

# Use siRNA to knowdown Cebp $\alpha$ in 3T3-L1

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## ABSTRACT

## INTRODUCTION

We choose two target gene from paper.

Tranditinal PCR is an in vitro techniques which allows the amplification of a specific DNA region that lies between two regions of known DNA sequence. Here are three phases of PCR, including exponential phase, linear phase and plateau phase. Nowadays, we

Relative PCR, 荧光是怎么与扩增数相关的。

The method of siRNA to knowdown the expression of gene.(Why we use dsRNA).

The points, which we should metation.

电转 (受用面广, 但有毒性)

Two siRNA , one qPCR primer, one positive control (GADPH)

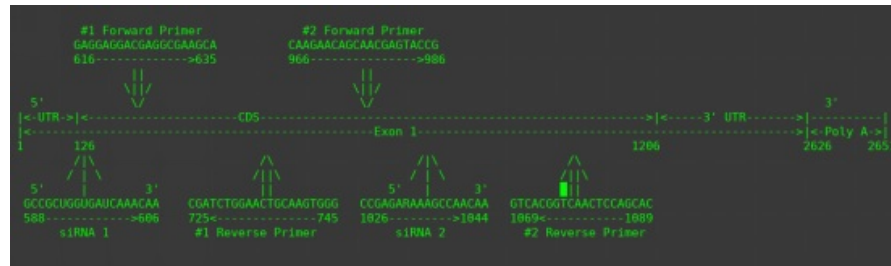
## MATERIALS AND METHODS

Firstly, from the He Y, Li Y, Zhao T, Wang Y, Sun C (2013), we choose the CCAAT/enhancer-binding protein alpha from Mus musculus. Cebp $\alpha$  encodes a transcription factor that contains a basic leucine zipper (bZIP) domain and recognizes the CCAAT motif in the promoters of target genes. The encoded protein functions in homodimers and also heterodimers with CCAAT/enhancer-binding protein beta and gamma. Activity of this protein can modulate the expression of genes involved in cell cycle regulation as well as in body weight homeostasis. The target sequence is following, and Accession ID: NM\_007678.3 from [https://www.ncbi.nlm.nih.gov/nuccore/NM\\_007678.3](https://www.ncbi.nlm.nih.gov/nuccore/NM_007678.3).

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1 ttcgcgacc cgaagctgcg cgggcgcgag ccagttgggg cactgggtgg gcggcggcga
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121 tcccc.../atgg agtcggccga cttctacgag gtggagccgc ggccccgat gagcagtcac
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 361 gccgacctct tccagcacag ccgacagcag gagaaggcca aggcggcgccg gggccccgcg  
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 481 tccgcggggg cgcacgggcc cctcccgcc tacggctgtg cggcgcccg ctacctggac  
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 601 aaacaagagc cccgcgagga ggacgaggcg aagcagctgg cgctggccgg cctcttcccc  
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 901 ctccgcacgg gagcgccgg cggtggcagc ggtgccgtg cgggcaaagc caagaagtcg  
 961 gtggacaaga acagcaacga gtaccgggta cggcggaac gcaacaacat cgcggtgcgc  
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 1741 gtgtcctcac cccagctac agggaggtgg agggctccta atcccttct tttgcacct  
 1801 ccactacat cccccccc cactcagct tacaacaggc cagtttctt gggtgagttc  
 1861 atggagaatg ggggcaccac cccagtcag accagaaagc tgagtttga gttagccatg  
 1921 tggtaggaga cagagacct ggtttctggg cttgtgggg tgggggatag gagacacgg  
 1981 ggaccattag cttgtgtgt actgtatgt gccagccgt gttgctgaag gaactgaag  
 2041 cacaatcga ccatccaga gggactggag ttatgacaag ctcccaaatt atttgttt  
 2101 atcatccga atcaacact gtatctgtc tctgtgtcc agcgggtcct tgtgcaatg  
 2161 cagtgtgcac gtctatgta aaccaccatt ttatttggtc tttgtttt ttttggtt  
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 2581 gtttcatgct agatgtcgt gtattatat ctataatata aacatatca actcaaaaaa  
 2641 aaaaaaaaa a

Then, we use BLOCK\_iT RNAi Designer and GeneBank to design siRNA and qPCR primers as following



**Figure 1.** The siRNA and qPCR primers for Cebp- $\alpha$

We use absolute qPCR to compare the effectivity of two qPCR primers. Prepare the PCR mixture shown below. Divide Primer-1&2 premixers into seven new tubes, respectively (63µl each). cDNA was added into tubes (7µl for 1:1, 1:5, 1:10, 1:25, 1:125, 1:3125, and control group). Then divide qPCR mixture into each well. After qPCR, draw standard curve and calculate the E from  $10^{-1/\text{slope}} - 1$  and observe the melt curves.

