213 CAAGCAGAAGAAGAAGCCACCCTGAAGCAGATCGCCAAAAGAAATCCTCGTGAA
214 CGAAGAGGATATTAAGGGCTACAGAGTGACCAGCACCGGCAAGCCCGAGTTCAC
215 CAACCTGAAGGTGTACCACGACATCAAGGACATTACCGCCCGGAAAGAGATTATT
216 GAGAACGCCGAGCTGCTGGATCAGATTGCCAAGATCCTGACCATCTACCAGAGC
217 AGCGAGGACATCCAGGAAGAAGTACCAATCTGAACTCCGAGCTGACCCAGGAA
218 GAGATCGAGCAGATCTCTAATCTGAAGGGCTATACCGGCACCCACAACCTGAGCC
219 TGAAGGCCATCAACCTGATCCTGGACGAGCTGTGGCACACCAACGACAACCAGA
220 TCGCTATCTTCAACCGGCTGAAGCTGGTGCCCAAGAAGGTGGACCTGTCCCAGC
221 AGAAAGAGATCCCCACCACCCTGGTGGACGACTTCATCCTGAGCCCCGTCGTGA
222 AGAGAAGCTTCATCCAGAGCATCAAAGTGATCAACGCCATCATCAAGAAGTACGG
223 CCTGCCCAACGACATCATTATCGAGCTGGCCCGCGAGAAGAAGTCCAAGGACGC
224 CCAGAAAATGATCAACGAGATGCAGAAGCGGAACCGGCAGACCAACGAGCGGAT
225 CGAGGAAATCATCCGGACCACCGGCAAAGAGAACGCCAAGTACCTGATCGAGAA
226 GATCAAGCTGCACGACATGCAGGAAGGCAAGTGCCTGTACAGCCTGGAAGCCAT
227 CCCTCTGGAAGATCTGCTGAACAACCCCTTCAACTATGAGGTGGACCACATCATC
228 CCCAGAAGCGTGTCTTCGACAACAGCTTCAACAACAAGGTGCTCGTGAAGCAG
229 GAAGAAAACAGCAAGAAGGGCAACCGGACCCCATTCCAGTACCTGAGCAGCAGC
230 GACAGCAAGATCAGCTACGAAACCTTCAAGAAGCACATCCTGAATCTGGCCAAG
231 GGCAAGGGCAGAATCAGCAAGACCAAGAAAAGAGTATCTGCTGGAAGAACGGGAC
232 ATCAACAGGTTCTCCGTGCAGAAAAGACTTCATCAACCGGAACCTGGTGGATACCA
233 GATACGCCACCAGAGGCCTGATGAACCTGCTGCGGAGCTACTTCAGAGTGAACA
234 ACCTGGACGTGAAAGTGAAGTCCATCAATGGCGGCTTCACCAGCTTTCTGCGGC
235 GGAAGTGAAGTTTAAAGAAAAGAGCGGAACAAGGGGTACAAGCACCACGCCGAG
236 GACGCCCTGATCATTGCCAACGCCGATTTTCATCTTCAAAGAGTGGAAGAAACTGG
237 ACAAGGCCAAAAAAGTGATGGAAAACCAAGATGTTTCGAGGAAAAGCAGGCCGAGA
238 GCATGCCCCGAGATCGAAACCGAGCAGGAGTACAAAGAGATCTTCATCACCCCCC
239 ACCAGATCAAGCACATTAAGGACTTCAAGGACTACAAGTACAGCCACCGGGTGG
240 ACAAGAAGCCTAATAGAAAAGCTGATTAACGACACCCTGTACTCCACCCGGAAGGA
241 CGACAAGGGCAACACCCTGATCGTGAACAATCTGAACGGCCTGTACGACAAGGA
242 CAATGACAAGCTGAAAAAGCTGATCAACAAGAGCCCCGAAAAGCTGCTGATGTA
243 CCACCACGACCCCGAGACCTACCAGAACTGAAGCTGATTATGGAACAGTACGG
244 CGACGAGAAGAATCCCCTGTACAAGTACTACGAGGAAACCGGGAACCTACCTGAC
245 CAAGTACTCCAAAAGGACAACGGCCCCGTGATCAAGAAGATTAAGTATTACGGC
246 AACAACTGAACGCCATCTGGACATCACCGACGACTACCCCAACAGCAGAAAC

