

Supplemental Table S1. Sequences of the sgRNA used to target IDH2 and MYBL2 and the ssODN sequence.

sgRNA	Sequence (5'-3')
<i>MYBL2</i>	TTGGCAGCTGGCTCCCTC
<i>IDH2_1</i>	TGGACCAAGGCCATCACCAT
<i>IDH2_2</i>	CTGGCCTACCTGGTCGCCAT
<i>IDH2_R172K</i> ssODN	tgcaaaaacatcccacgcctagtcctggctggactaaaccgataacgatcgaaa gcacgcgcatgcgaccaggtaggccagggtggagagggat

Supplemental Table S2. Primers sequence for sgRNA constructs. sgRNA sequence should be added to Primer FusionPCR_1F and FusionPCR_2R sequence in 5' (sgRNA forward sequence in FusionPCR_1F and sgRNA reverse sequence in FusionPCR_2R).

Name	Sequence (5'-3')
FusionPCR_1F	GTTTTAGAGCTAGAAATAGCAAG
FusionPCR_1R	CCGGCAGACGACGATTATGACGGAAAAAGCACCGACTCGGTGCCAC
FusionPCR_2F	AAAAAACCTCCCACACCTCC
FusionPCR_2R	GGTGTTCGTCCTTCCACAA
FusionPCR_3F	GTTGTGGTTGTCCAACACTC
FusionPCR_3R	CCGGCAGACGACGATTATGACGG
FusionPCR_4F	GGGTCAATTAGTTCATAGCCC
FusionPCR_4R	GGTGTTCGTCCTTCCACAA
FusionPCR_5F	AGCCCATATATGGAGTTCCG

Supplemental Table S3. Primers used in PCR 1 for library preparation.

Off-target	Primer Forward (5'-3')	Primer Reverse (5'-3')
sgRNA1_1	GATGATTGCCATAGCCTCAG	ATCCTATCTCCCACACTGTG
sgRNA1_2	GTACTCTAGCCTGGTGACAG	AGAATGGGAGGGGGAATAAG
sgRNA1_3	AGAGGTCATCTGTGTCCAGG	CTGGGACTCGGCCTCTGAA
sgRNA1_4	TGAAAGGAGGGTGAGCCG	GAAGGTTCCCCCTCATTG
sgRNA1_5	AGTATCACTGGCATCTCTGC	CTGAGGAGGCCAGAATGACT
sgRNA1_6	CCATATGGGAGGGCGGTAGC	CAGAACAGATTCCCCACAG
sgRNA1_7	CCTACCAGTGGAGGCCTTGAG	GCTTCGATCCTGTTCCCTCC
sgRNA1_8	TGTTGGACTAGATCACTCTG	GCCCTTAGAGGGTAAACAAC
sgRNA1_9	CGCCAGGTCTGAATGGAAG	GCCTCTGTGAACCTCCTC
sgRNA1_10	GCCCTGTCAATGAAGTGAAG	CCACAAATGGCTGCAGAAC

sgRNA1_11	AAGGCCCTGTCAATGAAC	TTCACTGCTAGGTTGCCAC
sgRNA1_12	GTTGGGATTACAGGTATGAG	TAGTCAAGGTCTTATTGCAC
On-target	TTATCTCTGCCTCACAGAG	CAAAGTCTGTGGCCTTGAC
sgRNA2_1	TGTGTGTGGTTGGAGGATG	AGCCATTCTCCTGTACAGC
sgRNA2_2	CTGAAAGCGTATAGCTATCC	GGCCTTGGGTATGAAATGAAG
sgRNA2_3	CCACTGTTGGTGTGAGGAAG	GCATGTCCCTAACCTTACTC
sgRNA2_4	AGCCCTACTGTAATGCTTG	ATGTCATCCATCAGTCCCCG
Adapter sequence for Forward primer	TACACTCTTCCCTACACGACGCTTCCGATCT	
Adapter sequence for Reverse primer	GTGACTGGAGTTCAGACGTGTGCTTTCCGATCT	

Supplemental Table S4. Primers used in PCR 2 for library preparation.

