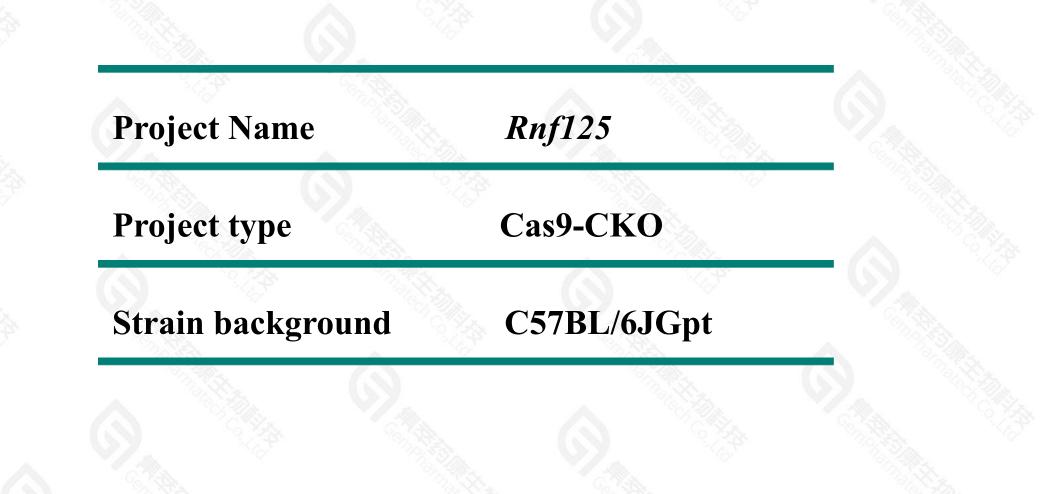


Rnf125 Cas9-CKO Strategy

Designer: Qiong Zhou

Project Overview





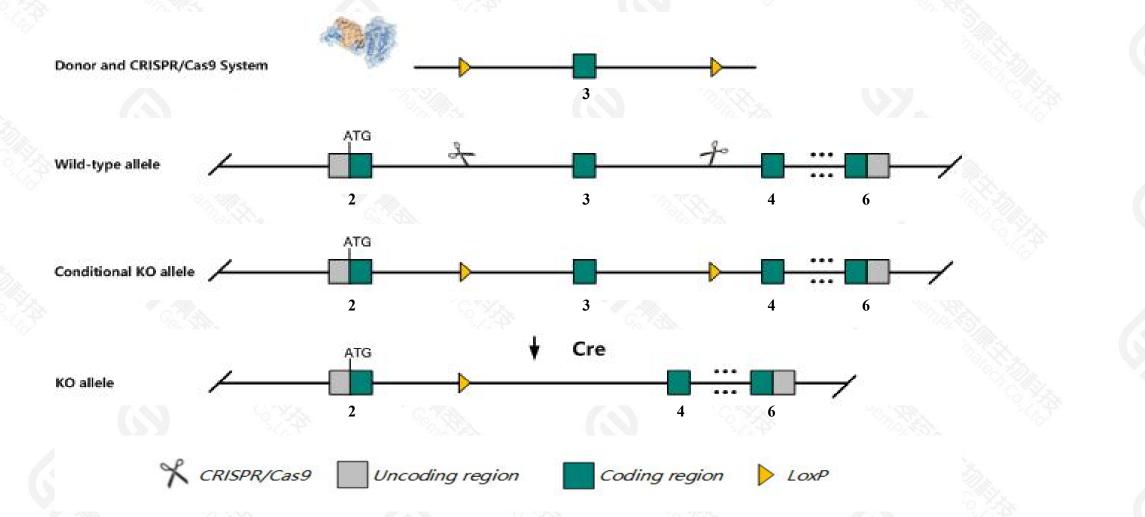
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Conditional Knockout strategy

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This model will use CRISPR/Cas9 technology to edit the *Rnf125* gene. The schematic diagram is as follows:



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Technical routes



The Rnf125 gene has 2 transcripts. According to the structure of Rnf125 gene, exon3 of Rnf125-201(ENSMUST00000050004.3) transcript is recommended as the knockout region. The region contains 95bp coding sequence. Knock out the region will result in disruption of protein function.

> In this project we use CRISPR/Cas9 technology to modify *Rnf125* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

> The flox mice will be 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.