247 AAGGTCGTGAAGCTGTCCCTGAAGCCCTACAGATTCGACGTGTACCTGGACAAT
248 GGCGTGTACAAGTTCGTGACCGTGAAGAATCTGGATGTGATCAAAAAAGAAAAT
249 ACTACGAAGTGAATAGCAAGTGCTATGAGGAAGCTAAGAAGCTGAAGAAGATCA
250 GCAACCAGGCCGAGTTTATCGCCTCCTTCTACAAGAACGATCTGATCAAGATCAA
251 CGGCGAGCTGTATAGAGTGATCGGCGTGAACAACGACCTGCTGAACCGGATCGA
252 AGTGAACATGATCGACATCACCTACCGCGAGTACCTGGAAAACATGAACGACAAG
253 AGGCCCCCCCACATCATTAAAGACAATCGCCTCCAAGACCCAGAGCATTAAAGAAGT
254 ACAGCACAGACATTCTGGGCAACCTGTATGAAGTGAAATCTAAGAAGCACCCCTCA
255 GATCATCAAAAAGGGACTAGTTCCGGCGGCAGCGCTTCTCCAAAGCGTCCGCGTGAC
256 CGTCACGATGGAGAATTGGGTGGACGCAAACGTGCAAGAGGTTAA
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281 **Supplemental Figure 1.** Off-target editing at *OsSPL17* by ABE-P1S. **a**, Schematic

282 view of the potential off-target site 1 of sgRNA1 in *OsSPL17*. The mismatch base in

283 *OsSPL17* is shown in lowercase. The OsmiR156 binding site in *OsSPL17* is highlighted

284 in red. **b**, Sequencing chromatogram of Line 3 at the potential off-target site 1 in

285 *OsSPL17*. Arrow points to the position with an edited base.

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302 **Supplemental Table 1** The base editing windows of ABE-P1 and ABE-P1S at
 303 different target sites.