Name	Adaptador PCR2. Sequence (5' - 3')
TruSeq Universal Adapter_Forwar	AATGATAACGGCGACCACCGAGATC TACACTCTTCCCTACACGACGCTTCCGATCT
TruSeq_NB4_RNP-Ed	CAAGCAGAAGACGGCATACGAGAT GATCTGGTACTGGAGTTCAGACGTGTGCTTTCCGATCT
TruSeq_NB4-Cas9-Ed	CAAGCAGAAGACGGCATACGAGAT TGGTCAGTGA CTGGAGTTCAGACGTGTGCTTTCCGATCT

Green nucleotides represent homolog sequence to primers for PCR 1. Indexes, which are tag sequences to mark each experiment, are showed as red nucleotides.

Supplemental Table S5. Primers used to amplify Cas9 cassette from hCas9 vector

Name	Sequence (5'-3')
Cas9_F	TCTGCTCTGATGCCGCATAG
Cas9_R	CTGCGCAGATCTGCTATGGC

Supplemental Table S6. Primers used to amplify targeted region in *MYBL2* and *IDH2* for T7 and RFLP assays and ICE analysis.

Target	Forward sequence (5'-3')	Reverse sequence (5'-3')
<i>MYBL2</i>	CTTCCCACCCCTGTAGCAGG	CCACATGCTGCAAATGTCTCAG
<i>IDH2</i>	ACTCCAGAGCCCACACATT	ATGCCGGGATTACAAGTGTC

Supplemental Table S7. Primers used to detect Cas9 lentiCRISPR V2 integration in cell lines.

Name	Sequence (5'-3')
Cell_Cas9_F	CGAGTACTTCACCGTGTATAACG
Cell_Cas9_R	CTCTTCGATCCGCTTCATTCTCT

Supplemental Table S8. Primers sequence for U6-sgRNA-terminator cassette amplification in PX458 vector. Recognition AflII site is indicated in italics.

Name	Sequence (5'-3)
pU6_sgRNA_F_AflII	AGCTGCCTTAAGGGTCTGGCCTTTGCTGG
pU6_sgRNA_R_AflII	AGCTGCCTTAAGGGTACCTCTAGAGCCATTG

Supplemental Table S9. Results of NHEJ obtained with ICE analysis with different sg*IDH2* in HEK293 cells.

Conditions			250 ng PCR	
	sg <i>IDH2_1</i>	sg <i>IDH2_2</i>	sg <i>IDH2_1</i> + sg <i>IDH2_2</i>	Cas9 sg <i>IDH2_1</i> + sg <i>IDH2_2</i>
Exp. 1	20	10	14	2
Exp. 2	10	16	44	1
Exp. 3	5	8	13	5
Exp. 4	0	0	13	-
Average NHEJ (%±SEM)	8.75±3.3	8.5±4.26	21±7.7	2.6±1.2

Supplemental Table S10. Results of NHEJ obtained with ICE analysis with different optimizations in HEK293 cells.

Conditions	150 ng hCas9 7ng sg <i>MYBL2</i>	250ng hCas9 12 ng sg <i>MYBL2</i>	250 ng hCas9 35ng sg <i>MYBL2</i>	250 ng hCas9 60ng sg <i>MYBL2</i>	500 ng hCas9 23.3 ng sg <i>MYBL2</i>	250 ng hCas9 35ng sg <i>MYBL2-</i> p	250 ng PCR Cas9 35ng sg <i>MYBL2</i>	PX458- <i>MYBL2</i>
	150 ng hCas9 7ng sg <i>MYBL2</i>	250ng hCas9 12 ng sg <i>MYBL2</i>	250 ng hCas9 35ng sg <i>MYBL2</i>	250 ng hCas9 60ng sg <i>MYBL2</i>	500 ng hCas9 23.3 ng sg <i>MYBL2</i>	250 ng hCas9 35ng sg <i>MYBL2-</i> p	250 ng PCR Cas9 35ng sg <i>MYBL2</i>	PX458- <i>MYBL2</i>
Exp. 1	8	16	0	18	12	8	0	8
Exp. 2	6	29	6	24	12	5	1	11
Exp. 3	13	11	13	18	20	17	0	14
Exp. 4	0	0	14	0	0	17	-	13
Average NHEJ (%±SEM)	6.75 ±2.7	14 ±6	8.25 ±3.3	15 ±5.2	11±4	11.75 ±3.1	0.3 ±0.3	11.5 ±1.3

Supplemental Table S11. NHEJ efficiencies obtained with ICE analysis in NB4-Cas9 cells using sg*IDH2* constructs or NB4 cells using RNPs.

