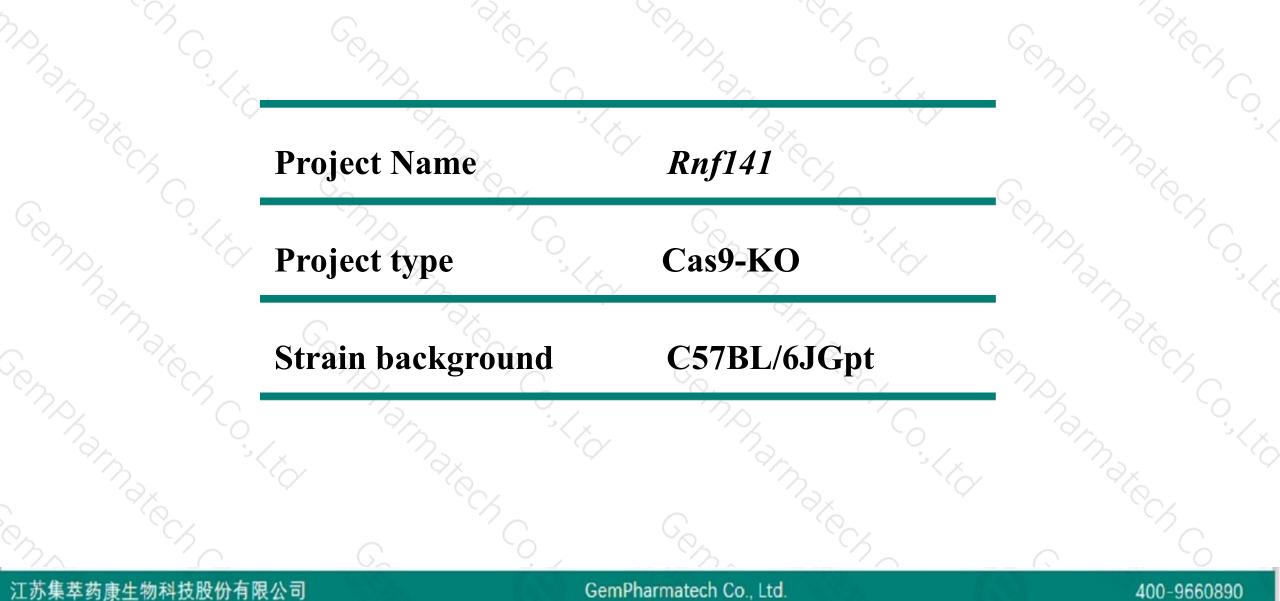


Rnf141 Cas9-KO Strategy

Designer: Yanhua Shen Reviewer: Xueting Zhang Design Date: 2019-09-02

Project Overview

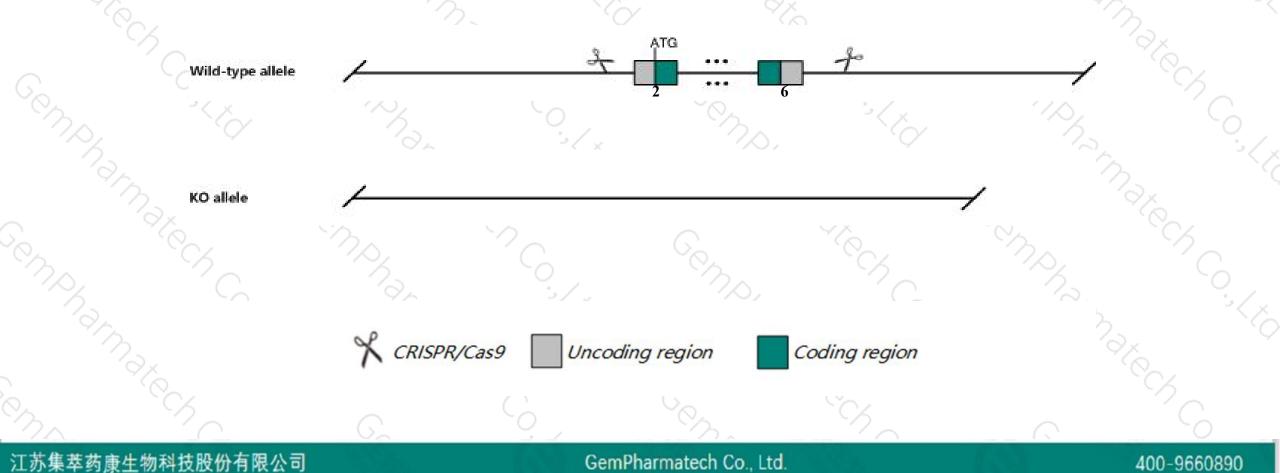




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Rnf141 gene. The schematic diagram is as follows:





The Rnf141 gene has 12 transcripts. According to the structure of Rnf141 gene, exon2-exon6 of Rnf141-209 (ENSMUST00000177236.7) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.

> In this project we use CRISPR/Cas9 technology to modify Rnf141 gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a targeted allele exhibit decreased litter size but normal spermatogeness and testes weight.
- The knockout region is about 1 kb from the 3th end of the *Ampd3* gene, which may affect the 3-terminal regulation of the gene.
 Transcripts 202, 212 are unaffected.
- The Rnf141 gene is located on the Chr7. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Notice

Gene information (NCBI)



\$?

Rnf141 ring finger protein 141 [Mus musculus (house mouse)]

Gene ID: 67150, updated on 12-Aug-2019

Summary

 Official Symbol
 Rnf141 provided by MGI

 Official Full Name
 ring finger protein 141 provided by MGI

 Primary source
 MGI:MGI:1914400

 See related
 Ensembl:ENSMUSG00000030788

 Gene type
 protein coding

 RefSeq status
 PROVISIONAL

 Organism
 Mus musculus

 Lineage
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

 Also known as
 ZFP36; ZNF230; AA792898; AU022812; 2610110L04Rik

 Expression
 Ubiquitous expression in lung adult (RPKM 5.5), subcutaneous fat pad adult (RPKM 5.1) and 28 other tissues See more human all

Transcript information (Ensembl)



The gene has 12 transcripts, all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|------------|----------------------|------|--------------|-------------------------|----------------|------------|-------------------------------|
| Rnf141-209 | ENSMUST00000177236.7 | 4032 | <u>230aa</u> | Protein coding | CCDS40086 | Q99MB7 | TSL:1 GENCODE basic APPRIS P1 |
| Rnf141-201 | ENSMUST00000106682.9 | 1101 | <u>230aa</u> | Protein coding | CCDS40086 | Q99MB7 | TSL:3 GENCODE basic APPRIS P1 |
| Rnf141-204 | ENSMUST00000175981.7 | 2333 | <u>133aa</u> | Protein coding | 84 | H3BJU0 | TSL:1 GENCODE basic |
| Rnf141-207 | ENSMUST00000176716.2 | 1080 | <u>87aa</u> | Protein coding | <u>62</u> | A0A1B0GT51 | TSL:2 GENCODE basic |
| Rnf141-210 | ENSMUST00000177462.7 | 859 | <u>180aa</u> | Protein coding | à.7 | H3BJB4 | TSL:5 GENCODE basic |
| Rnf141-203 | ENSMUST00000175648.1 | 422 | <u>59aa</u> | Protein coding | 87 | H3BJX9 | CDS 5' incomplete TSL:3 |
| Rnf141-211 | ENSMUST00000177520.1 | 419 | <u>75aa</u> | Protein coding | 81 | H3BJE9 | CDS 3' incomplete TSL:3 |
| Rnf141-208 | ENSMUST00000176746.7 | 317 | <u>21aa</u> | Protein coding | 62 | H3BKH1 | CDS 3' incomplete TSL:2 |
| Rnf141-206 | ENSMUST00000176210.1 | 647 | <u>28aa</u> | Nonsense mediated decay | 15 | H3BK28 | CDS 5' incomplete TSL:2 |
| Rnf141-212 | ENSMUST00000210070.1 | 4423 | No protein | Retained intron | 8 . | - | TSL:NA |
| Rnf141-202 | ENSMUST00000148367.1 | 793 | No protein | Retained intron | 81 | 2 | TSL:1 |
| Rnf141-205 | ENSMUST00000176048.1 | 614 | No protein | Retained intron | 62 | 2 | TSL:2 |

The strategy is based on the design of Rnf141-209 transcript, The transcription is shown below