sgRNA	Target gene	Base editor	Genotype of mutations	Base editing positions
sgRNA1	<i>OsSPL14</i>	ABE-P1	T ₅ -C ₅ (6), T ₁₀ -C ₁₀ (4), T ₅ T ₇ -C ₅ C ₇ (6), T ₅ T ₁₀ -C ₅ C ₁₀ (2)	5, 7, 10
		ABE-P1S	T ₇ -C ₇ (1), T ₅ T ₇ -C ₅ C ₇ (3), T ₅ -T ₁₀ (1), T ₁ T ₅ T ₇ -C ₁ C ₅ C ₇ (1), T ₅ T ₇ T ₁₀ -C ₅ C ₇ C ₁₀ (4), T ₅ T ₇ T ₁₀ T ₁₂ -C ₅ C ₇ C ₁₀ C ₁₂ (1), T ₃ T ₅ T ₇ T ₁₀ T ₁₂ -C ₃ C ₅ C ₇ C ₁₀ C ₁₂ (1)	1, 3, 5, 7, 10, 12
sgRNA2	<i>SLR1</i>	ABE-P1	T ₆ -C ₆ (7)	6
		ABE-P1S	T ₆ -C ₆ (7)	6
sgRNA3	<i>OsSERK2</i>	ABE-P1	T ₆ -C ₆ (21), T ₆ T ₈ -C ₆ C ₈ (5)	6, 8
		ABE-P1S	T ₆ -C ₆ (11), T ₆ T ₈ -C ₆ C ₈ (10)	6, 8
sgRNA4	<i>Tms9-1</i>	ABE-P1	T ₅ -C ₅ (1)	5
		ABE-P1S	T ₅ -C ₅ (4)	5
sgRNA5	<i>OsNRT1.1B</i>	ABE-P1	A ₄ -G ₄ (1), A ₆ -G ₆ (2), A ₈ -G ₈ (6), A ₄ A ₆ -G ₄ G ₆ (1), A ₆ A ₈ -G ₆ G ₈ (1), A ₄ A ₆ A ₈ -G ₄ G ₆ G ₈ (15), A ₄ A ₆ A ₈ A ₁₂ -G ₄ G ₆ G ₈ G ₁₂ (1)	4, 6, 8, 12
		ABE-P1S	A ₆ -G ₆ (4), A ₈ -G ₈ (2), A ₄ A ₆ -G ₄ G ₆ (1), A ₄ A ₈ -G ₄ G ₈ (3), A ₆ A ₈ -G ₆ G ₈ (9), A ₄ A ₆ A ₈ -G ₄ G ₆ G ₈ (32), A ₄ A ₆ A ₈ A ₁₂ -G ₄ G ₆ G ₈ C ₁₂ (1)	4, 6, 8, 12
sgRNA6	<i>OsACC1</i>	ABE-P1	T ₁ -C ₄ (6), T ₇ -C ₇ (5), T ₁ T ₇ -C ₄ C ₇ (14)	4, 7
		ABE-P1S	T ₄ -C ₄ (1), T ₇ -C ₇ (20), T ₂ T ₇ -C ₂ C ₇ (1), T ₄ T ₇ -C ₄ C ₇ (9)	2, 4, 7
sgRNA7	<i>OsDEP1</i>	ABE-P1	A ₅ -G ₅ (1), A ₆ -G ₆ (1), A ₅ A ₆ -G ₅ G ₆ (30), A ₃ A ₅ A ₆ -G ₃ G ₅ G ₆ (8)	3, 5, 6
		ABE-P1S	A ₅ A ₆ -G ₅ G ₆ (21), A ₃ A ₅ A ₆ -G ₃ G ₅ G ₆ (4)	3, 5, 6

304 Note: For the base editors ABE-P1 and ABE-P1S, the base editing position was
 305 counted from the PAM-distal end, scoring the PAM sequence as positions 21-23.

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323 **Supplemental Table 2** The base editing windows of ABE-P2, ABE-P2S, ABE-P5 and
 324 ABE-P5S at different target sites.