Conditions	sg <i>IDH2_1</i> + sg <i>IDH2_2</i>	RNPs
Exp. 1	10	78
Exp. 2	4	78
Exp. 3	0	67
Average NHEJ (%±SEM)	4.6±2.9	74.33±3.6

Original Images from this work

Figure 2B_original

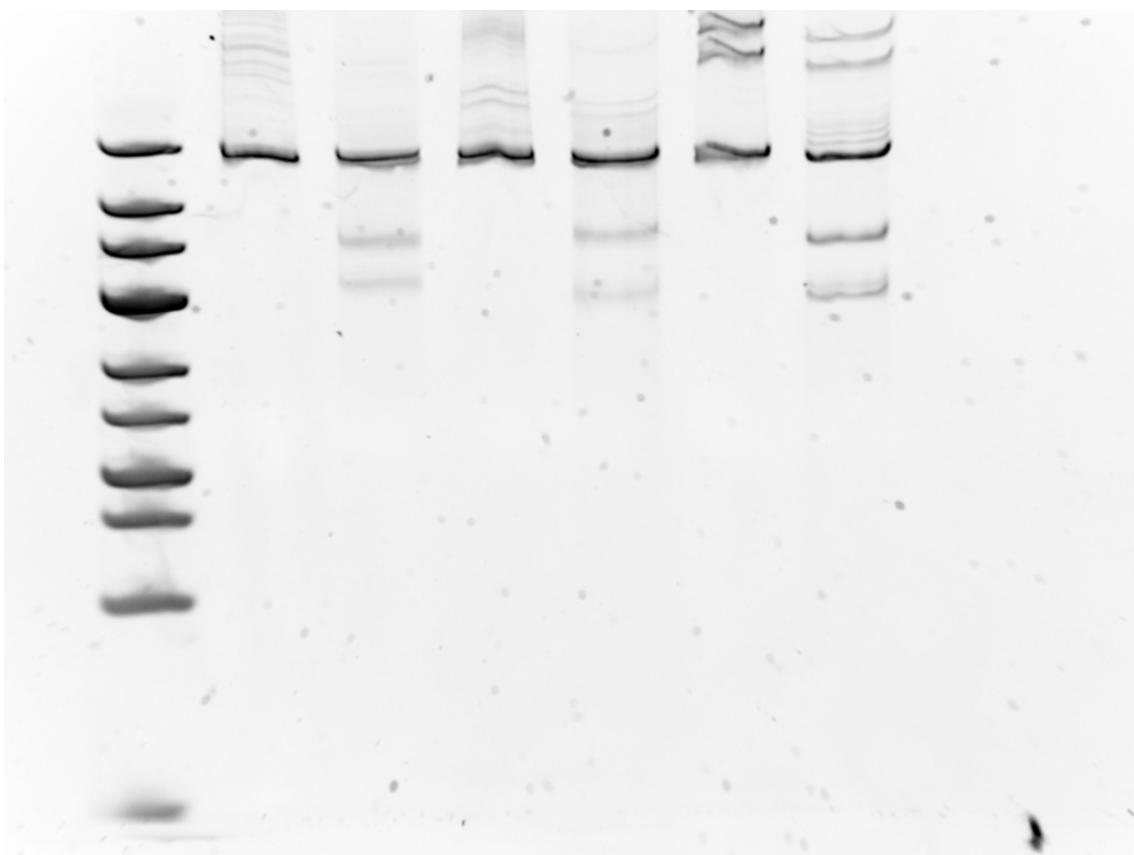


Figure 5A_original

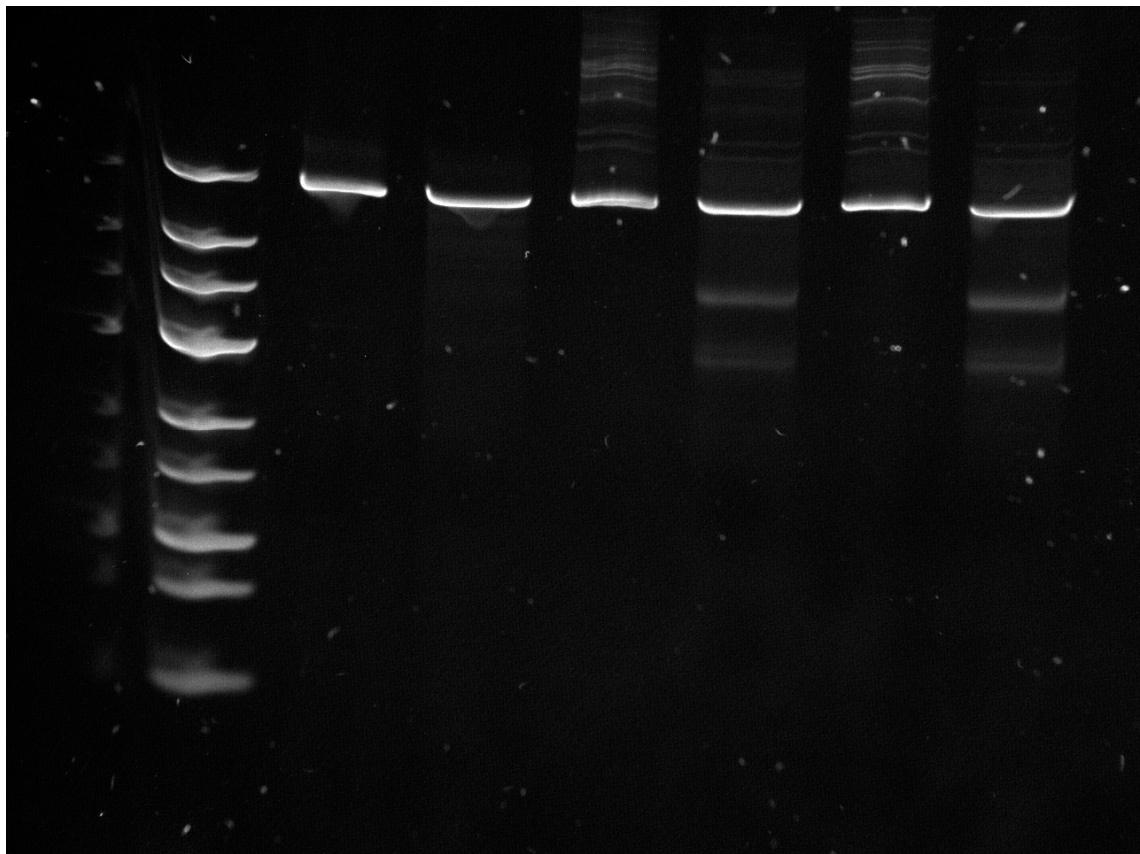