< Rnf141-209 protein coding

Reverse strand

- 30.93 kb ---

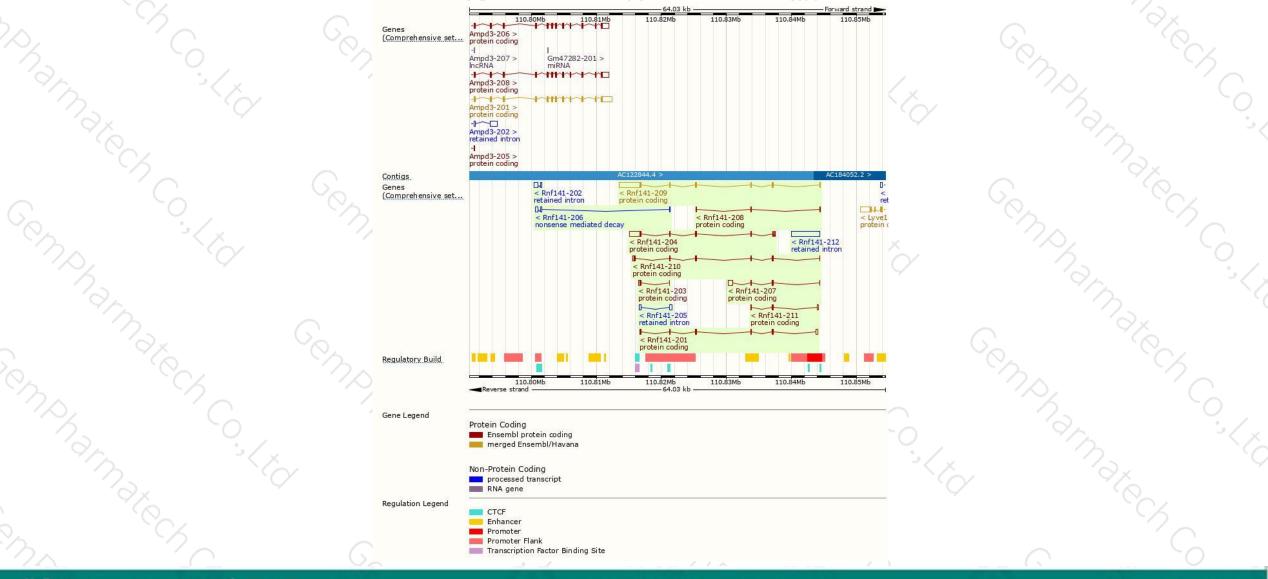
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400-9660890

Genomic location distribution





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GemPharmatech Co., Ltd.

400-9660890

Protein domain

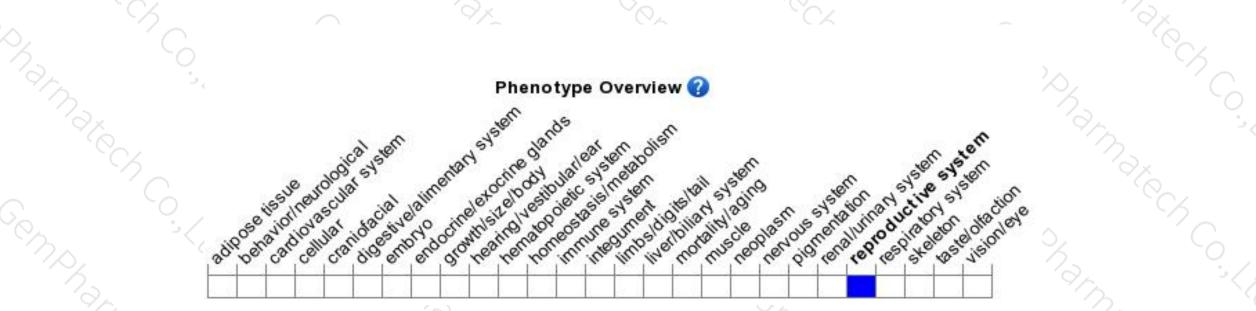




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Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(http://www.informatics.jax.org/).

According to the existing MGI data, Mice homozygous for a targeted allele exhibit decreased litter size but normal spermatogeness and testes weight.



If you have any questions, you are welcome to inquire. Tel: 400-9660890