Reagent	Volume( $\mu$ L)	Total volume	Final concentration
SYBR Premix ExIaqII(The RNase Plus)(2x	10	390	1x
PCR Forward Primer(10 $\mu$ M)	0.8	28	0.4 $\mu$ M
PCR Reverse Primer(10 $\mu$ M)	0.8	28	0.4 $\mu$ M
ROX reference Dye(50x)	0.8	14	1x
Template(<100g)	2	~	
dWater	6	210	
Total	20	630	

To transfect siRNA to 3T3-L cell, we use electroporation. Then we isolate RNA from cell and reverse RNA to cDNA. Finally we use qPCR to measure the expression of Cebp- $\alpha$ . Firstly, we prepare three PCR mixture as following table. (Table 1)

Reagent	Volume (3.5 tubes)	18srRNA premix (60 tubes)
SYBR Premix EX Taq II(Tli RNaseH plus)(2x)	3.5	600
PCR Forward Primer (10μl)	2.8	48
PCR Reverse Primer (10μl)	1.4	48
ROX Reference Dye	2.8	48
Template (<100 ng)	7	
H <sub>2</sub> O(sterile distilled water)	21	360
Total	70	1080

Table 1.

Then, we made a PCR set-up sheet in 96-well PCR plate as following table.

	18s rRNA			GAPDH			18s rRNA			Target gene			
	#1	#2	#3	#1	#2	#3	#1	#2	#3	#1	#2	#3	
NC-1													Test 1-1
NC-2													Test 1-2
NC-3													Test 1-3
PC-1													Test 2-1
PC-2													Test 2-2
PC-3													Test 2-3
													NTC
													Target Gene
				NC-1			NC-2			NC-3			

Table 2.

For test sample:  $2^{-[(Ct_{\text{target gene}} - Ct_{18s\text{rRNA}}) - (Ct_{18s\text{RNA}})]}$

For postive control  $2^{-[(Ct_{\text{GAPDH}} - Ct_{18s\text{rRNA}}) - (Ct_{\text{GAPDH gene}} - Ct_{18s\text{rRNA}})]}$

RESULTS

The primer Pricebpa-MX2 is better than Pricebpa-MX1 because the E is closer 100% than Pricebpa-MX1.

