Ikzf4 Cas9-KO Strategy

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Project Overview

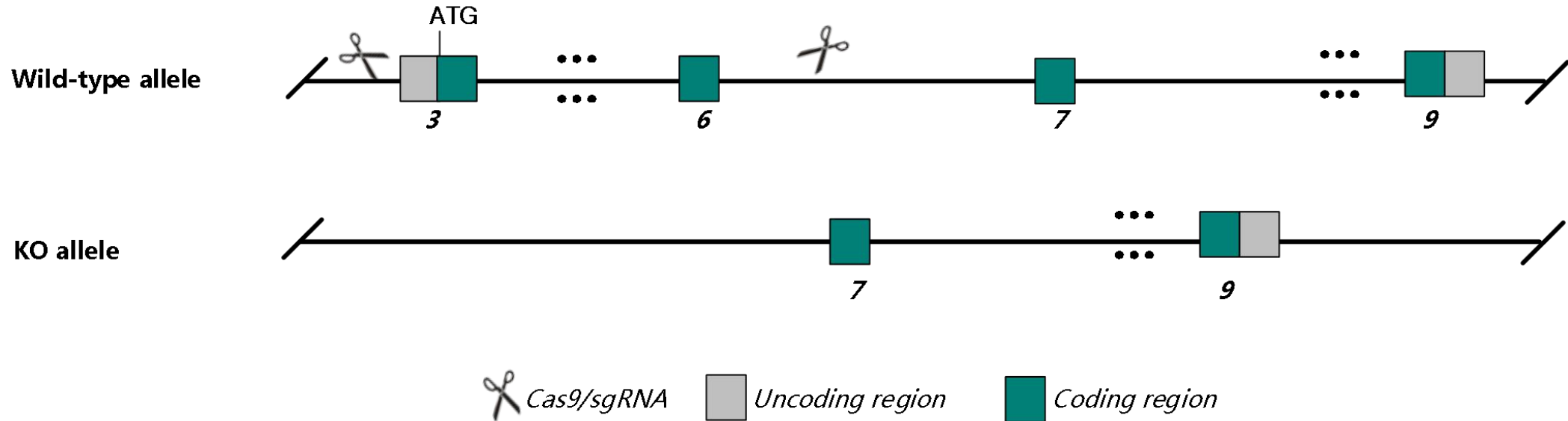|	
Project Name	*Ikzf4*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ikzf4* gene. The schematic diagram is as follows:

Technical routes

➢ The *Ikzf4* gene has 10 transcripts. According to the structure of *Ikzf4* gene, exon3-exon6 of *Ikzf4-210*

 (ENSMUST00000238712.1) 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 *Ikzf4* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ The *Ikzf4* gene is located on the Chr10. 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.

➢ *Gm26876* gene will be deleted.

➢ 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）

Ikzf4 IKAROS family zinc finger 4 [Mus musculus (house mouse)]

Gene ID: 22781, updated on 13-Mar-2020

Summary

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Official Symbol	Ikzf4 provided by MGI
Official Full Name	IKAROS family zinc finger 4 provided by MGI
Primary source	MGI:MGI:1343139
See related	Ensembl:ENSMUSG00000002578
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	A630026H08Rik, Eos, Zfpn1a4, Znfn1a4
Expression	Broad expression in whole brain E14.5 (RPKM 4.1), CNS E14 (RPKM 4.1) and 24 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ikzf4-201	ENSMUST00000133342.9	5150	586aa	Protein coding	CCDS24284	Q8C208	TSL:2 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Ikzf4-210	ENSMUST00000238712.1	5251	539aa	Protein coding	-	-	GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
Ikzf4-209	ENSMUST00000238610.1	5173	539aa	Protein coding	-	-	GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
Ikzf4-204	ENSMUST00000222067.1	2688	533aa	Protein coding	-	Q8C208	TSL:1 GENCODE basic
Ikzf4-203	ENSMUST00000221150.1	2213	686aa	Protein coding	-	Q8C208	TSL:1 GENCODE basic
Ikzf4-208	ENSMUST00000223162.1	3449	71aa	Nonsense mediated decay	-	A0A1Y7VK04	TSL:1
Ikzf4-206	ENSMUST00000222901.1	490	45aa	Nonsense mediated decay	-	A0A1Y7VK30	CDS 5' incomplete TSL:5
Ikzf4-205	ENSMUST00000222899.1	363	No protein	Processed transcript	-	-	TSL:5
Ikzf4-207	ENSMUST00000223145.1	358	No protein	Processed transcript	-	-	TSL:3
Ikzf4-202	ENSMUST00000221022.1	350	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Ikzf4-210* transcript,the transcription is shown below
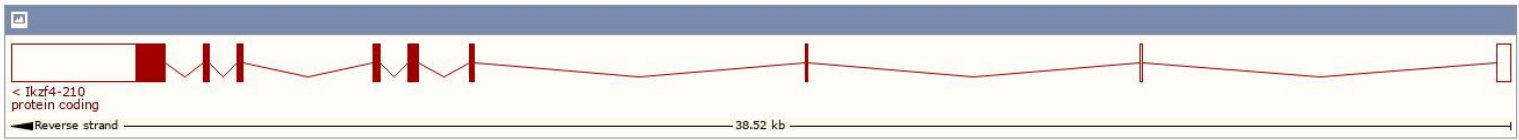
Genomic location distribution