sgRNA	Target gene	Base editor	Genotype of mutations	Base editing positions
sgRNA8	<i>SPX-MSF2</i>	ABE-P2	T ₁ -C ₁ (1), T ₉ -C ₉ (2), T ₁₅ -C ₁₅ (1)	1, 9, 15
		ABE-P2S	T ₃ -C ₃ (1), T ₆ -C ₆ (1), T ₉ -C ₉ (3), T ₁₅ -C ₁₅ (1), T ₉ T ₁₂ -C ₉ C ₁₂ (1)	3, 6, 9, 12, 15
sgRNA9	<i>OsSPL14</i>	ABE-P2	T ₆ -C ₆ (1), T ₁₀ -C ₁₀ (3), T ₆ T ₁₀ -C ₆ C ₁₀ (2), T ₈ T ₁₀ -C ₈ C ₁₀ (3), T ₆ T ₈ T ₁₀ -C ₆ C ₈ C ₁₀ (1), T ₁₀ T ₁₄ -C ₁₀ C ₁₄ (1)	6, 8, 10, 14
		<i>OsSPL17</i>	ABE-P2	T ₈ -C ₈ (2), T ₁₂ -C ₁₂ (2), T ₈ T ₁₀ -C ₈ C ₁₀ (3), T ₆ T ₁₀ T ₁₂ -C ₆ C ₁₀ C ₁₂ (3), T ₈ T ₁₀ T ₁₂ -C ₈ C ₁₀ C ₁₂ (2), T ₈ T ₁₀ T ₁₂ T ₁₄ -C ₈ C ₁₀ C ₁₂ C ₁₄ (1)
	<i>OsSPL14</i>	ABE-P2S	T ₈ -C ₈ (1), T ₁₀ -C ₁₀ (6), T ₁₂ -C ₁₂ (4), T ₁₄ -C ₁₄ (1), T ₈ T ₁₀ -C ₈ C ₁₀ (1), T ₈ T ₁₂ -C ₈ C ₁₂ (1), T ₈ T ₁₄ -C ₈ C ₁₄ (2), T ₁₀ T ₁₄ -C ₁₀ C ₁₄ (1), T ₁₂ T ₁₄ -C ₁₂ C ₁₄ (1), T ₈ T ₁₂ T ₁₄ -C ₈ C ₁₂ C ₁₄ (1), T ₆ T ₁₂ T ₁₇ -C ₆ C ₁₂ C ₁₇ (1)	6, 8, 10, 12, 14, 17
	<i>OsSPL17</i>	ABE-P2S	T ₈ -C ₈ (2), T ₁₀ -C ₁₀ (7), T ₁₂ -C ₁₂ (2), T ₈ T ₁₀ -C ₈ C ₁₀ (4), T ₈ T ₁₂ -C ₈ C ₁₂ (1), T ₁₀ T ₁₂ -C ₁₀ C ₁₂ (1), T ₁₀ T ₁₄ -C ₁₀ C ₁₄ (2), T ₈ T ₁₀ T ₁₂ -C ₈ C ₁₀ C ₁₂ (2), T ₁₀ T ₁₂ T ₁₄ -C ₁₀ C ₁₂ C ₁₄ (1)	8, 10, 12, 14
	<i>OsSPL16</i>	ABE-P2S	T ₁₀ -C ₁₀ (4), T ₁₂ -C ₁₂ (1), T ₁₄ -C ₁₄ (2), T ₆ T ₈ -C ₆ C ₈ (1), T ₁₀ T ₁₂ -C ₁₀ C ₁₂ (1), T ₁₂ T ₁₄ -C ₁₂ C ₁₄ (1)	6, 8, 10, 12, 14
sgRNA10	<i>OsSPL18</i>	ABE-P2S	T ₁₀ -C ₁₀ (2), T ₁₂ -C ₁₂ (2), T ₁₄ -C ₁₄ (2), T ₁₇ -C ₁₇ (1), T ₈ T ₁₂ -C ₈ C ₁₂ (1), T ₁₀ T ₁₂ -C ₁₀ C ₁₂ (3), T ₁₀ T ₁₄ -C ₁₀ C ₁₄ (2), T ₁₀ T ₁₂ T ₁₄ -C ₁₀ C ₁₂ C ₁₄ (1)	8, 10, 12, 14, 17
		<i>OsSPL13</i>	ABE-P5	T ₁₁ -C ₁₁ (1)
sgRNA11	<i>OsSPL13</i>	ABE-P5S	T ₉ -C ₉ (1), T ₇ -C ₇ (1)	7, 9
		sgRNA12	<i>SNB</i>	ABE-P5
ABE-P5S	A ₄ -G ₄ (1), A ₈ -G ₈ (2), A ₉ -G ₉ (18)			4, 8, 9

325 Note: For the base editors ABE-P2, ABE-P2S, ABE-P5 and ABE-P5S, the base editing
 326 position was counted from the PAM-distal end, scoring the PAM sequence as positions
 327 22-27.

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343 **Supplemental Table 3** The base editing frequencies of ABE-P1 and ABE-P1S at
 344 potential off-target sites of sgRNA1.

