

# Targeting the Highly Expressed microRNA miR-146b with CRISPR/Cas9n Gene Editing System in Thyroid Cancer



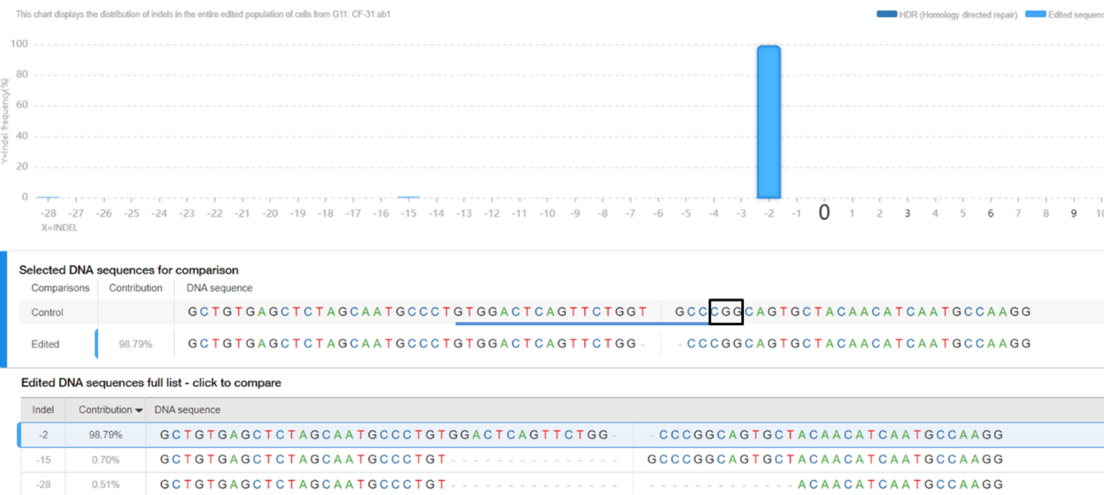
**Figure S1.** Validation of *MIR146B* gene editing for GuideA-targeted region in KTC2-Cl1 using the SeqScreener Gene App. Black square indicates the PAM sequence adjacent to the sgRNA underlined in blue.



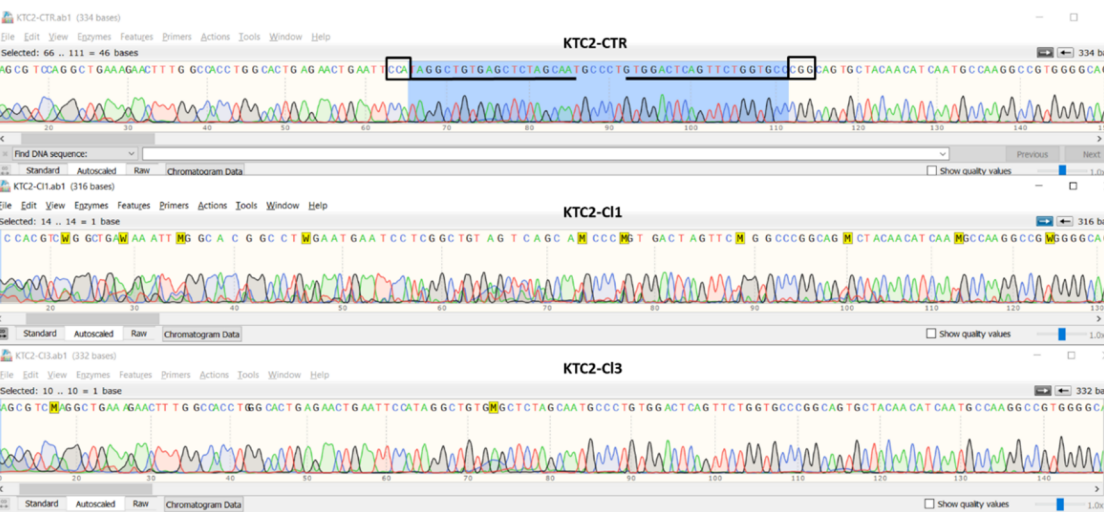
**Figure S2.** Validation of *MIR146B* gene editing for GuideB-targeted region in KTC2-Cl1 using the SeqScreener Gene App. Black square indicates the PAM sequence adjacent to the sgRNA underlined in blue.