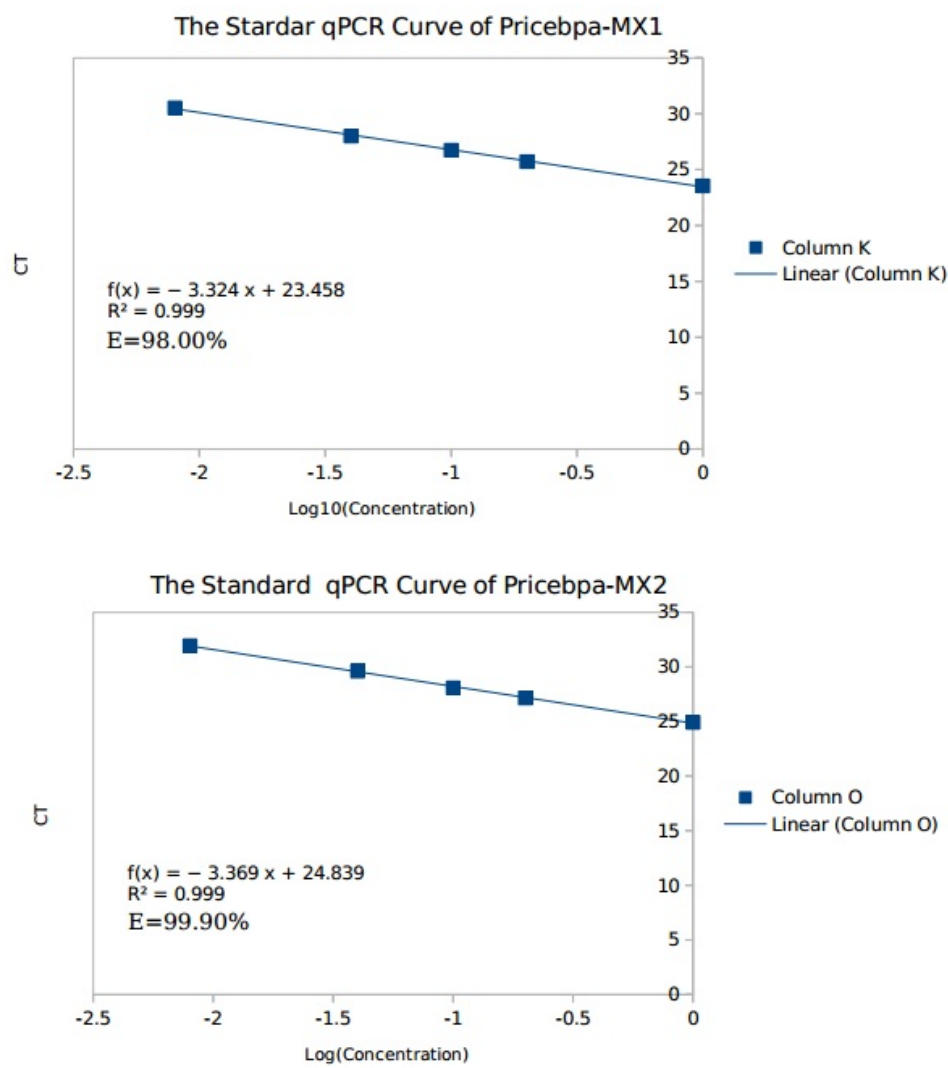
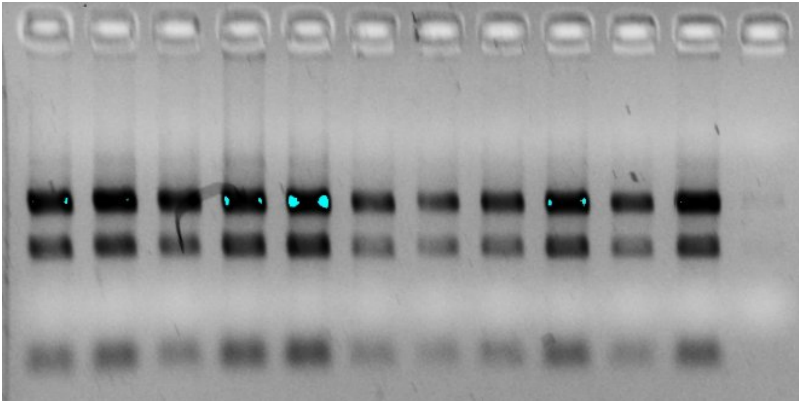


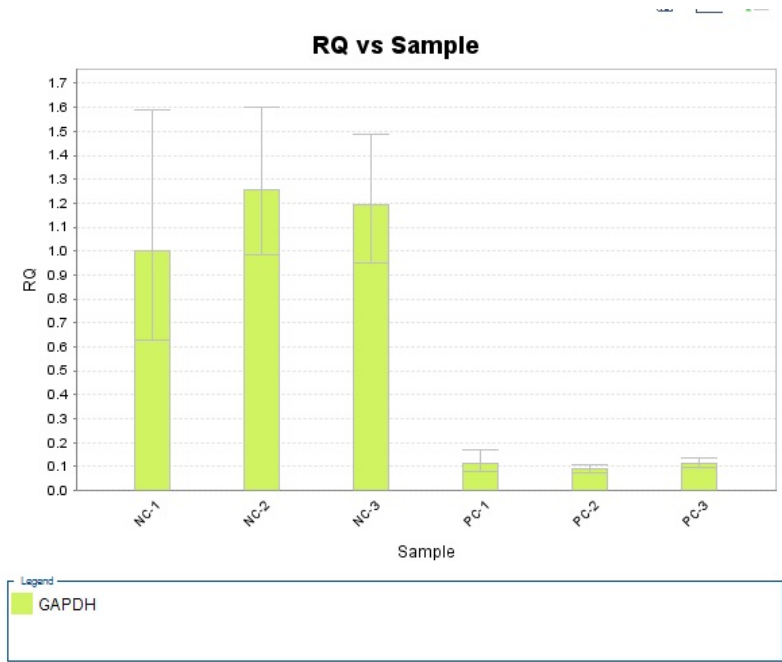
Figure 2. The standard qPCR curve of Pricebpa-MX1 and Pricebpa-MX2.

Figure 3.      Figure 4.

