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GemPharmatech

Rnf10 Cas9-KO Strategy

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Reviewer **Huan Fan**

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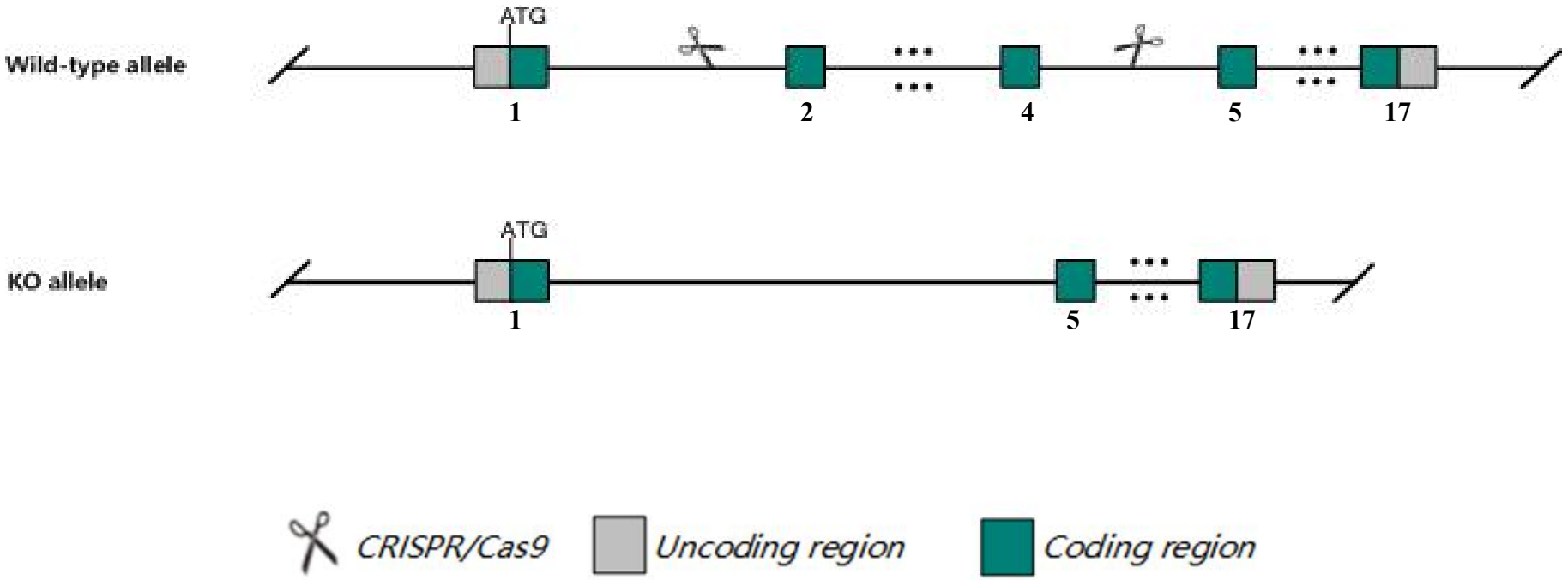
Project Overview

Project Name	***Rnf10***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnf10* gene. The schematic diagram is as follows:



Technical routes

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The *Rnf10* gene has 11 transcripts. According to the structure of *Rnf10* gene, exon2-exon4 of *Rnf10-201* (ENSMUST00000040555.14) transcript is recommended as the knockout region.The region contains 488bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Rnf10* gene. The brief process is as follows: gRNA was transcribed in vitro.Cas9 and gRNA 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.

Notice

The *Rnf10* gene is located on the Chr5. 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.

Gene information NCBI

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Rnf10 ring finger protein 10 [Mus musculus (house mouse)]