Site	Chr	Position	Guide-PAM sequence	Base editor	Mismatch numbers	Number of genotyped lines	Number of edited lines	Editing efficiency
On target	8	25275163	AGAGAGAGCACAGCTCGAGTCGG	ABE-P1	0	48	18	37.5%
				ABE-P1S	0	17	12	70.6%
Off-target 1	9	18918918	AGAGAGAGCACAGCTgGAGTCGG	ABE-P1	1	8	0	0
				ABE-P1S	1	8	1	12.5%
Off-target 2	1	24179644	tGAtcGgGCACAGCTCGcGTCGG	ABE-P1	5	8	0	0
				ABE-P1S	5	8	0	0
Off-target 3	3	36137080	AGAaAGAGCAtgGgTCGAGTCGG	ABE-P1	4	8	0	0
				ABE-P1S	4	8	0	0
Off-target 4	3	8596704	AGAGtGAGCACAGCggGAGaCGG	ABE-P1	4	8	0	0
				ABE-P1S	4	8	0	0
Off-target 5	4	23025825	gGAGAGcGCgCgGCTCGAGgCGG	ABE-P1	5	8	0	0
				ABE-P1S	5	8	0	0
Off-target 6	5	10284901	AGAGtGtGCAgAGtTCGAGTCGG	ABE-P1	4	8	0	0
				ABE-P1S	4	8	0	0
Off-target 7	7	19030423	AGAGAGAGCtCgGCTCGgcTCGG	ABE-P1	4	8	0	0
				ABE-P1S	4	8	0	0
Off-target 8	10	1012640	AGAGAGAtCtCAGaTCGAGgCGG	ABE-P1	4	8	0	0
				ABE-P1S	4	8	0	0
Off-target 9	7	20804240	AGAcAGAGCACAGCaaGAaTCGG	ABE-P1	4	8	0	0
				ABE-P1S	4	8	0	0

345 Note: Nucleotides of PAM sequence are written in bold, and the mismatch bases in
 346 potential off-targets are shown in lowercase.

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359 **Supplemental Table 4** The base editing frequencies of ABE-P1 and ABE-P1S at
 360 potential off-target sites of sgRNA6.

Site	Chr	Position	Guide-PAM sequence	Base editor	Mismatch numbers	Number of genotyped lines	Number of edited lines	Editing efficiency
On target	5	13065463	CCCAGACCGCATTGAGTGTATG	ABE-P1	0	36	25	69.4%
				ABE-P1S	0	42	31	73.8%
Off-target 1	8	22061977	CATAGCACTCAActCaGT TGGG	ABE-P1	4	8	0	0
				ABE-P1S	4	8	0	0
Off-target 2	5	17365477	aATAGCACTCA TGaGaTCTTGG	ABE-P1	4	8	0	0
				ABE-P1S	4	8	0	0
Off-target 3	3	26476439	CATAGCACT lAATGtGGgCgGAG	ABE-P1	4	8	0	0
				ABE-P1S	4	8	0	0

361 Note: Nucleotides of PAM sequence are written in bold, and the mismatch bases in
 362 potential off-targets are shown in lowercase.

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364 **Supplemental Table 5** The base editing frequencies of ABE-P2S at potential off-target
 365 sites of sgRNA9.

Site	Chr	Position	Guide-PAM sequence	Mismatch numbers	Number of genotyped lines	Number of edited lines	Editing efficiency
On target 1	8	25275156	ACAGAAGAGAGAGAGCACAG CTCGAGT	0	36	20	55.6%
On target 2	9	18918911	ACAGAAGAGAGAGAGCACAG CTGGAGT	0	36	22	61.1%
Off-target 1	9	19647839	ACAGAAGAGAGAGAGCACAct CGGAGT	2	8	0	0
Off-target 2	11	17631827	ACAGAAGAGAGAGAGCACAct CCGGGT	2	8	0	0
Off-target 3	8	26505555	ACAGAAGAGAGAGAGCACAct CCGGGT	2	8	0	0
Off-target 4	3	36137083	ACgGAAGAGAAAGAGCA tGgTCGAGT	5	8	0	0

366 Note: Nucleotides of PAM sequence are written in bold, and the mismatch bases in
 367 potential off-targets are shown in lowercase.

