

Edit-R™ Lentiviral sgRNA Positive Controls

Product Description:

The following protocol is an example of thermal cycling and cleavage conditions for a DNA mismatch detection assay using T7 Endonuclease I (T7EI) and the Edit-R Lentiviral sgRNA Control primer set utilizing genomic DNA (gDNA) from direct cell lysis. For direct cell lysis, cells were treated for gene editing in a 96-well format.

- Lyse cells in 100 µL of 1x Phusion High-Fidelity buffer with additives

Reagent	Volume	Final concentration
5x Phusion HF Buffer	20 µL	1x
Proteinase K (~ 20 mg/mL)	5 µL	~ 1 mg/mL
RNase A (10 mg/mL)	5 µL	0.5 mg/mL
Water, nuclease free	70 µL	N/A

- Seal the 96-well plate with a plate seal to minimize evaporation and cross contamination. Incubate for 15-30 minutes at 56 °C, followed by deactivation for 5 minutes at 96 °C. Briefly centrifuge plate to collect liquid at bottom of wells.

- Set up 50 µL PCR for each sample to be analyzed.

Note: Other PCR reagents can be used provided that PCR optimization is performed for mismatch detection conditions and testing compatibility with direct cell lysis or purified gDNA.

Reagent	Volume	Final concentration
5x Phusion HF buffer	10 µL	1x
Forward primer (50 µM)	0.5 µL	500 nM
Reverse primer (50 µM)	0.5 µL	500 nM
dNTPs (10 mM)	1 µL	200 µM each
Phusion Hot Start II High-Fidelity DNA Polymerase (2 U/µL)	1 µL	0.04 U/µL
Water, nuclease free	32 µL	N/A
Cell lysate	5 µL	N/A

- Thermal cycling condition.

Cycle step	Temperature	Time	Cycle(s)
Initial denaturation	98 °C	3 min	1
Denature	98 °C	10 s	10
Touchdown annealing	72 °C - 1 °C/cycle	15 s	
Extension	72 °C	30 s	
Denature	98 °C	10 s	25
Annealing	62 °C	15 s	
Extension	72 °C	30 s	
Final extension	72 °C	10 min	1

- Heat PCR samples to 95 °C for 10 minutes and then slowly (> 15 minutes) cool to room temperature (~ 25 °C).
- PCR product (~ 5 µL) can be run on 2% agarose gel to confirm amplification.
- Set up 15 µL reactions for mismatch detection assay using T7EI. Be sure to include at least one sample without the T7EI enzyme (No enzyme negative control) and/or Untreated (no gene editing negative control).

Note: Other mismatch detection assays can be used following the manufacturer's recommended protocol.

Reagents	Volume	Final concentration
PCR from gDNA (300-500 ng/reaction)	10 µL	variable
Water, nuclease free	3 µL	N/A
NEBuffer 2 (10x)	1.5 µL	1x
T7 Endonuclease I (10 U/µL)	0.5 µL	0.33 U/µL

- Incubate for 25 minutes at 37 °C.
- Immediately run entire reaction volume with appropriate gel loading buffer on 2% agarose gel, since T7EI enzyme cannot be heat inactivated. Compare samples with expected gene editing to the No enzyme and/or Untreated negative controls.

Gene target	Species	Primer	Sequence	Tm* (°C)	MW	Extinction coefficient	Expected band sizes (bp)	
							No editing	With editing
PPIB	Human	Forward	GAAGCTAGGCTCCGCTCCTT	64.0	6044.0	176184	505	~ 330, ~ 174
		Reverse	CTCTGCAGGTACGTTTGCTG	64.3	6115.0	178151		
Ppib	Mouse	Forward	CCAGCCTGTTTGTGGATTT	64.2	6105.1	176905	572	~ 409, ~ 163
		Reverse	ACTGTGAGGCTGCCAGATTT	64.2	6148.1	191297		
Ppib	Rat	Forward	TGCCATTTCTCACTCCCTA	60.4	5938.9	165727	524	~ 342, ~ 170
		Reverse	GGCTACCGCTACAATGGAC	62.4	6111.0	197820		
DNMT3B	Human	Forward	TGAGAAGGAGCCACTTGCTT	64.4	6157.1	197197	544	~ 335, ~ 209
		Reverse	GACCAAGAACGGGAAAGTCA	64.4	6193.1	220800		
Dnmt3b	Mouse	Forward	ACTTGGTGATTGGTGAAGC	64.3	6228.1	199164	561	~ 372, ~ 189
		Reverse	TTAAGCCACACCTCCTCTG	64.5	5972.9	174218		
Dnmt3b	Rat	Forward	GGCATTGATCCCATGTAACC	60.4	6077.0	189330	532	~ 319, ~ 212
		Reverse	CTCCGAGCTGCTAAGAGGAA	62.4	6151.0	201754		

*Tm calculated specifically for use with Phusion DNA polymerases. Tm should be calculated for specific DNA polymerases and PCR reagents using appropriate parameters.

Materials:

- Thermo Scientific™ Phusion™ Hot Start II High-Fidelity DNA Polymerase, 2 U/µL (Cat #F-549S)
- T7 Endonuclease I, 10 U/µL (NEB, Cat #M0302S)
- Thermo Scientific™ Proteinase K, ~ 20 mg/mL (Cat #E00492)
- Thermo Scientific™ RNase A, 10 mg/mL (Cat #EN0531)
- Thermo Scientific™ 5x Phusion HF Buffer (Cat #F-518L)
- NEBuffer 2 (NEB, Cat #B7002S)

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