Figure S1. Map diagrams of the lentiviral, packaging plasmid backbones and partial sequencing results of the sgRNAs. (A) Map of the lentiviral and packaging plasmid backbones. (B) The sequences of each of the sgRNAs used.

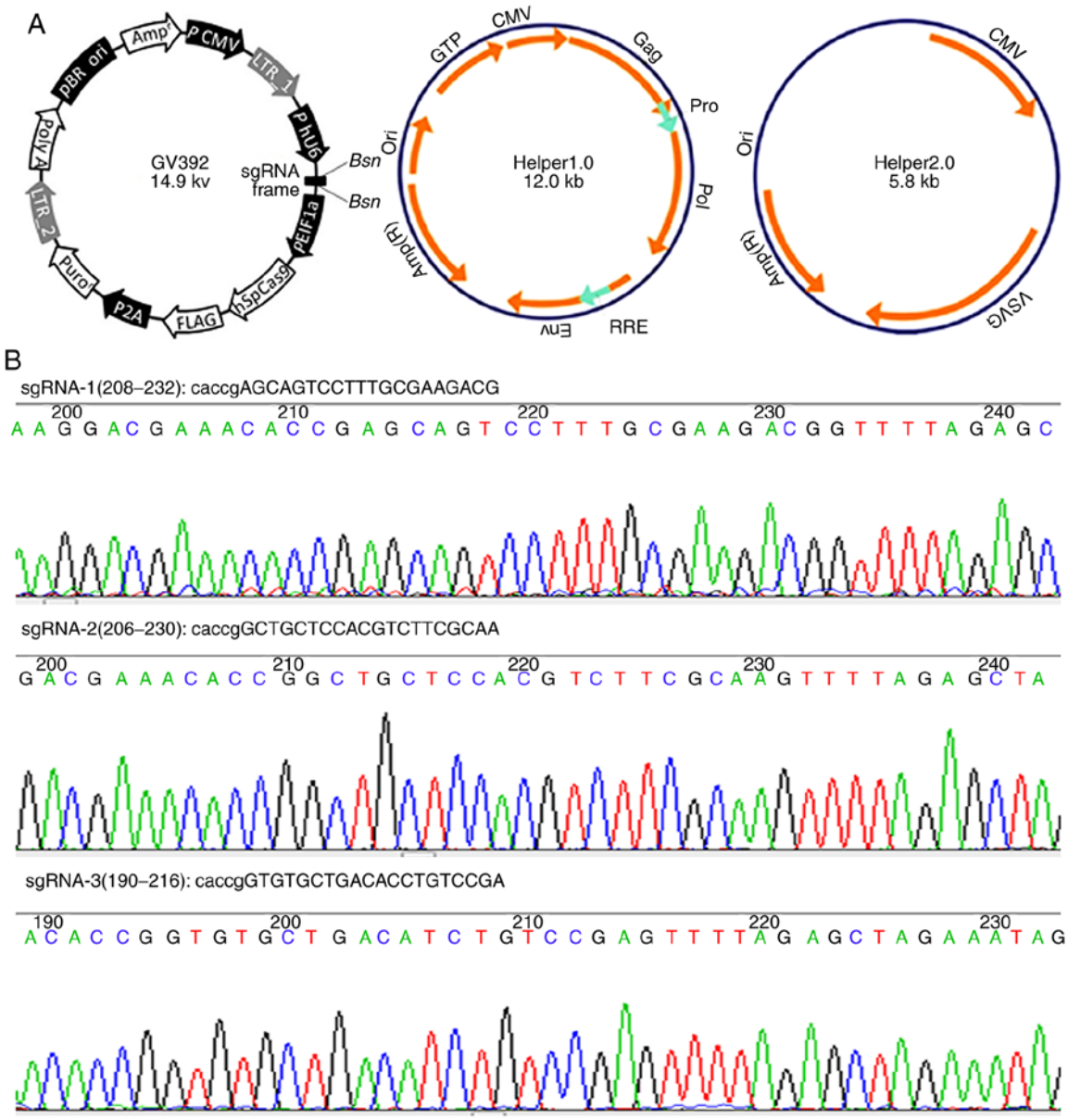
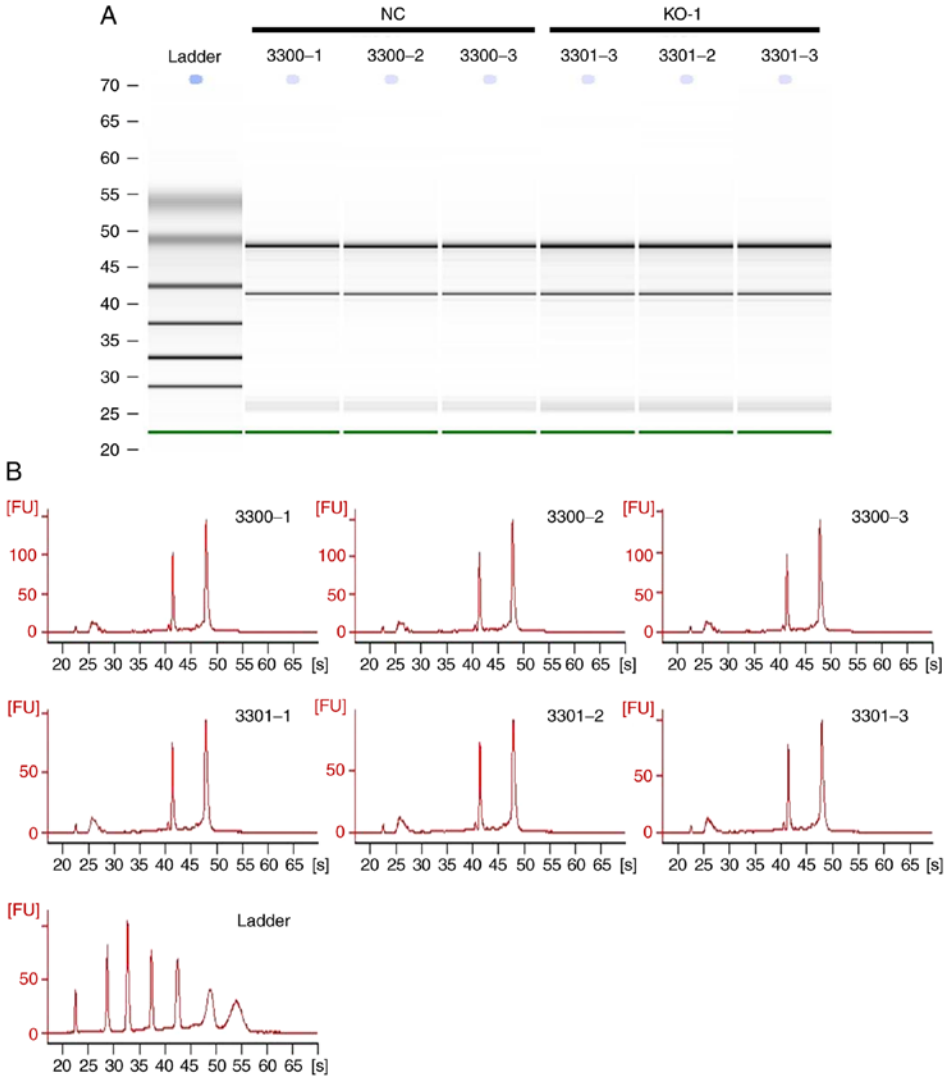


