Rnase10 Cas9-CKO Strategy

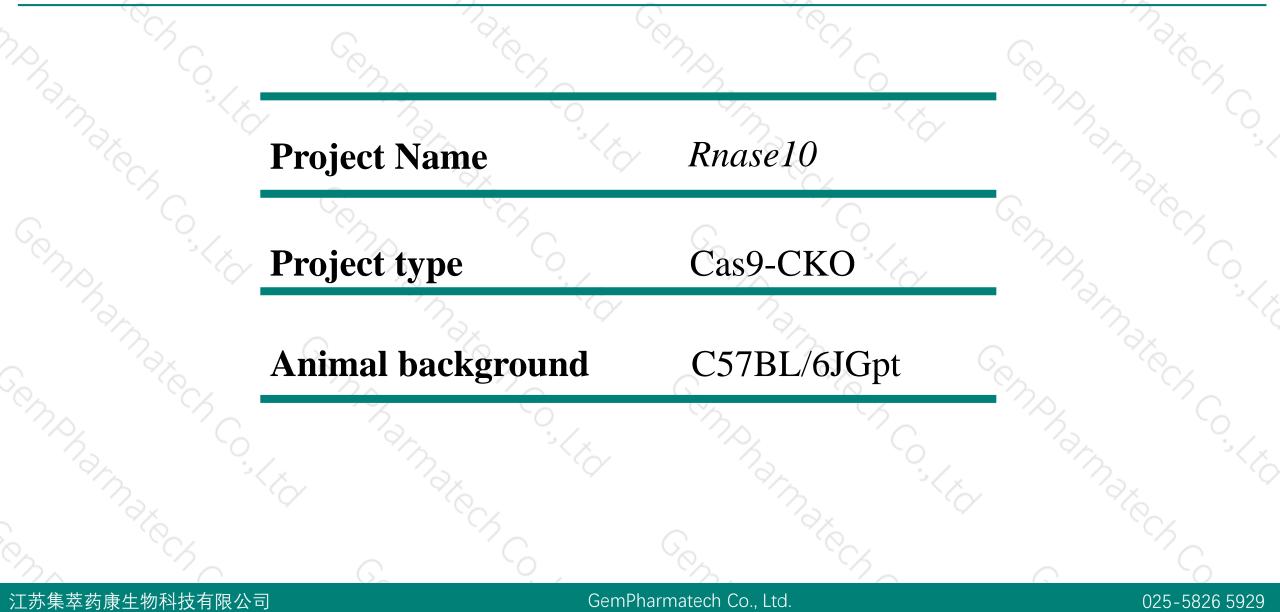
Designer: Reviewer :

Design Date:

Daohua Xu Huimin Su 2019-9-28

Project Overview

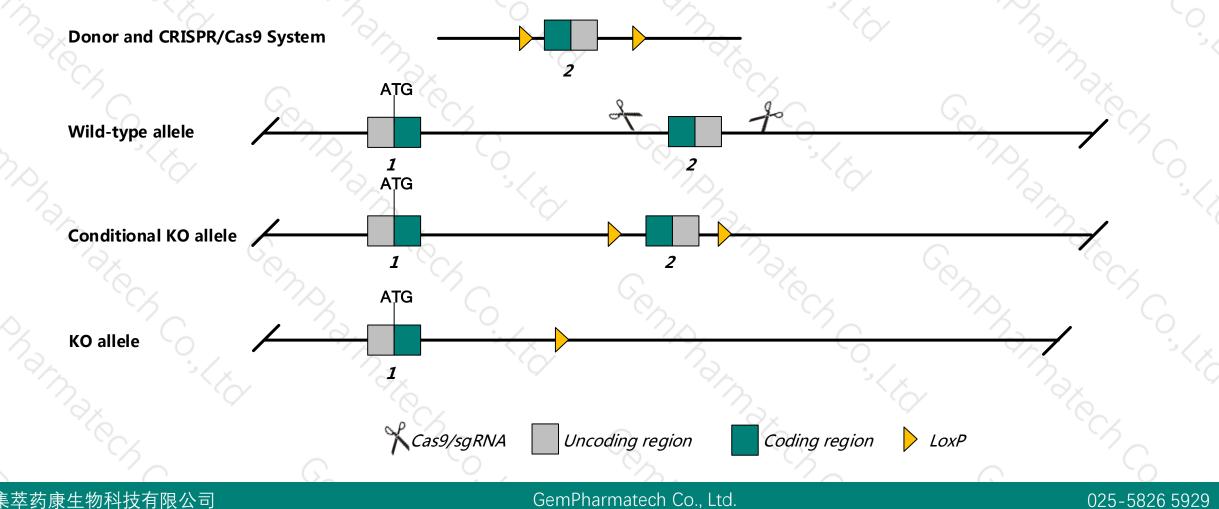




Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Rnase10* gene. The schematic diagram is as follows:



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- The *Rnase10* gene has 2 transcripts, According to the structure of *Rnase10* gene, exon2 of *Rnase10-201* transcript is recommended as the knockout region. The region contains the most of coding sequence. Knock out the region, result in destruction of protein.
- This project uses CRISPR/Cas9 technology to modify *Rnase10* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed, Cas9, sgRNA and donor were microinjected into fertilized eggs of C57BL/6JGpt mice and homologous recombination was carried out to obtain F0 mice. A stable and hereditary F1 generation mouse model was obtained by mating F0 generation mice with C57BL/6JGpt mice which were confirmed positive by PCR-sequencing.
- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

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Notice



- According to the existing MGI data, Homozygous disruption of this gene leads to decreased bone mineral density, alterations in B cell, T cell and NK cell number, and abnormal circulating glucose, creatinine, chloride and serum albumin levels.
- The *Rnase10* gene is located in the Chr14. If the knockout mice are mixed with other mice, two target genes are avoided on the same chromosome as possible, otherwise the offspring of mice with double gene positive and homozygous gene knockout can not be obtained.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)



2 ?

