Ikzf1 Cas9-CKO Strategy

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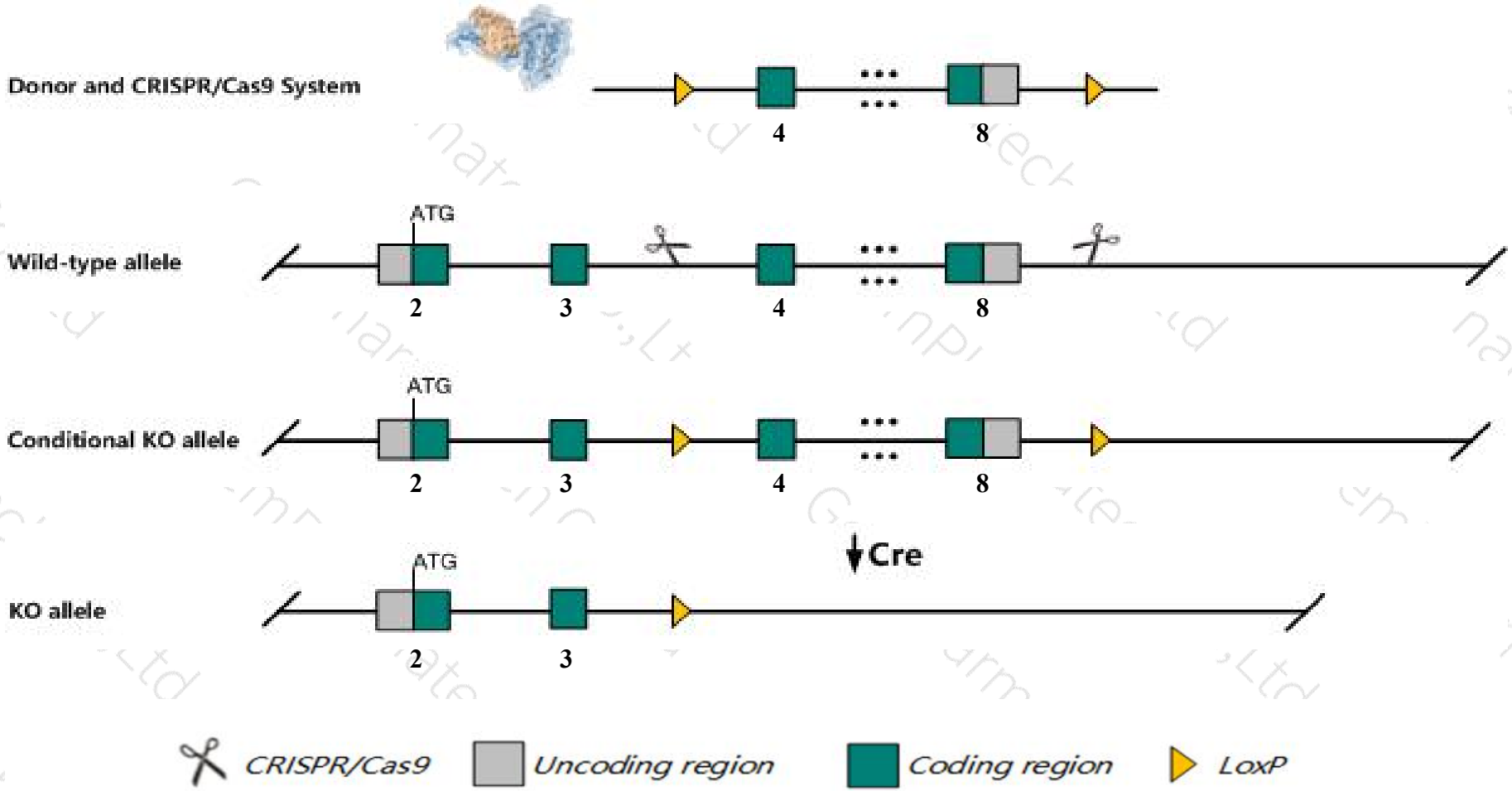
Project Overview