Figure S2. Quantity control of the RNA samples for use in chip assay. (A) RNA electrophoresis. Black bands from top to bottom represent 28S, 18S and 5S rRNA, respectively. (B) Agilent 2100 Bioanalyzer detection map results. Peaks from left to right represent the subunits of the ribosomes. Values on x-axis represent time (sec), and values on y-axis represent fluorescence intensity. (C) RNA concentration and purity. NC, negative control, cells transfected with scrambled sgRNA; KO, knockout.

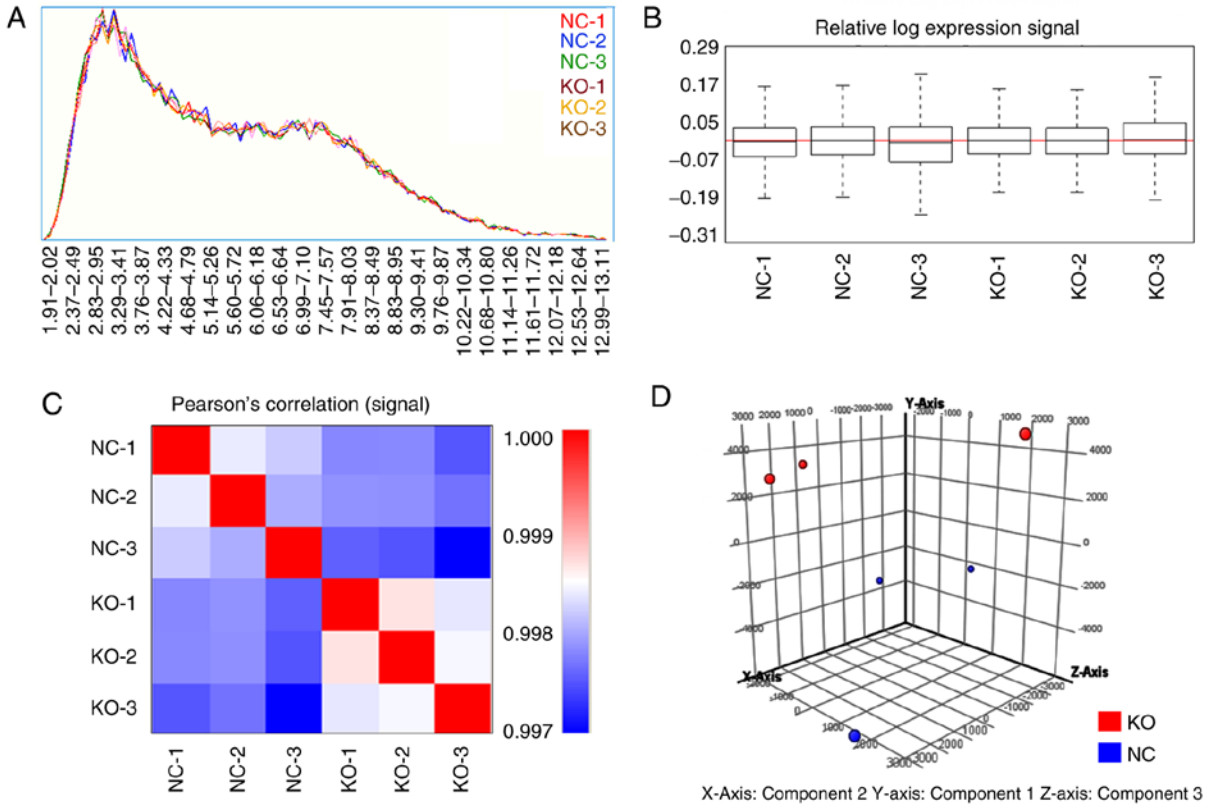


C

Sample	Name	Thermo NanoDrop 200		Agilent 2100 Bioanalyzer	
		Concentration*	A260/A280	RIN	28S/18S
3300–1	NC	1101.9	2.05	9.7	1.9
3300–2	NC	1193.6	2.04	9.7	1.9
3300–3	NC	1087.2	2.00	9.6	1.8
3301–1	KO	857.1	2.05	9.5	2.2
3301–2	KO	889.8	2.03	9.3	2.2
3301–3	KO	903.1	2.05	9.4	2.3

*Unit: ng/μl

Figure S3. Quantity control results of the chip signal. (A) Signal histogram. The x-axis indicates the probe expression value interval and the y-axis indicates the probe statistics in the expression value interval. (B) Relative signal emitted by each sample as indicated by the box plot. (C) Pearson's correlation analysis of fluorescence intensity signals emitted by each sample. Red color indicates high correlation and blue color indicates low correlation. (D) Principal components analysis. High similarity was observed within both NC and KO group, while large differences were observed between the NC and KO groups.



X-Axis: Component 2 Y-axis: Component 1 Z-axis: Component 3

Table SI. Sequences of the RhoE- and NC-sgRNA oligos.

