

1 **Supplementary data**

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3 **Title:**

4 **Identification and characterization of rabbit ROSA26 for gene**
5 **knock-in and stable reporter gene expression**

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22 **Supp. Table 1.** Primers used in the present study.

	SIZE	sequences
For indel detection	F1/R1, 2kb	F1: 5'- agccctaaattcaagccctgtg-3' R1: 5'- agaagcctgtcccctaaacta-3' Pseq: 5'- ggggagtgaaaccagcagacg-3'
For Rosa-EGFP ki detection	F2/R2, 0.8 kb	F2: 5'- ctccccagcaggcagaagt-3' R2: 5'- aaggtgagaaacaggcagaaatagt-3'
For Rosa-Cre reporter ki detection	F3/R3, 1.5 kb	F3: 5'-agaagcctgtcccctaaacta-3' R3: 5'-cggcggcggtcacgaactcc-3'
5'-GSP		5'- gattacgccaagctt caggttcagggggaggtgtgggaggtt-3'
3'-GSPs		5'- gattacgccaagctt ggctgtgctctggggctccggtcctca-3' 5'- gattacgccaagctt attcttcgggccatcctgtattgtgtag-3'
For Realtime-PCR	F4/R4, 66 bp F5/R5, 79 bp	F4: 5'- agaagaggctgtgctctgg -3' R4: 5'- cagcaagtgtcgtccact -3' F5: 5'- aggctggcctcaactttgta -3' R5: 5'- acagccagtcaagtgtcgtc-3'

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38 **Supp. Table 2.** Weight comparison of rbRosa26-GFP and rbRosa26-Cre-reporter knock-in rabbits (F1
39 generation) with their age matched controls.
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	Weight (kg) ± SD (n)		
Age	rbRosa26-GFP ki	rbRosa26-Cre reporter ki	WT
5 months	3.27 ± 0.26 (9)		3.29 ± 0.07 (4)
4 months		2.70 ± 0.04 (5)	2.79 ± 0.10 (4)

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43 **Supp. Fig. 1. Off target analysis of in founder rabbits.** (A) Only one off target match is identified to be
 44 within an exon region of a gene. It is in the 3' UTR of Has2 gene. Red characters are the seed + PAM
 45 sequence in the sgRNA. (B) T7 endonuclease I assay revealed gene editing events in the on target region
 46 but none at the off target region in all founder animals examined. wt: wild type. M: NEB 100 bp DNA
 47 Ladder marker. On target: samples are from the on target region (i.e. rbRosa26). Off target: samples are
 48 from the off target regions (3' UTR of Has2) from founder #1 to #4. #1 and #2: breeding founders of
 49 rbRosa26-GFP knock-in rabbits. #3 and #4: breeding founders of rbRosa26-Cre-reporter knock-in rabbits.
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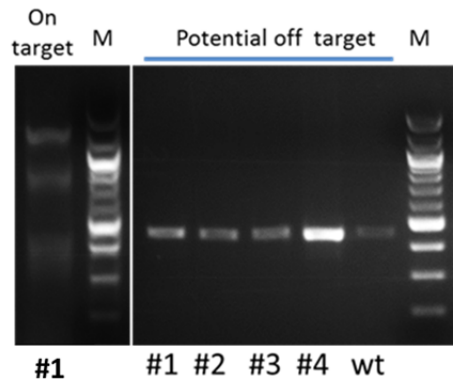
A. Off target match identified on the 3' UTR of Has2

Gene HAS2

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137491005 AATTTTATCAAAAATATTTTATTTTACAAAAAATCAATTATACTATACATCCTATACTGG
137491065 AAGTACATTGAATAATTGCTAAAATAAATACAGGCAATTAATTCACCTTTTTATAAGAAT
137491125 GAGAGAATTTGACATTTGAATGTTATCAAAGCTTAACTTAGAACATAAATAGTTAAAAAG
137491185 TCAAAGTCAAGTTTTAGTCTCATTATTTGGCATGGTATGTTTGTTCACCAAGCTCTCT
137491245 GATCCGTGAGAGTCTGAGTTTAAGAATCTTATGTACCTTTTGTAACTCTGAAGGTAGAATG
137491305 TGCAGCTTTTCTTAGGCAGGATAGATATAACATAGATGTCTACATGGAAAGGAAGCAGA
137491365 AGGGCAGGAAGCCACATTTTAACATTTCTCTACACGTCTCTGCTTCAGAACAAGGCTTT
137491425 GAAATTATTCATGCATTCGTGATGATGCTTTGTAACACAGGTCTACACAGCACCAGCTATA
137491485 AGGCAAGATTGAATGTTTACAAAAGTCAAATTGGATAATTGAGGTCCCATAGTAAGTAAAG
137491545 TTCAGAGCACCTGGTTCATCCAGTTTTCTATGTGCCAATTCCTTGACATACTACTTAACC
137491605 TTGATATCATTTCCTACT
  
```

B. T7 endonuclease I assay



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56 **Supp. Fig. 2. Donor DNA sequence and annotation**

57 rbRosa26-EGFP donor DNA sequence:

5'-

acaatgccatgcttcaactgtgtgtgtgtttttttataagacttttaaagtctgatgggaagacacccaaggacagtattcttcagag
cttcggtgttcagagagagctctcagacagttgcctttctatataatacaattctcaatcccacatccagagacgataaattcacagtgtgtgt
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atacttaagtcgctgatattctattcatagatgaaactcgggcctcatggtctcgo **GGCTAGCAGATCTGTAGGGCGCAGTAGTCCA**
Splicing Acceptor
GGGTTTCCTTGATGATGTCATACTTATCCTGTCCCTTTTTTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGT
CTTCCAGTGGGGATCGACGGTATCGATAAGCTTGGTACCGCGGGCCCGGGATCCACCGGTCGCCACC**ATGGTGA**
GCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAG
TTCAGCGTGTCGCGCAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGC
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Homologous Arm

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rbRosa26-cre-reporter donor DNA sequence:

5'-

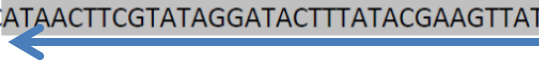
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Homologous Arm

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Splicing Acceptor
ATGATGTCATACTTATCCTGTCCCTTTTTTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGCTTTCCAGTAA
GAATTCCTCGATCGAGGGACCTA**ATAACTTCGTATAGCATACATTATACGAAGTTAT**ATTAAAGGGTTCCGCAAGCT
TTCGCCACC**ATGGTGAGCAAGGGCGAGGAGGTCATCAAAGAGTTCATGCGCTCAAGGTGCGCATGGAGGGCTC**
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LoxP2272

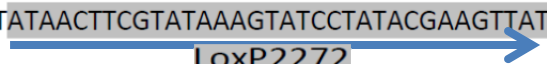


EGFP cDNA

LoxP



LoxP2272



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Homologous Arm
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68 *Homologous Arm* EGFP cDNA TdTomato cDNA Splicing Acceptor LoxP LoxP2272

69 26 bp sequence (5'-ggagcatgcagcttttctgggtt-3') were deleted to destroy sgRNA target.

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