Project Name	***Ikzf1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ikzf1* gene. The schematic diagram is as follows:



Technical routes

- The *Ikzf1* gene has 6 transcripts. According to the structure of *Ikzf1* gene, exon4-exon8 of *Ikzf1-204* (ENSMUST00000076700.10) transcript is recommended as the knockout region.The region contains most of coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Ikzf1* 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

- According to the existing MGI data,Homozygous mutants have a variety of T, B, and hematopoeitic cell maturation defects. Heterozygotes for one allele exhibit dominant negative effects and mice develop lymphoproliferative disorders.

- The *Ikzf1* gene is located on the Chr11. 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）

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Ikzf1 IKAROS family zinc finger 1 [*Mus musculus* (house mouse)]

Gene ID: 22778, updated on 22-Oct-2019

Summary

Official Symbol	Ikzf1 provided by MGI
Official Full Name	IKAROS family zinc finger 1 provided by MGI
Primary source	MGI:MGI:1342540
See related	Ensembl:ENSMUSG00000018654
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	LyF-1; hlk-1; Ikaros; Zfpn1a1; Znfn1a1; mKIAA4227; 5832432G11Rik
Summary	The protein encoded by this gene belongs to a family of transcription factors that are characterized by a set of four DNA-binding zinc fingers at the N-terminus and two C-terminal zinc fingers involved in protein dimerization. It is regulated by both epigenetic and transcription factors. This protein is a transcriptional regulator of hematopoietic cell development and homeostasis. In addition, it is required to confer temporal competence to retinal progenitor cells during embryogenesis, demonstrating an essential function in nervous system development. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Sep 2014]
Expression	Biased expression in thymus adult (RPKM 67.8), spleen adult (RPKM 38.3) and 5 other tissues See more
Orthologs	human all