No.	5'	Stem	3'
sgRNA-NC-a	CACCg	CGCTTCCGCGGCCCGTTCAA	
sgRNA-NC-b	aaac	TTGAACGGGCCGCGGAAGCG	c
RhoE-sgRNA-1-a	CACCg	AGCAGTCCTTTGCGAAGACG	
RhoE-sgRNA-1-b	aaac	CGTCTTCGCAAAGGACTGCT	c
RhoE-sgRNA-2-a	CACCg	GCTGCTCCACGTCTTCGCAA	
RhoE-sgRNA-2-b	aaac	TTGCGAAGACGTGGAGCAGC	c
RhoE-sgRNA-3-a	CACCg	GTGTGCTGACATCTGTCCGA	
RhoE-sgRNA-3-b	aaac	TCGGACAGATGTCAGCACAC	c

sgRNA, single guide RNA.

Table SII. Sequences of PCR primers and fragments of products before and after Cruiser nuclease digestion.

Number	Primer sequence (5'→3')	Amplicon size (bp)	Fragment 1 (bp)	Fragment 2 (bp)
sgRNA-1[a]	GTTGGAGAGGAGTAAAGAGCCG TGAAGTGTCCCACAGGCTCAAC	833	303	530
sgRNA-2[a]	GTTGGAGAGGAGTAAAGAGCCG TGAAGTGTCCCACAGGCTCAAC	833	298	535
sgRNA-3	GAACCACTGAGTCACGCAGAAT TATCAACTGTGTGCCCTAACCC	738	247	491

[a]sgRNA-1 and sgRNA-2 share the same pair of PCR primers. sgRNA, single guide RNA.

Table SIII. Sequences of primers used for the reverse transcription quantitative PCR validation of target genes.

Gene	Upstream (5'-3')	Downstream (5'-3')
GAPDH	TTCAACGGCACAGTCAAGG	CTCAGCACCAGCATCACC
ELK1	CAAAGGGTGCAGGAATGAC	TCTAAGGGGTTTGGACTGG
TIMP3	TTGCCTTGCTTTGTGACCT	CGTAGTGTTTGGACTGATAG
IL6ST	AAATGTGGTCGGCAAGTCC	GGTTTAGATGGCGGTGTCC
DNAJB12	GTGATGGCGGGCTAGGAGT	CCAGCAGTTGTTTCGGAGG
SOD3	GTGGCTCTGTCACCTGGAC	GAGTGCGTGTCGCCTATCT
FTH1	CCAGAACTACCACCAGGACTC	CAGTTTCTCAGCATGTTCCCT
Ccnb1	GAACGGCTGTTAGTGTTTAGGT	ATTCTTGACTGTTCGCTGACTT
ADAM10	TTATGGGAATTGCCCTGAT	GTGCCTGGAAGTGGTTTAG
CXCL12	ATATTCATCCGTGCCCTCG	GCAATGCCACCACCTGTAAC
JAK2	TCAAGAGGGAAACATAAGGAA	ATACCCGTCAATTAACGACAC
CDK2	CCTGGATGAAGACGGACGG	GGGGCACTGGTTTAGTCACAT
CDK4	ATTGGTGTCGGTGCCTATG	TCACGAACTGTGCTGACGG
CDK6	AGACCTCCTTCTGAAATGC	GTCTTGGAAGTACGGGTGA
CCNA1	GCCAAGCATGGATTTGATA	TCCTCTGCATATTCCGTTA
CCNE1	TGATTCAGCGTGCGTGGAC	AAGACGGGAAGTGGGGAGG
SCAP	GACTGAAAGGCTTCGTGAG	ATGATGGGAATGGGGTAGG
MAP3K1	GTTCCCTGTAAAATACCCT	TAGTTTGCTTGTGCTACCC
CBL	AGCCTTGCTGTAACTCACCCTG	TGTAACGTACCCAATAGCCCAC
DUSP1	GTTCCCAAGCAGTCATAACAAT	GGTAGGTATGTCAAGCACGAAG
BCL2LL1	AGGATCGGAGACGAGTTCAA	CCATACCAGACGGAAGATGA