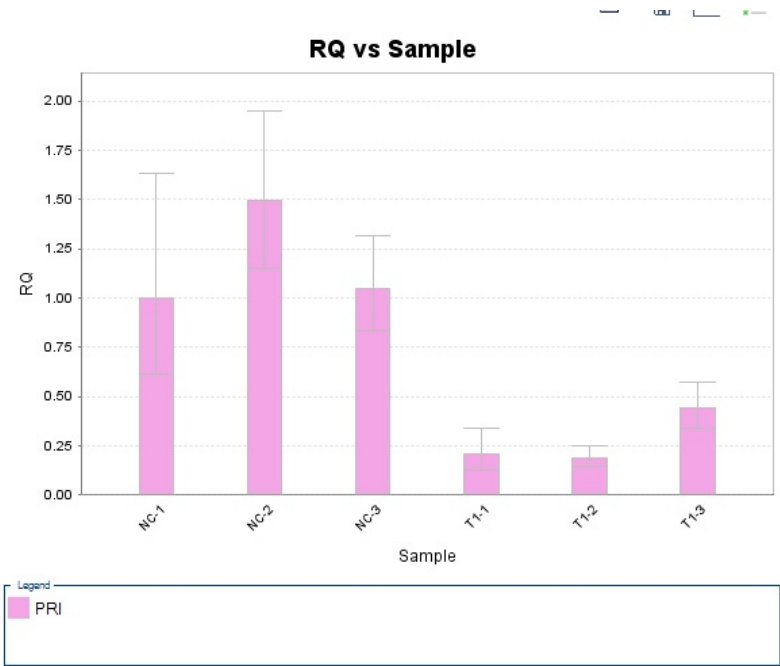
The  
Gel analysis of total RNA.  
Primer amplification efficiency: 杂峰  
siRNA efficient: knowdown efficiency



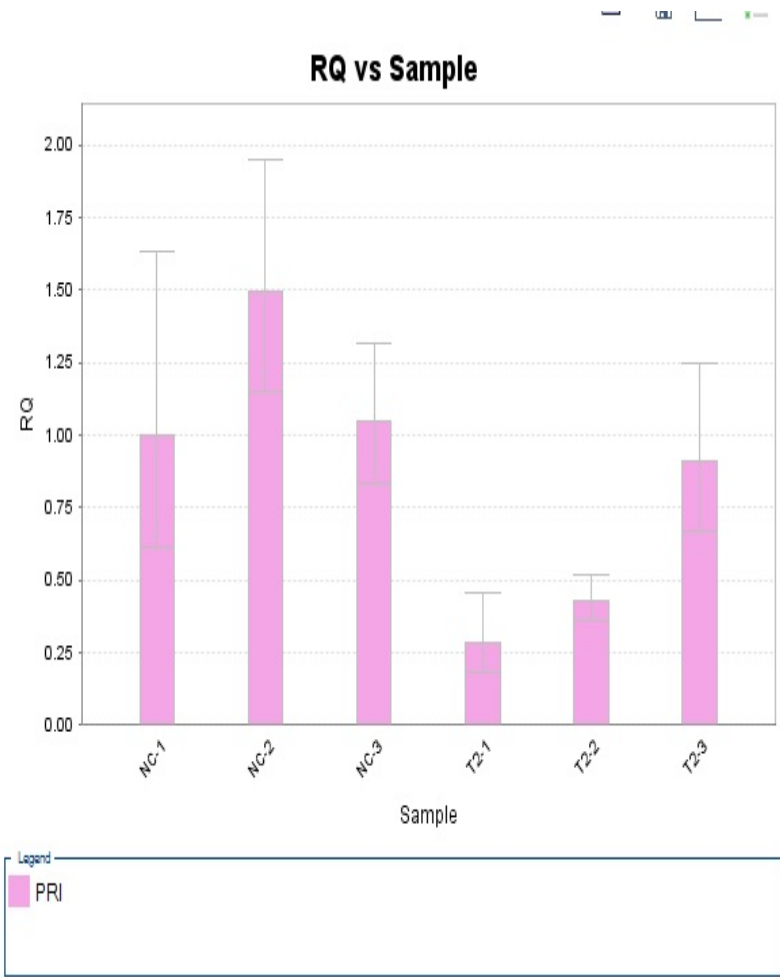
**Figure 5.** The Gel Graph of 4 isolativte RNAs. (From left to right: Postive Control, Negative control, siRNA 1, siRNA 2



**Figure 6.** The experssion of GADPH



**Figure 7.** The experssion of Cebp  $\alpha$  with siRNA



**Figure 8.** The expressino of Cebp  $\alpha$  with siRNA 2

## DISCUSSION

E%>100% 有非特异性扩增, E%<100% 效率

## CONCLUSION

## ACKNOWLEDGEMENTS

Xu wenxin and I finish this work together. *Conlict of interest statement.* None declared.

## REFERENCES

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- Pfaffl, M. W. (2001). A new mathematical model for relative quantification in real-time RT-PCR. *Nucleic Acids Research*, 29(9), e45.

图要有图注, p value