Rnase10 ribonuclease, RNase A family, 10 (non-active) [Mus musculus (house mouse)]

Gene ID: 75019, updated on 23-Oct-2018

Summary

 Official Symbol
 Rnase10 provided by MGI

 Official Full Name
 ribonuclease, RNase A family, 10 (non-active) provided by MGI

 Primary source
 MGI:MGI:1922269

 See related
 Ensembl:ENSMUSG0000021872

 Gene type
 protein coding

 RefSeq status
 VALIDATED

 Organism
 Mus musculus

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

 Also known as
 Rah1; 4930474F22Rik

 Expression
 Restricted expression toward genital fat pad adult (RPKM 393.6) See more

 Orthologs
 human all

Transcript information (Ensembl)

The gene has 2 transcripts, and all transcripts are shown below :

Show/hide o	columns (1 hidden)								Filter	
Name 🍦	Transcript ID 🛛 🍦	bp 🖕	Protein 🖕	Biotype 🍦	CCDS 🍦	UniProt 🖕	RefSeq 🍦		Flags	\$
Rnase10-201	ENSMUST00000022424.7	1629	<u>245aa</u>	Protein coding	<u>CCDS27030</u> ജ	<u>E9QPU5</u> @	<u>NM 029145</u> മ <u>NP 083421</u> മ	TSL:1	GENCODE basic	APPRIS P3
Rnase10-202	ENSMUST00000164632.1	1521	<u>208aa</u>	Protein coding	<u>CCDS49480</u> ജ	<u>G3UWD1</u> മ	<u>NM 001162863</u> ଜ NP 001156335ଜ	TSL:1	GENCODE basic	APPRIS ALT2

The strategy is based on the design of *Rnase10-201* transcript, The transcription is shown below :

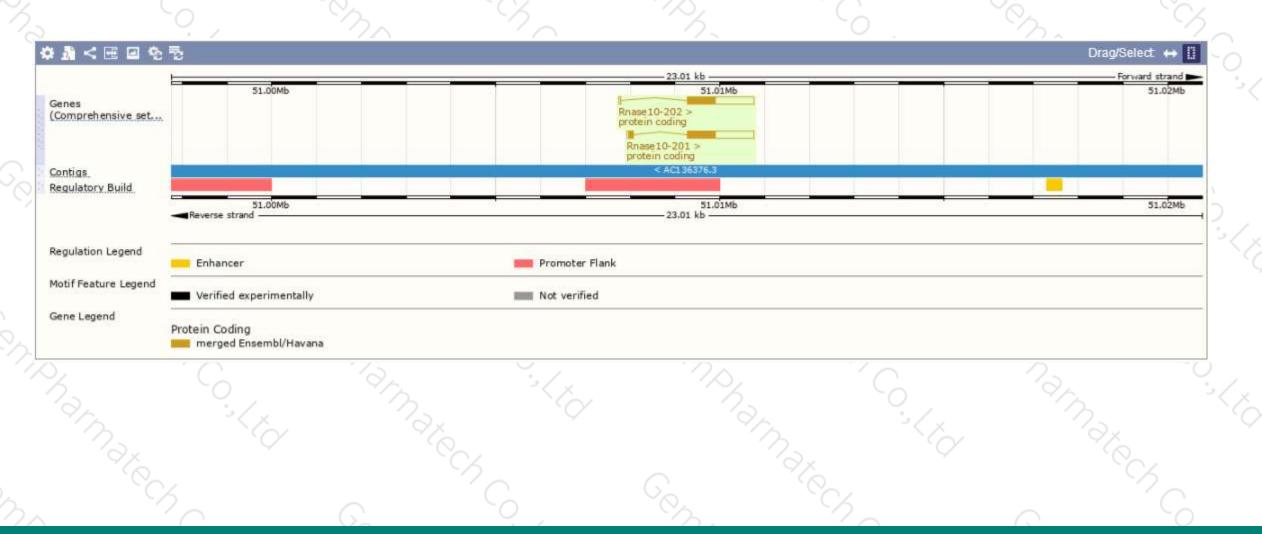
	- 2.83 kb	- Forward strand
Page 10, 201 >		
protein coding		

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Genomic location distribution





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Mouse phenotype description(MGI)

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Phenotype Overview 🕜

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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, Homozygous disruption of this gene leads to decreased bone mineral density, alterations in B cell, T cell and NK cell number, and abnormal circulating glucose, creatinine, chloride and serum albumin levels.

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If you have any questions, you are welcome to inquire. Tel: 025-5864 1534