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Supplemental Table 6 The target sites and primers for all sgRNAs used in this study.

sgRNA	Target site	Forward primer 5'-3'	Reverse Primer 5'-3'
sgRNA1	AGAGAGAGCACAGCTCGAGT	TGTGAGAGAGAGCACAGCTCGAGT	AAACTCGAGCTGTGCTCTCTCT
sgRNA2	AGTGCACGGTGTCCGTGGCC	TGTGAGTGCACGGTGTCCGTGGCC	AAACGGCCACGGACACCGTGCCT
sgRNA3	GCCGGACAGCTCCATTGCC	TGTGGCCGGACAGCTCCATTGCC	AAACGGCAATGGAGCTGTCCGGC
sgRNA4	GCCGAGGCTGAGCAGCTTG	TGTGGCCGAGGCTGAGCAGCTTG	AAACCAAGCTGCTCAGCCTCGGC
sgRNA5	ACTAGATATCTAAACCATTA	TGTGACTAGATACTAAACCATTA	AAACTAATGGTTTAGATACTAGT
sgRNA6	CATAGCACTCAATGCGGTCT	TGTGCATAGCACTCAATGCGGTCT	AAACAGACCCGATTGAGTGTATG
sgRNA7	AGACAAGCTTGGCCCTCTTT	TGTGAGACAAGCTTGGCCCTCTTT	AAACAAAGAGGGCCAAGCTTGTCT
sgRNA8	AGATGACCATCAACAAATCCA	TGTGTGAGATGACCATCAACAAATCCA	AAACTGGATTGTGTGATGGTCACTCA
sgRNA9	ACAGAAGAGAGAGAGCACAGC	TGTGTGACAGAAGAGAGAGAGCACAGC	AAACGCTGTGCTCTCTCTCTCTGTCA
sgRNA10	ACAGAAGAGAGAGAGCACAAT	TGTGTGACAGAAGAGAGAGAGCACAAT	AAACATTGTGCTCTCTCTCTCTGTCA
sgRNA11	ACAGAAGAGAGGGAGCATGC	TGTGTGACAGAAGAGAGGGAGCATGC	AAACGCATGCTCCCTCTCTCTGTCA
sgRNA12	CGTAGAGAATCCTGATGATGC	TGTGTGCGTAGAGAATCCTGATGATGC	AAACGCATCATCAGATTCTCTACGCA

Supplemental Table 7 Primers for on-target site amplification and sequencing.

Primer name	Primer sequence 5'-3'	Purpose
OsSPL14-F	AGGGTTCCAAGCAGCGTAAGGA	Amplify all the <i>OsSPL14</i> target sites
OsSPL14-R	TGGTGCTGGGGCTGGACCGTTC	
OsSPL14seq-F	TCTCCGGTGGTATCCAGTGGCAC	Sanger sequencing primer
SLR1-F	GCGCAATTATTACTAGCTATAGC	Amplify the <i>SLR1</i> target site
SLR1-R	AGCCGTCGCCACCACCGTAAGG	
SLR1seq-F	CGTCGACGAGCTGCTGGCG	Sanger sequencing primer
OsSERK2-F	CCATCTGCACGCATGACTT	Amplify the <i>OsSERK2</i> target site
OsSERK2-R	AGAGTTGTACGTACAATACAGCAG	
OsSERK2seq-F	GCTTCGTGGAGCATGAGGT	Sanger sequencing primer
Tms9-1-F	TGCCGTCGTACCGGCAGTCG	Amplify the <i>Tms9-1</i> target site
Tms9-1-R	CACGAGGCCTCCGACATGATGC	
Tms9-1seq-F	CTCCATGCCGCTCTGCGTGCTG	Sanger sequencing primer
OsNRT1.1B-F	GGGAGTTTCATGATTGGAGGCACG	Amplify the <i>OsNRT1.1B</i> target site
OsNRT1.1B-R	GTGCTACCTCGCCAGTGCTCATC	
OsNRT1.1Bseq-F	CTGTGACATTTGCAACCACAC	Sanger sequencing primer
OsACC1-F	GCAATCTGTTTCCTCGTGCTGGAC	Amplify the <i>OsACC1</i> target site
OsACC1-R	CTTGAAGCGATTTGTGTGTCAGCAC	
OsACC1seq-F	GGCATTGCTGGACTTCAACCG	Sanger sequencing primer
OsDEP1-F	CTCTTTCACACTCGCTCGCTCG	Amplify the <i>OsDEP1</i> target site
OsDEP1-R	AGCACAGCACAGTGTCAAGAAC	
OsDEP1seq-F	AGGAGATCCGATTCGCCGCG	Sanger sequencing primer
SPX-MSF2-F	AGCACACACACAGACAGTGTGTC	Amplify the <i>SPX-MSF2</i> target site
SPX-MSF2-R	GGCAACTTAGGTTGGCATTGCC	
SPX-MSF2seq-F	CGCTGCATGCATGCAGGCGCGT	Sanger sequencing primer
OsSPL17-F	GGGTTCCAAGCAGTGTGAGGGA	Amplify the <i>OsSPL17</i> target site
OsSPL17-R	GGACCTCGTTCAGCACAACCC	