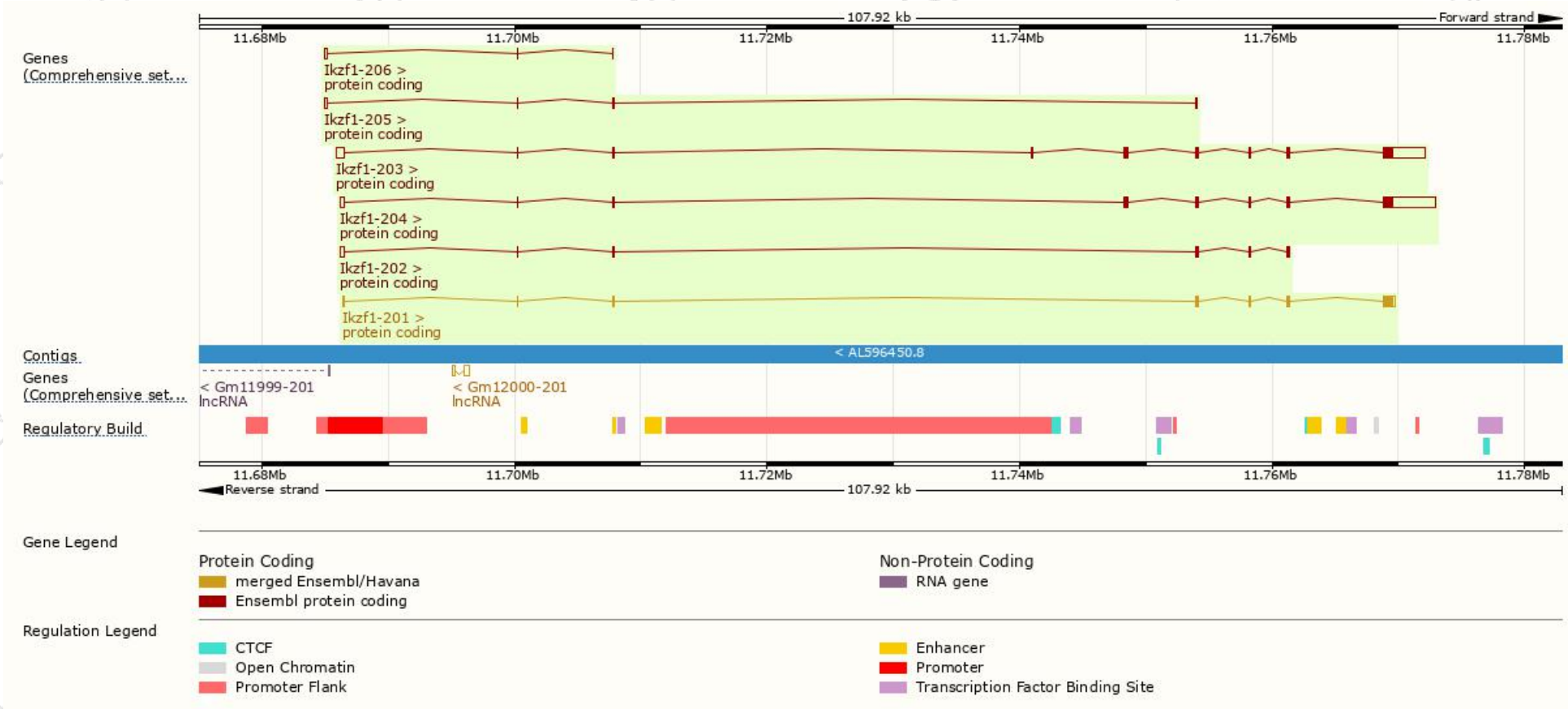
Transcript information（Ensembl）

The gene has 6 transcripts,all transcripts are shown below:

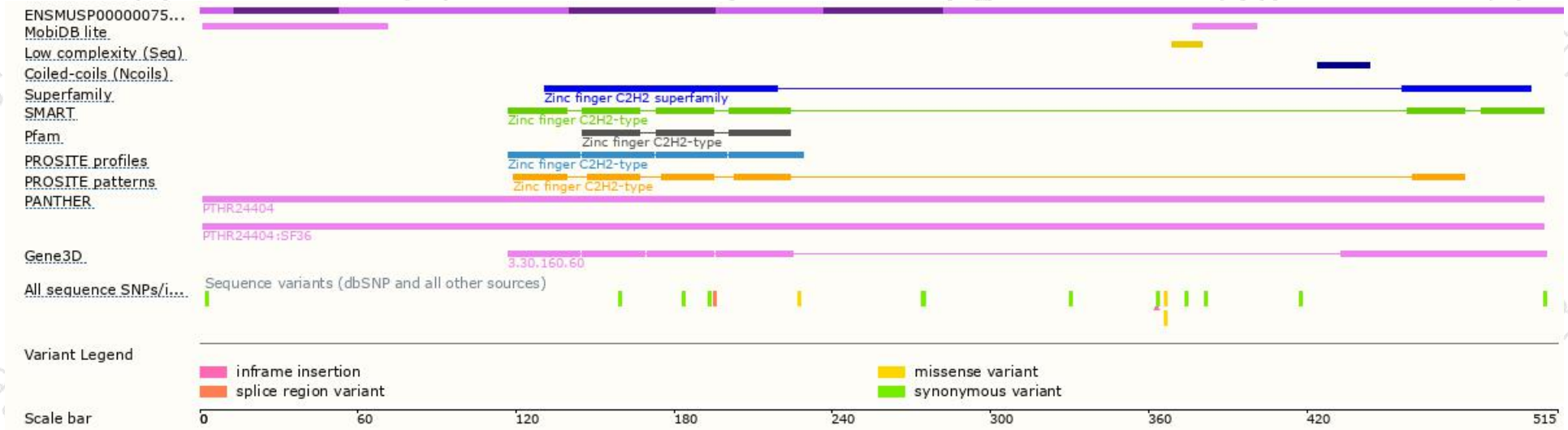
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ikzf1-204	ENSMUST00000076700.10	5163	515aa	Protein coding	CCDS24436	G5E8H3	TSL:1 GENCODE basic APPRIS P4
Ikzf1-201	ENSMUST00000018798.6	1542	428aa	Protein coding	CCDS24437	Q5SWU0	TSL:1 GENCODE basic APPRIS ALT1
Ikzf1-203	ENSMUST00000065433.11	4697	535aa	Protein coding	-	Q5SWT9	TSL:5 GENCODE basic APPRIS ALT1
Ikzf1-202	ENSMUST00000048122.12	911	198aa	Protein coding	-	Q8C9X3	TSL:1 GENCODE basic
Ikzf1-205	ENSMUST00000126058.7	446	79aa	Protein coding	-	Q5SWT7	CDS 3' incomplete TSL:3
Ikzf1-206	ENSMUST00000141436.7	242	18aa	Protein coding	-	Q5SWT6	CDS 3' incomplete TSL:5