Gene ID: 50849, updated on 31-Jan-2019

Summary

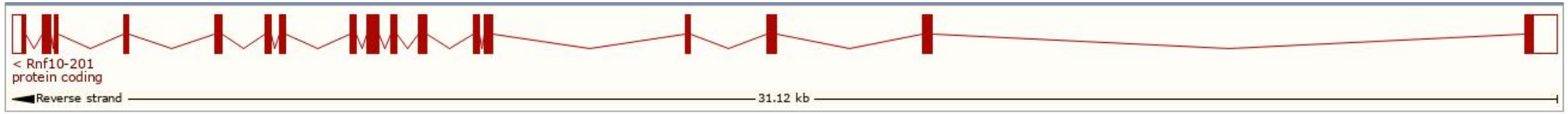
Official Symbol	Rnf10 provided by MGI
Official Full Name	ring finger protein 10 provided byMGI
Primary source	MGI:MGI:1859162
See related	Ensembl:ENSMUSG00000041740
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA675014, RIE2, mKIAA0262
Summary	The protein encoding this gene is a member of the really interesting new gene finger protein family. Members of this family contain protein motifs similar to zinc finger domains and are involved in many processes that include transcriptional regulation, DNA repair and signal transduction. Expression of this gene is upregulated during neuronal differentiation of cultured cells, and inhibition of its expression impairs differentiation and cell cycle exit, providing evidence for a function in neuronal differentiation. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Oct 2014]
Expression	Ubiquitous expression in adrenal adult (RPKM 116.7), testis adult (RPKM 98.0) and 28 other tissuesSee more
Orthologs	human all

Transcript information Ensembl

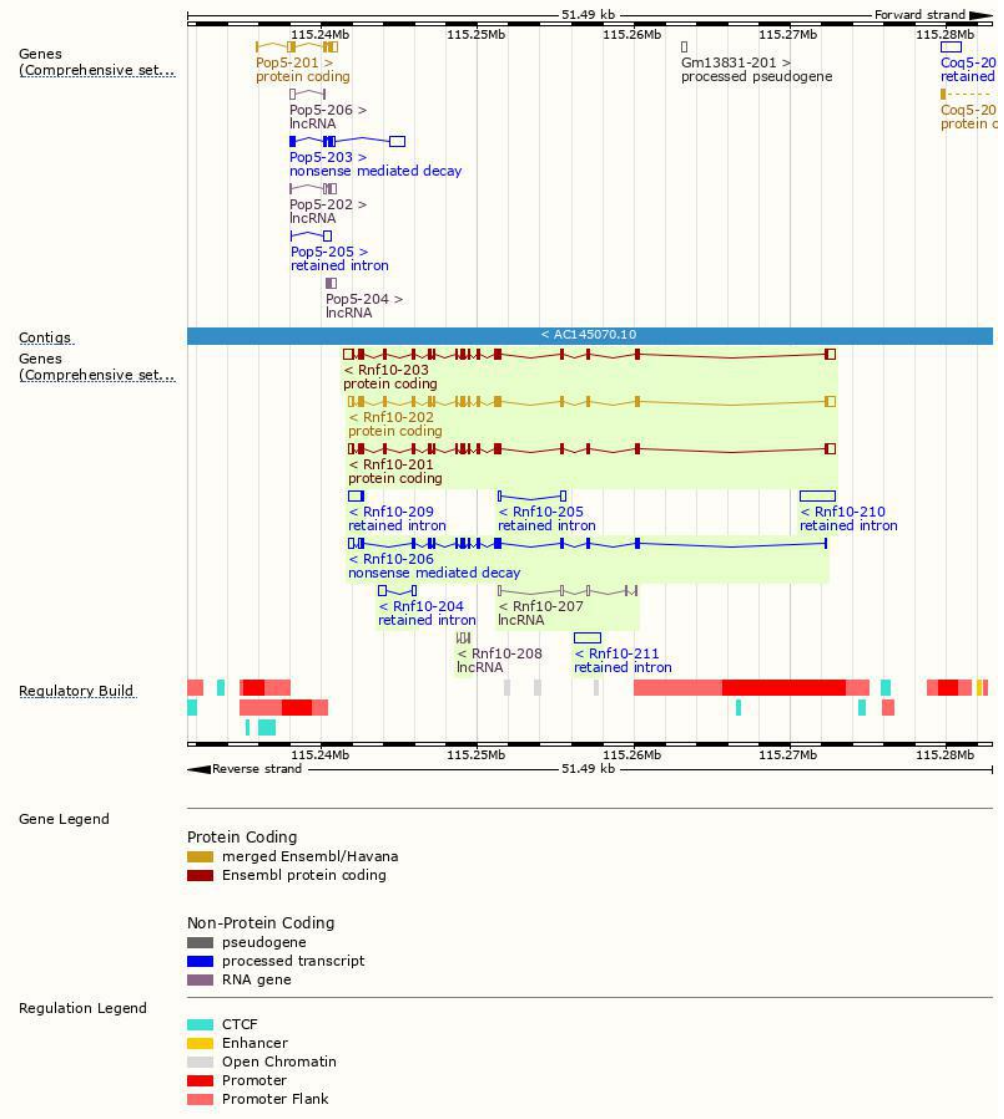
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf10-203	ENSMUST00000112097.7	3476	805aa	Protein coding	CCDS80381	D3Z1N2	TSL:1 GENCODE basic APPRIS ALT2
Rnf10-202	ENSMUST00000112096.8	3112	804aa	Protein coding	CCDS19584	Q3UIW5	TSL:1 GENCODE basic APPRIS P3
Rnf10-201	ENSMUST00000040555.14	3106	803aa	Protein coding	CCDS80380	H7BX06	TSL:1 GENCODE basic APPRIS ALT2
Rnf10-206	ENSMUST00000139853.1	2408	656aa	Nonsense mediated decay	-	F7AN16	CDS 5' incomplete TSL:5
Rnf10-210	ENSMUST00000200923.1	2276	No protein	Retained intron	-	-	TSL:NA
Rnf10-211	ENSMUST00000202855.1	1672	No protein	Retained intron	-	-	TSL:NA
Rnf10-209	ENSMUST00000153553.1	833	No protein	Retained intron	-	-	TSL:5
Rnf10-204	ENSMUST00000128954.1	657	No protein	Retained intron	-	-	TSL:2
Rnf10-205	ENSMUST00000133276.1	447	No protein	Retained intron	-	-	TSL:3
Rnf10-207	ENSMUST00000151085.1	600	No protein	lncRNA	-	-	TSL:2
Rnf10-208	ENSMUST00000152613.1	364	No protein	lncRNA	-	-	TSL:1

