Zfp536 Cas9-CKO Strategy

Designer: Daohua Xu

Design Date: 2019-7-18

Project Overview



Project Name

Zfp536

Project type

Cas9-CKO

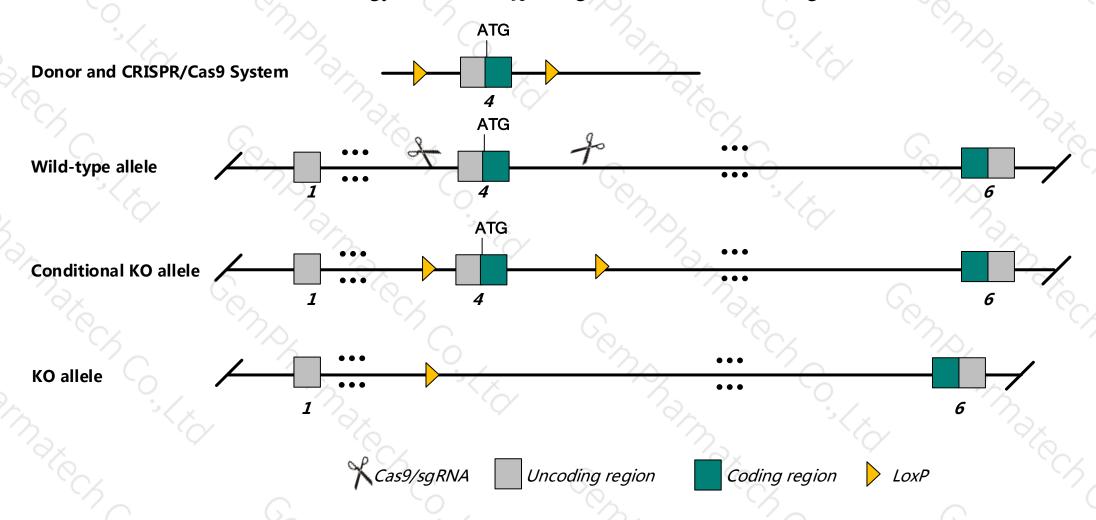
Strain background

C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Zfp536 gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Zfp536* gene has 10 transcripts. According to the structure of *Zfp536* gene, exon4 of *Zfp536*-202 (ENSMUST00000175941.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Zfp536* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA 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 was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

Notice



- The Zfp536 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)



Zfp536 zinc finger protein 536 [Mus musculus (house mouse)]

Gene ID: 243937, updated on 8-Dec-2018

Summary

Official Symbol Zfp536 provided by MGI

Official Full Name zinc finger protein 536 provided by MGI

Primary source MGI:MGI:1926102

See related Ensembl: ENSMUSG00000043456

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 Znf536; mKIAA0390; 9630010P11Rik

Expression Biased expression in cerebellum adult (RPKM 1.6), CNS E14 (RPKM 1.5) and 13 other tissues See more

Orthologs human all

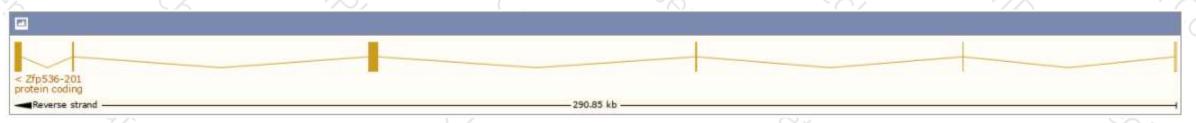
Transcript information (Ensembl)



The gene has 10 transcripts, and all transcripts are shown below:

