

A

Target	Cas9 target sequence	Strand	Nucleotide distance of SNPs from PAM
1	TGATGCAGCTGA <ins>g</ins> AAGTTGAAGG	+	8
2	AAGTTGAAGGCCGCGATG <ins>c</ins> AGG	+	1
3	TTGAAGGCCGCCGATG <ins>c</ins> AGGAGG	+	4
4	AAGGCCGCCGATG <ins>c</ins> AGGAGGAGG	+	7
5	CGCCGATG <ins>c</ins> AGGAGGAGG <ins>a</ins> GAGG	+	2, 12
6	GTAGACGATGAACTTGAAGAAGG	+	
7	CTC <ins>t</ins> CCTCCTCCT <ins>g</ins> CATCGGCGG	-	7, 17
8	TACCT <ins>c</ins> tCCTCCTCCT <ins>g</ins> CATCGG	-	4, 14

B

seq_id	sgRNA_id	Score	Sequence	strand	pos	%GC
5' 114nt eIF4E-1	Guide6	0.5841	GTAGACGATGAACTTGAAGG <ins>GG</ins>	+	101	40%
5' 114nt eIF4E-1	Guide4	0.1980	AAGGCCGCCGATGCGAGGAGG <ins>GG</ins>	+	74	70%
5' 114nt eIF4E-1	Guide7	0.1646	CTCTCTCTCTCTGCATCGG <ins>GG</ins>	-	58	70%
5' 114nt eIF4E-1	Guide5	0.1646	CGCCGATGCGAGGAGGAGG <ins>GG</ins>	+	79	70%
5' 114nt eIF4E-1	Guide1	0.1505	TGATGCAGCTGAGAAGTGA <ins>GG</ins>	+	55	45%
5' 114nt eIF4E-1	Guide3	0.1121	TTGAAGGCCGCCGATGCAAGG <ins>GG</ins>	+	71	65%
5' 114nt eIF4E-1	Guide8	0.0776	TACCTCTCTCTCTGCAT <ins>GG</ins>	-	61	65%
5' 114nt eIF4E-1	Guide2	0.0041	AAGTTGAAGGCCGCCGATGC <ins>GG</ins>	+	68	60%

Supplementary Figure 2. (A) Analysis of SNPs in the Cas9 target sequences in the first 114 nucleotides of the *eIF4E1*. In red nucleotides identifying the location of the SNP. In yellow is highlighted the Cas9 PAM sequence. (B) CRISPR-P score prediction of Cas9 targets. The score range from 0 to 1, the high score predicts the high effectiveness of sgRNA. Presumably best target (score > 0.50), intermediate (0.20 < score < 0.50) low (score < 0.2) CRISPRP <http://crispr.hzau.edu.cn/CRISPR2/>