Protein domain

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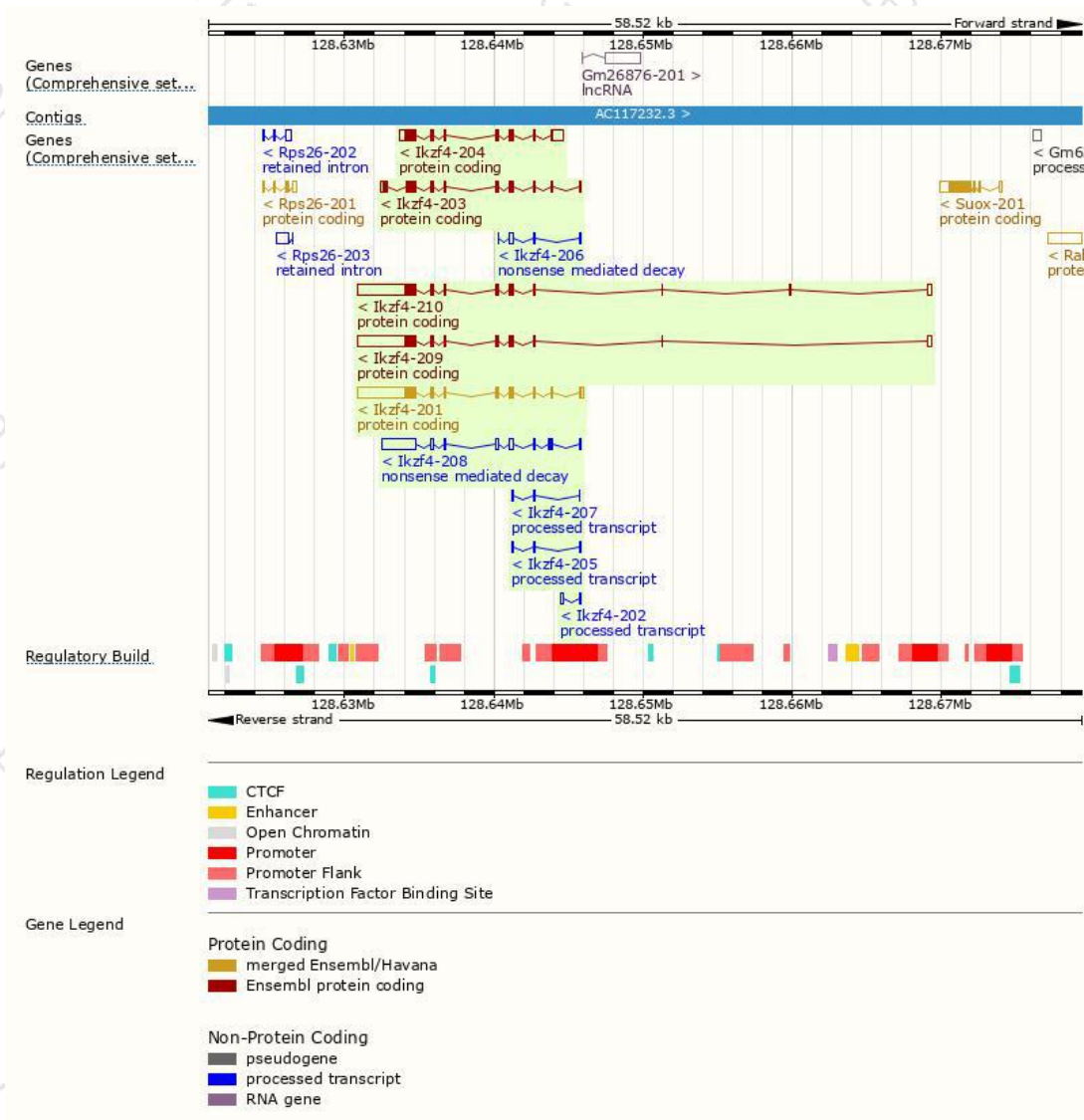
If you have any questions, you are welcome to inquire.
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