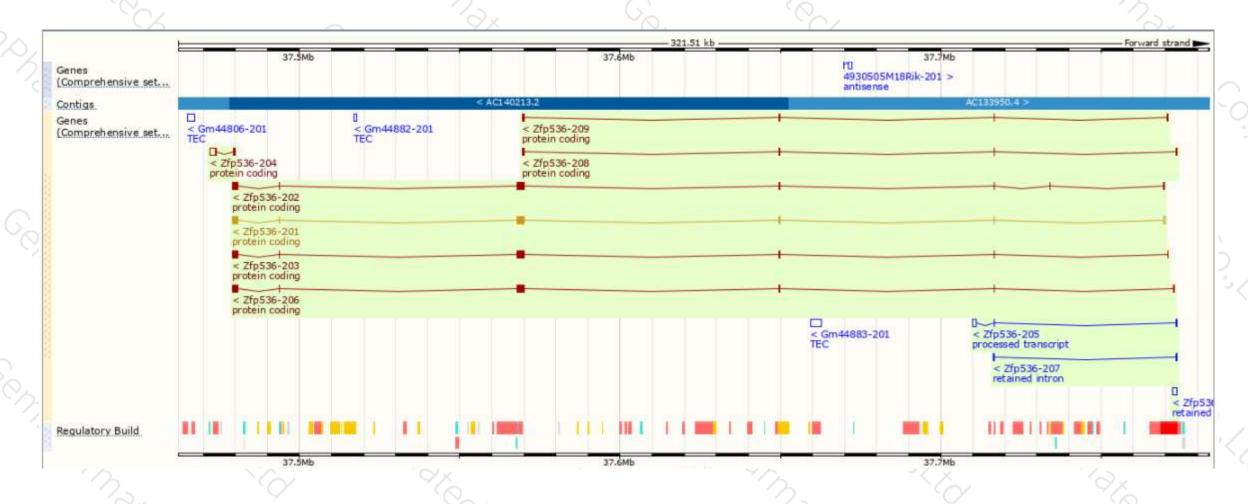
Show/hide columns (1 hidden) Filter								
Name 🍦	Transcript ID 👙	bp 👙	Protein 🍦	Biotype	CCDS	UniProt 👙	RefSeq	Flags 🝦
Zfp536-201	ENSMUST00000056338.12	4621	<u>1302aa</u>	Protein coding	CCDS21156₽	<u>Q8K083</u> ₽	NM 172385@ NP 759017@	TSL:1 GENCODE basic APPRIS P1
Zfp536-202	ENSMUST00000175941.7	4423	<u>1302aa</u>	Protein coding	<u>CCDS21156</u> @	<u>Q8K083</u> ₽	-	TSL:1 GENCODE basic APPRIS P1
Zfp536-206	ENSMUST00000176205.7	4372	<u>1302aa</u>	Protein coding	<u>CCDS21156</u> @	<u>Q8K083</u> ₽	-	TSL:1 GENCODE basic APPRIS P1
Zfp536-203	ENSMUST00000176114.7	4341	<u>1302aa</u>	Protein coding	<u>CCDS21156</u>	<u>Q8K083</u> ₽	-	TSL:1 GENCODE basic APPRIS P1
Zfp536-204	ENSMUST00000176129.1	2541	<u>281aa</u>	Protein coding	-	<u>Q3TR09</u> ₽	-	CDS 5' incomplete TSL:1
Zfp536-209	ENSMUST00000176680.7	818	<u>163aa</u>	Protein coding	-	<u>H3BK19</u> ₽	-	CDS 3' incomplete TSL:2
Zfp536-208	ENSMUST00000176534.7	738	<u>120aa</u>	Protein coding	-	H3BKM9₽	-	CDS 3' incomplete TSL:3
Zfp536-205	ENSMUST00000176137.1	1062	No protein	Processed transcript	-	-	-	TSL:1
Zfp536-210	ENSMUST00000206332.1	1203	No protein	Retained intron	-	-	-	TSL:NA
Zfp536-207	ENSMUST00000176297.1	439	No protein	Retained intron	-	-	-	TSL:2

The strategy is based on the design of Zfp536-202 transcript, The transcription is shown below



Genomic location distribution





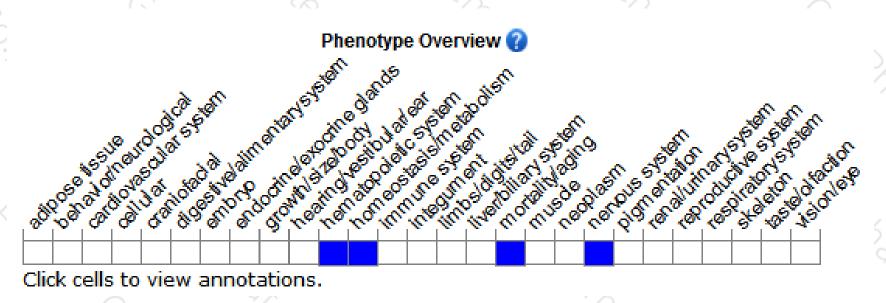
Protein domain





Mouse phenotype description(MGI)





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

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