The strategy is based on the design of *Rnf10-201*transcript,The transcription is shown below

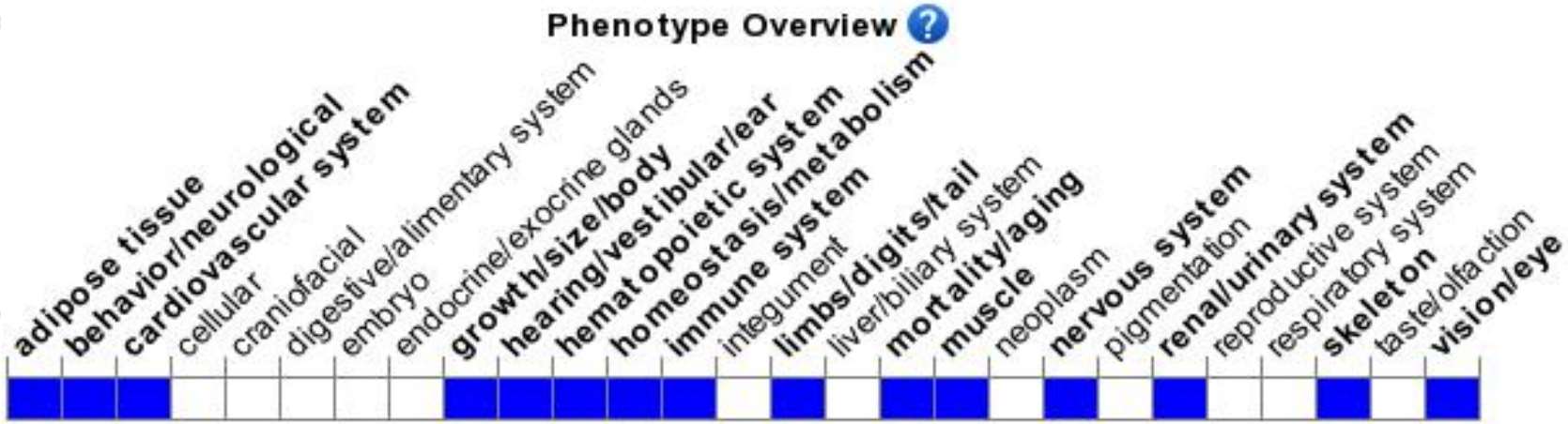


Genomic location distribution



Protein domain

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.

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