

Supplementary

Table S1 Target gene, sgRNA design and plasmid information

Target gene	Species	Plasmid	Target number	SgRNA sequence
LOC100506675	Human	PCA04859	KO1	Forward: GAAGTCTGTAGCTAAATCTC Downstream: AGACCAGATCTCAGCTTATC
LOC100506675	Human	PCA04859	KO2	Forward: AGCAATATTTATTGACCGT Downstream: CTGGGTAAACCAACTTAAA

Table S2 Primers for detecting sgRNA and Cruiser™ digestion information

Target number	Primers	Product length	Digested fragment
KO1	Forward: ATGATCTGACGCAGCGCACTGC Reverse: GCAAGGGCTATTCTGAAGGGTC	651 bp	187 bp/259 bp
KO2	Forward: GCTACCTTGGAGGAAAGTTGCTC Reverse: GCTGAGTAAGACAGGTACCCAG	647 bp	349 bp/451 bp

Table S3 Primers for confirmation of NR_120526 knockout

Primers	Product length (positive)	Product length (negative)
Forward: GTAATTTATTTGAATGAGGCTGG Reverse: AGAATCCCTCCACCTACCAAGAG	653bp	5964bp (theoretically)

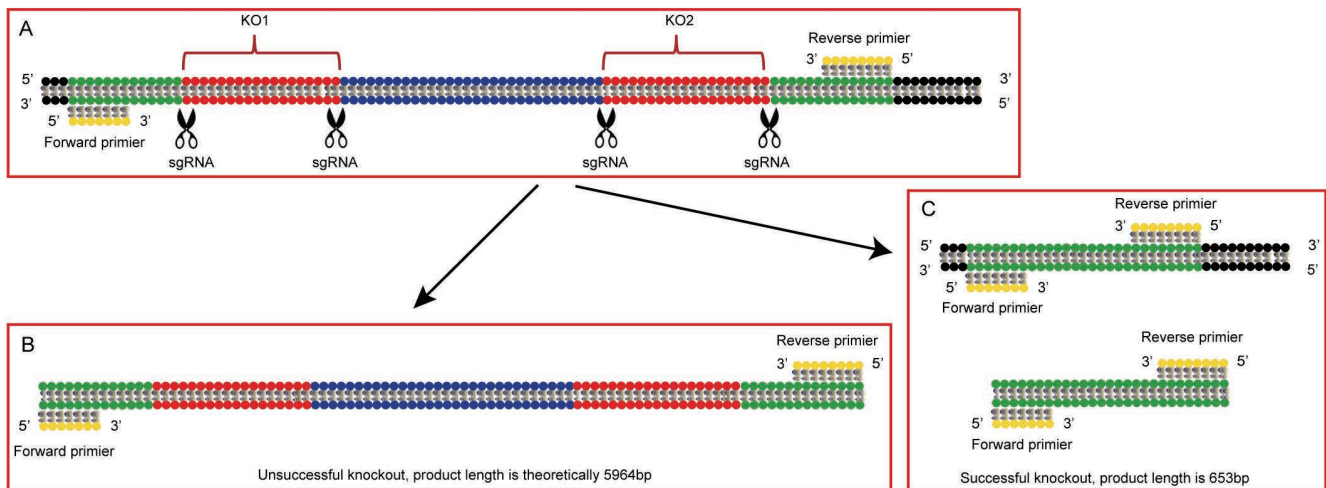


Figure S1 Schematic diagram for knockout of NR_120526 gene. (A) Design of sgRNAs and verification primers for NR_120526 gene knockout; (B) Amplified product for unsuccessful knockout NR_120526 gene; (C) Amplified product for successful knockout NR_120526 gene.

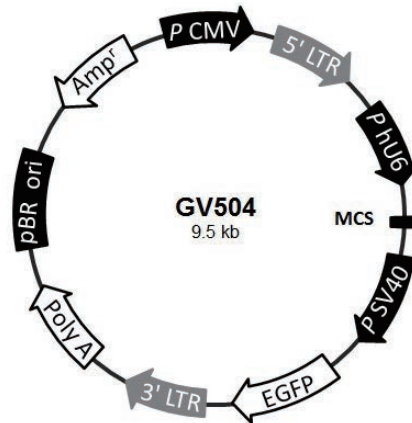


Figure S2 Plasmid information designed for knockout of NR_120526 gene.