The strategy is based on the design of *Ikzf1-204* transcript,The transcription is shown below

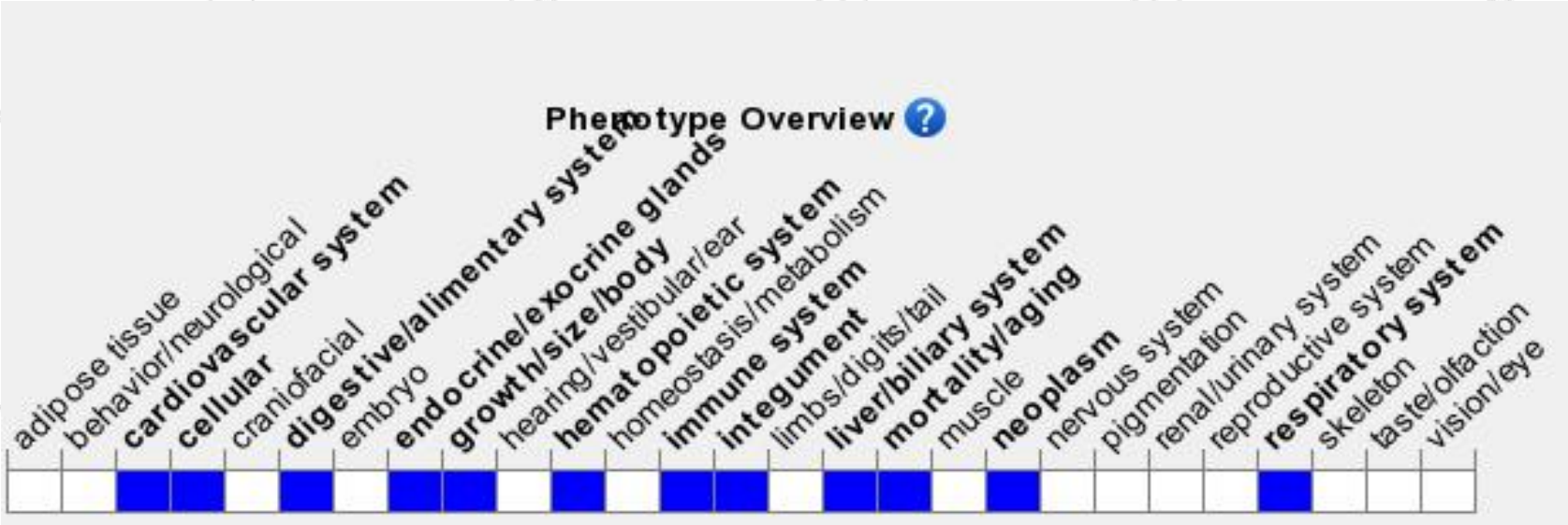
Genomic location distribution



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/).

According to the existing MGI data,Homozygous mutants have a variety of T, B, and hematopoeitic cell maturation defects. Heterozygotes for one allele exhibit dominant negative effects and mice develop lymphoproliferative disorders.

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

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