OsSPL17seq-F	ATGAACTCCATCCTCACCGCAG	Sanger sequencing primer
OsSPL16-F	TTGGCATCAGCAGCAGGCAGCAG	Amplify the <i>OsSPL16</i> target site
OsSPL16-R	AGAGACGACGACGTGCCATCCGATG	
OsSPL16seq-F	CAGCTGCTGCTGCTGCTTCAGTGTG	Sanger sequencing primer
OsSPL18-F	TGGGATCATCAAATCCGAGGAG	Amplify the <i>OsSPL18</i> target site
OsSPL18-R	CTGTCCATGCTCGGGCAGGCCG	
OsSPL18seq-F	CCTCCATGAGGGCGATCAGATA	Sanger sequencing primer
OsSPL13-F	ATTTGACAAGAGTGCATTATGCA	Amplify the <i>OsSPL13</i> target site
OsSPL13-R	AGCACTGCATATATGTAGCAGCAG	
OsSPL13seq-F	GCTTCATCATCATCTTGTC	Sanger sequencing primer
SNB-F	GGTTAGAATCATCCATTCATG	Amplify the <i>SNB</i> target site
SNB-R	CCAGCTTTAGTGCCCACTGTTC	
SNBseq-F	CTGGTAGCACGGTCACGATTCG	Sanger sequencing primer

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381 **Supplemental Table 8** Primers for off-target site amplification and sequencing.