Table S4 List of proteins that specifically bind to NR_120526

Protein name	Annotation	STRING_id
HSPA5	Heat shock 70kDa protein 5 (glucose-regulated protein, 78 kDa)	9606.ENSP00000324173
HSPD1	Heat shock 60kDa protein 1 (chaperonin)	9606.ENSP00000340019
SERPINB3	Serpin peptidase inhibitor, clade B (ovalbumin), member 3	9606.ENSP00000283752
RPLP0	Ribosomal protein, large, P0	9606.ENSP00000339027
PKM	Pyruvate kinase, muscle	9606.ENSP00000320171
ATP5A1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	9606.ENSP00000282050
KRT8	Keratin 8	9606.ENSP00000293308
LMNA	Lamin A/C	9606.ENSP00000357283
PKP1	Plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	9606.ENSP00000263946
VDAC2	Voltage-dependent anion channel 2	9606.ENSP00000361635
ILF3	Interleukin enhancer binding factor 3, 90 kDa	9606.ENSP00000404121
HADHA	Hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit	9606.ENSP00000370023
ILF2	Interleukin enhancer binding factor 2, 45 kDa	9606.ENSP00000355011
PARP1	Poly (ADP-ribose) polymerase 1	9606.ENSP00000355759
KRT86	Keratin 86	9606.ENSP00000452237
RPL22	Ribosomal protein L22	9606.ENSP00000346088
COX4I1	Cytochrome c oxidase subunit IV isoform 1	9606.ENSP00000253452
SSBP1	Single-stranded DNA binding protein 1, mitochondrial	9606.ENSP00000265304
SBSN	Suprabasin	9606.ENSP00000430242
RPS4X	Ribosomal protein S4, X-linked	9606.ENSP00000362744
PPIA	Peptidylprolyl isomerase A (cyclophilin A)	9606.ENSP00000419425
C1orf68	Chromosome 1 open reading frame 68	9606.ENSP00000354769
AK2	Adenylate kinase 2	9606.ENSP00000346921
P4HB	Prolyl 4-hydroxylase, beta polypeptide	9606.ENSP00000327801
RPSA	Ribosomal protein SA	9606.ENSP00000346067
KRT36	Keratin 36	9606.ENSP00000329165
VDAC1	Voltage-dependent anion channel 1	9606.ENSP00000265333
HSP90B1	Heat shock protein 90 kDa beta (Grp94), member 1	9606.ENSP00000299767
KRT84	Keratin 84	9606.ENSP00000257951

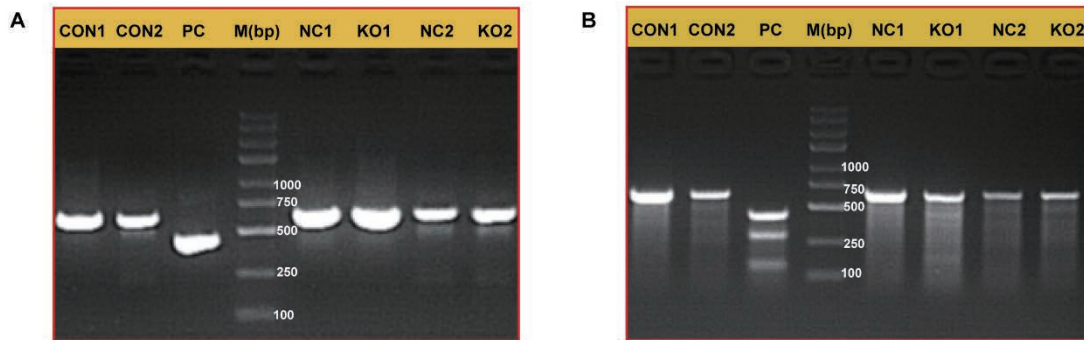


Figure S3 Results of screening for active NR_120526-sgRNA. The infection rate of K562 cells is 80%, and the recovery is 10 days after infection. (A) PCR detection of mixed clone pool; (B) PCR detection of mixed clone pool after Cruiser™ digestion (M stands for marker, PC stands for positive control, the size of the amplified fragment is 456bp, and the size of the digested fragment is 151bp and 303bp, respectively). CON, normal target K562 cells; NC, K562 cells infected with negative control virus; KO, K562 cells infected with LV-LOC100506675-sgRNA (04859-1).