**Figure S3.** Validation of *MIR146B* gene editing for GuideA-targeted region in KTC2-CI3 using the SeqScreener Gene App. Black square indicates the PAM sequence adjacent to the sgRNA underlined in blue.



**Figure S4.** Validation of *MIR146B* gene editing for GuideB-targeted region in KTC2-CI3 using the SeqScreener Gene App. Black square indicates the PAM sequence adjacent to the sgRNA underlined in blue.



**Figure S5.** Raw sanger sequencing data alignment for *MIR146B* gene used in SeqScreener Gene Editing. The blue highlighted region in KTC2-CTR indicates the region between two sgRNAs that are underlined in black. PAM sequences are indicated by black squares.

**Table S1.** Off-targets list of sgRNA A and sgRNA B.

sgRNA	Location	Number of Mismatches	Sequence (Including Mismatches)
sgRNA A	chr10:102436533 ( <i>MIR146B</i> ) - on target	0	TTGCTAGAGCTCACAGCCTATGG
	chr10:95817873	3	TTGCTgtAGCTCAgAGCCTAGGG
	chr12:106688991	3	TTcCTAGAGCTCACAGtCTcAGG
	chr13:58239277	3	gTGCTAGAGCTtcCAGCCTAGGG
	chr14:98114838	3	CCCTAtcCTGTGAGCTCTAGtAA
	chr16:24336061	3	CCCTAGGCccTGAGCTCTtGCAA
	chr16:65410481	3	CCCTAGGCTGTGAaCTCTAcCAG
	chr2:221546073	3	CCTTAGaCTGTGAaCTCTtGCAA
	chr21:19900603	3	cTGCTAGAGCTtcCAGCCTAAGG
	chr5:142679117	3	TTtCTAGgGCTCACAGctTAAGG
	chr6:122057654	2	TTGCTAGAGCTctCAGaCTAAGG
	chr7:101906218	3	TTGCTgGAGtTCACAGCCcATGG
	chrX:139912958	3	TTGCTAGgGCTctCAGCCTtAGG
sgRNA B	chr10:102436562 ( <i>MIR146B</i> ) - on target	0	GTGGACTCAGTTCTGGTGCCCGG
	chr1:22182587	3	GTGGcCTCAGTTCTGtTcCCTGG
	chr1:112028553	3	GgGGA CTCA GTgCTGGTGctAGG
	chr1:191533406	3	CCAGGctCCAGAACTGccTCCAC
	chr13:40338408	3	CCGGGCACCAGAACTagGgCCAC
	chr14:36482672	3	CCAGGatCCAGAACTGAGTCCAt
	chr14:85131510	3	GTGGACTCAGTTaTaaTGCCAGG
	chr14:102644835	2	tTGGtCTCAGTTCTGGTGcCTGG
	chr15:30264840	3	GTaGACTCAGTgCTGtTGCCGGG
	chr15:32273795	3	CCCGGCAaCAGcACTGAGTctAC
	chr15_KI270905v1_alt:2549795	3	GTaGACTCAGTgCTGtTGCCGGG
	chr15_KI270905v1_alt:4559480	3	CCCGGCAaCAGcACTGAGTctAC
	chr18:23820083	3	CCTGtCcCCAGAACTGAtTCCAC
	chr19:22351022	3	CCTGGggCCAGAgCTGAGTCCAC
	chr2:127624083	3	cTGGcCTCAGTTCTGGTcCCTGG
	chr2:231859595	3	CCAGGCACCAGAgCTGAagCCAC
	chr21:45459366	3	CCGGGCACCAGAAcAGAGcCctC
	chr4:2836889	3	GTGGgGCTCAGTTCTGGgGctTGG
	chr8:144181727	3	GTGGACTCAGcTaaGGTGCCTGG