- > The *Rnf125* gene is located on the Chr18. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Rnf125 ring finger protein 125 [Mus musculus (house mouse)]

Gene ID: 67664, updated on 7-Mar-2021

Summary

Official Symbol	Rnf125 provided by MGI
Official Full Name	ring finger protein 125 provided by <u>MGI</u>
Primary source	MGI:MGI:1914914
See related	Ensembl:ENSMUSG00000033107
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
	Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4930553F04Rik, C730049014, C730049014Rik
Expression	Broad expression in liver adult (RPKM 19.3), testis adult (RPKM 9.0) and 18 other tissuesSee more
Orthologs	human all

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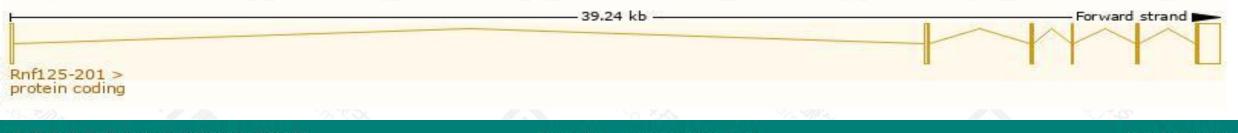
Transcript information (Ensembl)

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf125-201	ENSMUST0000050004.3	1348	<u>140aa</u>	Protein coding	CCDS29088		TSL:1, GENCODE basic,
Rnf125-202	ENSMUST00000234316.2	1406	<u>233aa</u>	Protein coding	-		GENCODE basic , APPRIS P1 ,

The strategy is based on the design of *Rnf125-201* transcript, the transcription is shown below:

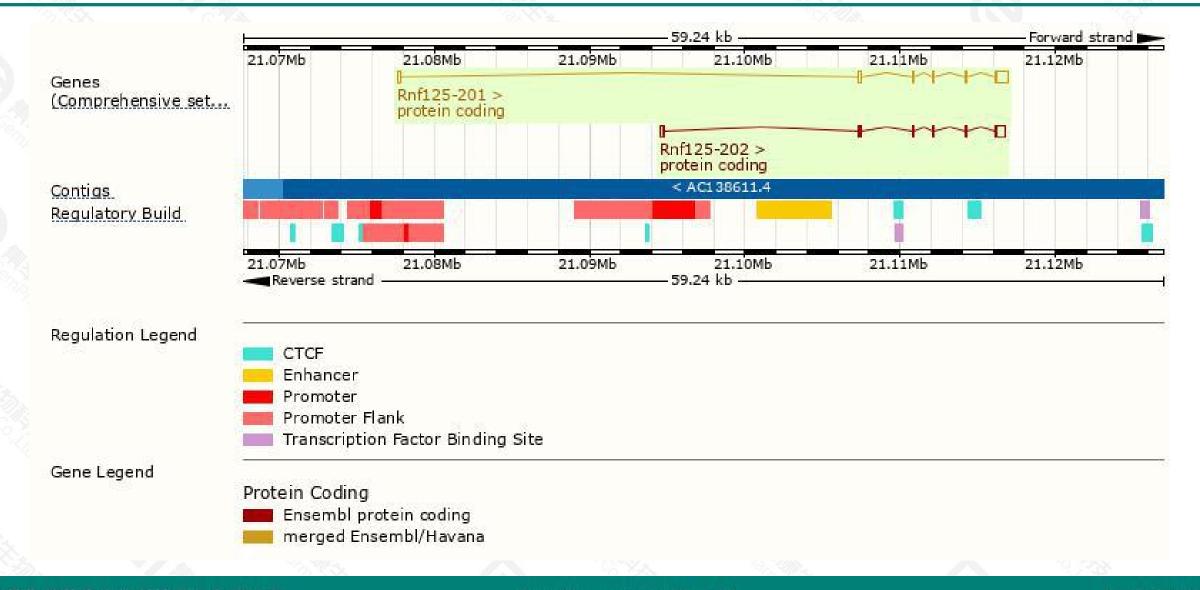


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Genomic location distribution





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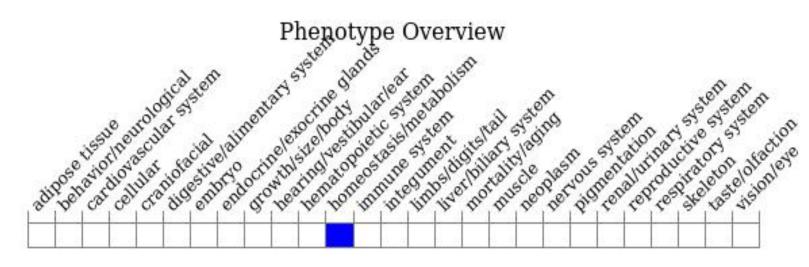
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Protein domain



fam.	Zinc finger C2HC RNF-type	Drought	induced 19 protein type, z	inc-binding domain	
ROSITE profiles	Zinc finger C2HC RNF-	type			
CONSIGNOUS AND	PTHR46016				
ANTHER	PTTTVTUDIO				
ANTHER	PTHR46016:SF2				
ANTHER Il sequence SNPs/i	PTHR46016:SF2	and all other sources)		
	PTHR46016:SF2)		

Mouse phenotype description(MGI)



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

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