Primer name	Primer sequence 5'-3'	Purpose
sgRNA1M1-F	GGGACCTCGTTCAGCACAACCCC	Amplify the off target site 1 for sgRNA1
sgRNA1M1-R	GCAGGTCCAGAAGCTTTGTGGTA	
sgRNA1M1seq-F	CTCGCCGCCATGTAGTTGCT	Sanger sequencing primer
sgRNA1M2-F	TTGCTCCCTAAACAACCTCCAG	Amplify the off target site 2 for sgRNA1
sgRNA1M2-R	CCTGGTGCAGAGAGTACAAATG	
sgRNA1M2seq-F	GTCAACCTGCACAGGGACAG	Sanger sequencing primer
sgRNA1M3-F	TGCAATGCATCTACTCCCTCAG	Amplify the off target site 3 for sgRNA1
sgRNA1M3-R	GATCACACTAGCGACAGCGAGC	
sgRNA1M3seq-F	TTGGACGGACGGAATATAAG	Sanger sequencing primer
sgRNA1M4-F	ACGAGAGCTTCCACTGAACGCA	Amplify the off target site 4 for sgRNA1
sgRNA1M4-R	AATCTGCCCGTGTGTCAGCAGAG	
sgRNA1M4seq-F	CGCCTCGGGATCAGCAGAT	Sanger sequencing primer
sgRNA1M5-F	TGCAGGTGGTCGGCGATCGCG	Amplify the off target site 5 for sgRNA1
sgRNA1M5-R	AGCGCGCGCAGCTTGGCCT	
sgRNA1M5seq-F	ACTACTGGAACACGCACCTA	Sanger sequencing primer
sgRNA1M6-F	GATCACAACCTGCTCGTAAGCTA	Amplify the off target site 6 for sgRNA1
sgRNA1M6-R	ATATGTCTTATCGGACACGAC	
sgRNA1M6seq-F	AGACGCAAGAACGACAAGC	Sanger sequencing primer
sgRNA1M7-F	CCAAACTCTATCTTGAGCCTTC	Amplify the off target site 7 for sgRNA1
sgRNA1M7-R	GAGTTCGACGAGGGAGAGAGA	
sgRNA1M7seq-F	CCAAAACCCTAATTCGAATC	Sanger sequencing primer
sgRNA1M8-F	ATATTCATAATCCCCCTAGAA	Amplify the off target site 8 for sgRNA1
sgRNA1M8-R	CCCCAACGCTTCGCGAATCGCA	
sgRNA1M8seq-F	GAGGGAATATACAGTGTA	Sanger sequencing primer
sgRNA1M9-F	CAGAGCCTGGACGGTTCTAC	Amplify the off target site 9 for sgRNA1
sgRNA1M9-R	ACAGTACAGCAAATCGCACGT	
sgRNA1M9seq-F	GAGTGCCCCGGCGTCGTCTC	Sanger sequencing primer

sgRNA6M1-F	CTCAACTCTTGGGATTGCAGTTGC	
sgRNA6M1-R	CCGATAAGGTTTGTATTACACAGG	Amplify the off target site 1 for sgRNA6
sgRNA6M1seq-F	GTAGCTAATGGTGATTGTATAC	Sanger sequencing primer
sgRNA6M2-F	GGGCATCAGTTTATGTTCTCCTGC	
sgRNA6M2-R	TTCCACTGGAGTAGCCTGTGAC	Amplify the off target site 2 for sgRNA6
sgRNA6M2seq-F	ATGCAATGAGAGGCATCAAGAG	Sanger sequencing primer
sgRNA6M3-F	CGAGAGAGTACAGCAGCAGCTG	
sgRNA6M3-R	CTCCGCCGCCTCGAGTTCCGTC	Amplify the off target site 3 for sgRNA6
sgRNA6M3seq-F	CCGCGCACCATCTCAACCG	Sanger sequencing primer
sgRNA9M1-F	GCAACAAGATGTTCTCCTCCG	
sgRNA9M1-R	CTGCCGCCGAAGTCTGCTGCTGC	Amplify the off target site 1 for sgRNA9
sgRNA9M1seq-F	TGACGACGGCGACGACGACG	Sanger sequencing primer
sgRNA9M2-F	ACACCTGCCAAGAGAATGGCA	
sgRNA9M2-R	CCGATAGCTGATCAGAACGC	Amplify the off target site 2 for sgRNA9
sgRNA9M2seq-F	GTGACAGCAGGAACCAAGAC	Sanger sequencing primer
sgRNA9M3-F	TTGGCATCAGCAGCAGGCAGCA	
sgRNA9M3-R	GAACCAGGCTGAGCTGCCGCC	Amplify the off target site 3 for sgRNA9
sgRNA9M3seq-F	GAAGACGGTAGCTCCTCCT	Sanger sequencing primer
sgRNA9M4-F	TATTATTCGTGCAATGCATCTA	
sgRNA9M4-R	ATGCGAGCGGTCTAACCGACGA	Amplify the off target site 4 for sgRNA9
sgRNA9M4seq-F	CATTCTCACTCTCCACTATTTC	Sanger sequencing primer

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