Figure 5B_original

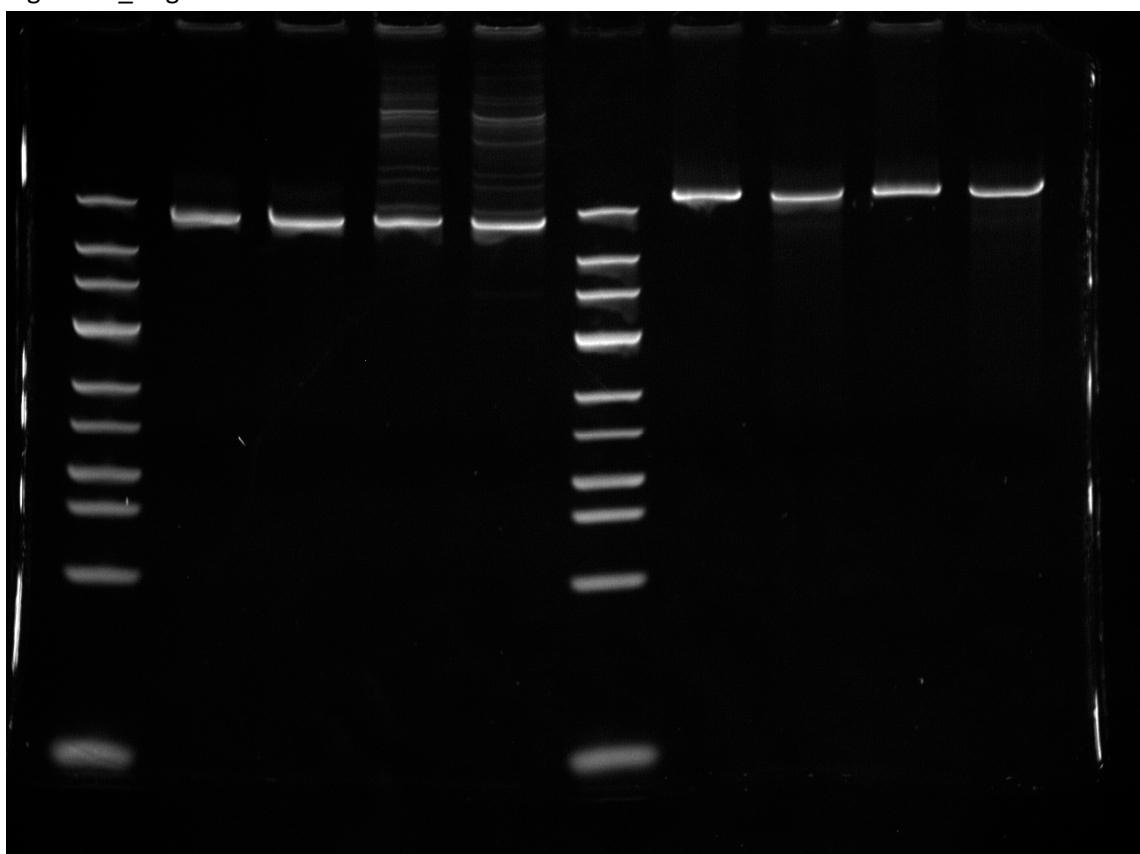


Figure 5C_original

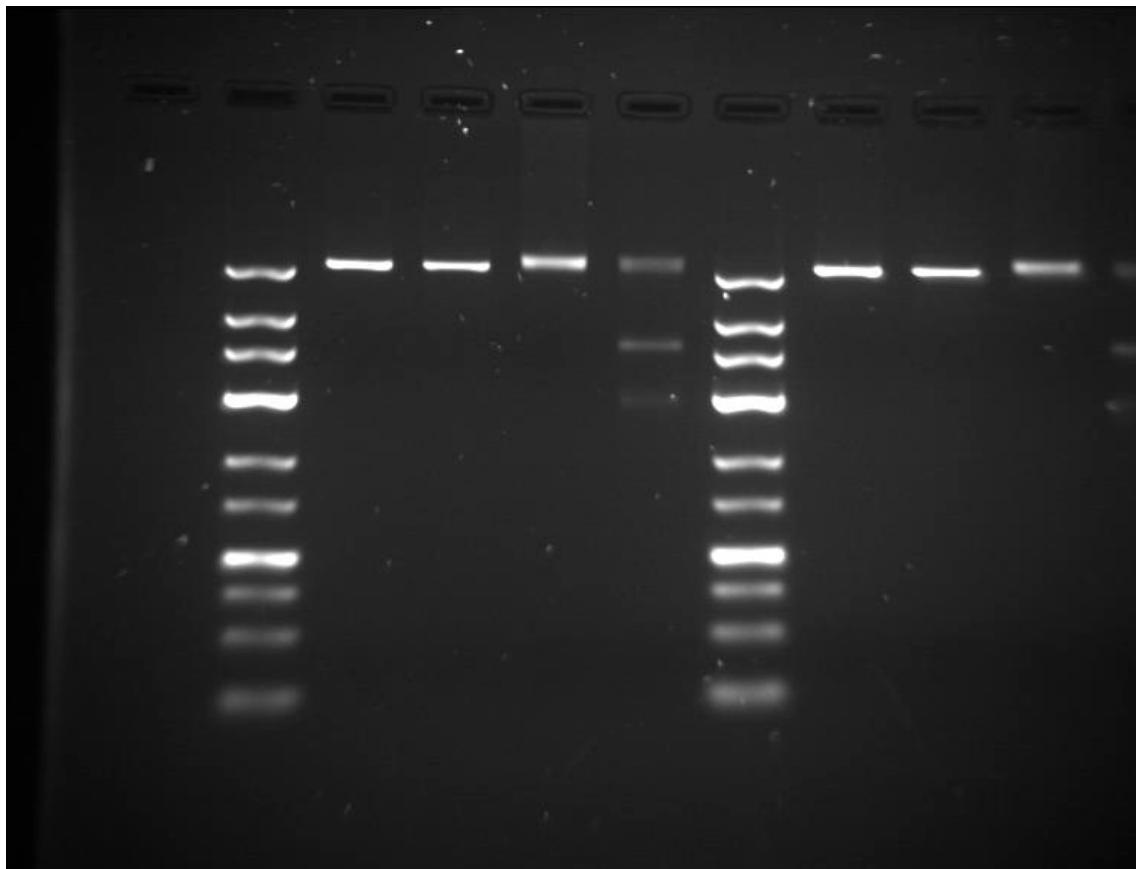


Figure 5D_original

