

Rnf14 Cas9-CKO Strategy

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Project Overview



Project Name

Rnf14

Project type

Cas9-CKO

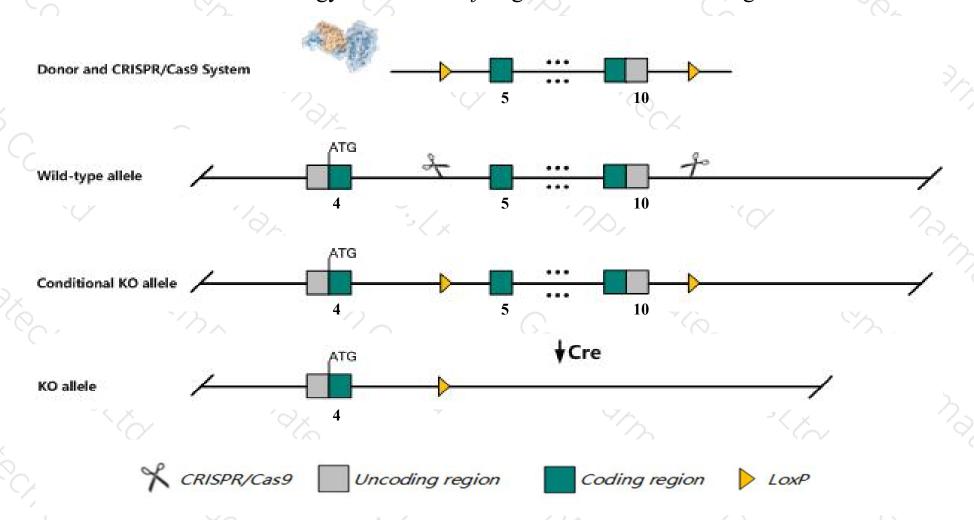
Strain background

C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Rnf14 gene. The schematic diagram is as follows:



Technical routes



- The *Rnf14* gene has 21 transcripts. According to the structure of *Rnf14* gene, exon5-exon10 of *Rnf14-203* (ENSMUST00000171461.2) transcript is recommended as the knockout region. The region contains most 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 *Rnf14* 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.

Notice



- ightharpoonup The effect on transcript *Rnf14*-206&210 is unknown.
- > Transcript *Rnf14*-207&213&221 may not be affected.
- The *Rnf14* 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)



Rnf14 ring finger protein 14 [Mus musculus (house mouse)]

Gene ID: 56736, updated on 24-Oct-2019

Summary

☆ ?

Official Symbol Rnf14 provided by MGI

Official Full Name ring finger protein 14 provided by MGI

Primary source MGI:MGI:1929668

See related Ensembl: ENSMUSG00000060450

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 Triad2; AA986456; AU041447; D7Bwg0165e; D18Ertd188e; 2310075C09Rik; 2610005D23Rik

Expression Ubiquitous expression in CNS E18 (RPKM 51.1), cortex adult (RPKM 38.6) and 28 other tissues See more

Orthologs <u>human</u> all

Genomic context



Location: 18 B3; 18 20.2 cM

See Rnf14 in Genome Data Viewer

Exon count: 15

Annotation release	Status	Assembly	Chr	Location	
108	current	GRCm38.p6 (GCF_000001635.26)	18	NC_000084.6 (3827746038317852)	
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	18	NC_000084.5 (3845628938477503)	

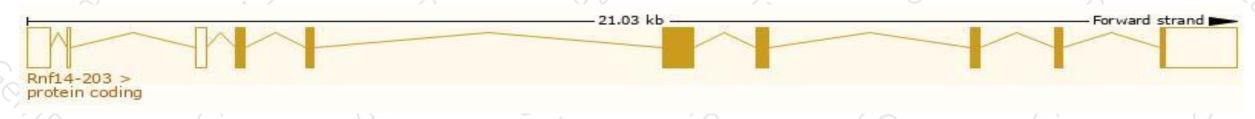
Transcript information (Ensembl)



The gene has 21 transcripts, all transcripts are shown below:

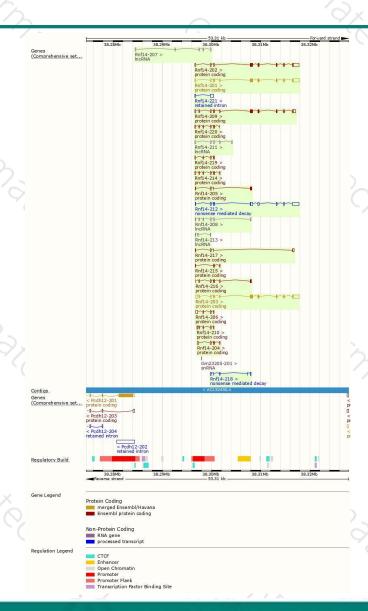
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf14-203	ENSMUST00000171461.2	3340	485aa	Protein coding	CCDS29200	Q9JI90	TSL:1 GENCODE basic APPRIS P1
Rnf14-201	ENSMUST00000072376.12	3040	485aa	Protein coding	CCDS29200	Q9JI90	TSL:1 GENCODE basic APPRIS P1
Rnf14-202	ENSMUST00000170811.7	2886	359aa	Protein coding	CCDS50261	G3XA54	TSL:1 GENCODE basic
Rnf14-209	ENSMUST00000236116.1	2410	485aa	Protein coding	CCDS29200	-	GENCODE basic APPRIS P1
Rnf14-216	ENSMUST00000237211.1	864	183aa	Protein coding	178		CDS 3' incomplete
Rnf14-214	ENSMUST00000236982.1	776	94aa	Protein coding	691	-	CDS 3' incomplete
Rnf14-204	ENSMUST00000235491.1	767	102aa	Protein coding	1/40	ů.	CDS 3' incomplete
Rnf14-206	ENSMUST00000235811.1	740	28aa	Protein coding	1.0	-	CDS 3' incomplete
Rnf14-205	ENSMUST00000235549.1	717	142aa	Protein coding	153		CDS 3' incomplete
Rnf14-210	ENSMUST00000236319.1	684	40aa	Protein coding	691	-	CDS 3' incomplete
Rnf14-220	ENSMUST00000237903.1	662	65aa	Protein coding	1/40	-	CDS 3' incomplete
Rnf14-217	ENSMUST00000237416.1	618	23aa	Protein coding	343	-	GENCODE basic
Rnf14-219	ENSMUST00000237824.1	530	49aa	Protein coding	153	- 6	CDS 3' incomplete
Rnf14-215	ENSMUST00000237089.1	364	87aa	Protein coding	686	-	CDS 3' incomplete
Rnf14-212	ENSMUST00000236649.1	2822	<u>79aa</u>	Nonsense mediated decay	1920	-	
Rnf14-218	ENSMUST00000237667.1	674	39aa	Nonsense mediated decay	3.23	-	
Rnf14-221	ENSMUST00000238031.1	796	No protein	Retained intron	-		
Rnf14-208	ENSMUST00000236032.1	778	No protein	IncRNA	6-8	-	
Rnf14-211	ENSMUST00000236353.1	743	No protein	IncRNA	(2)	-	
Rnf14-207	ENSMUST00000235812.1	548	No protein	IncRNA	188	-	
Rnf14-213	ENSMUST00000236690.1	424	No protein	IncRNA		-	

The strategy is based on the design of Rnf14-203 transcript, The transcription is shown below



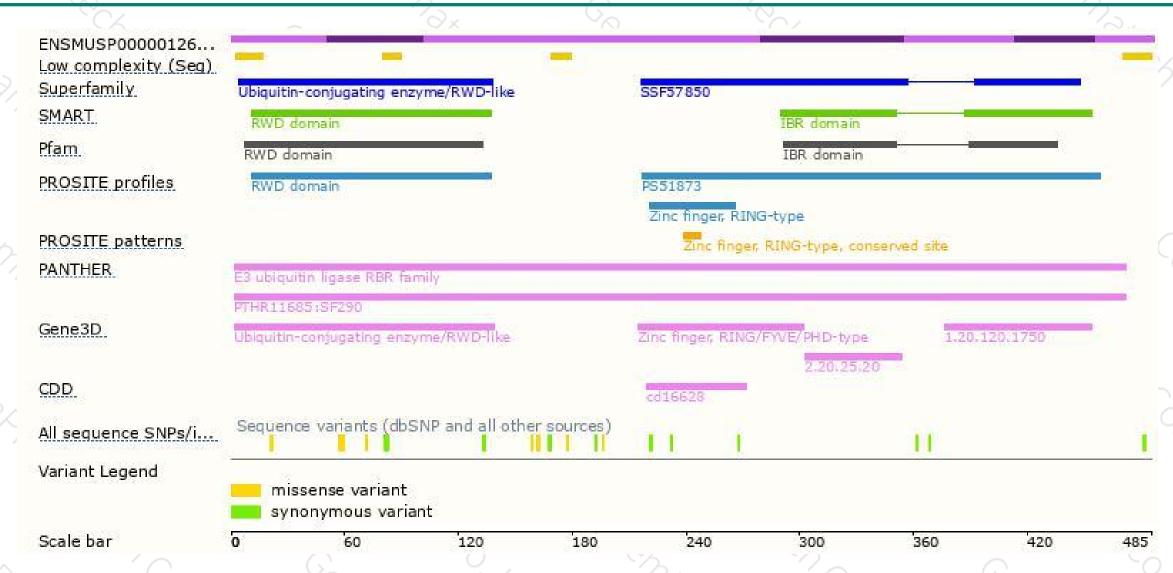
Genomic location distribution





Protein domain







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





