

# *Ikzf1* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***Ikzf1***

**Project type**

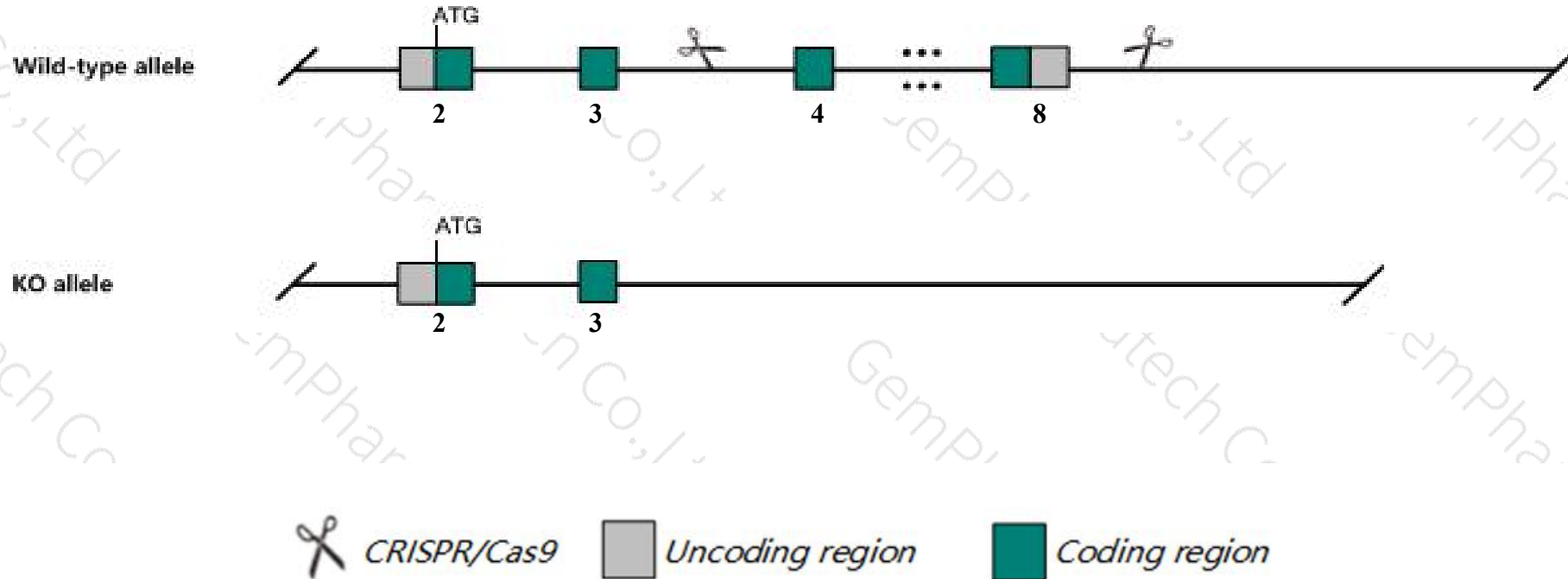
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- 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 1388bp 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 v

- According to the existing MGI data, Homozygous mutants have a variety of T, B, and hematopoietic 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## 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)

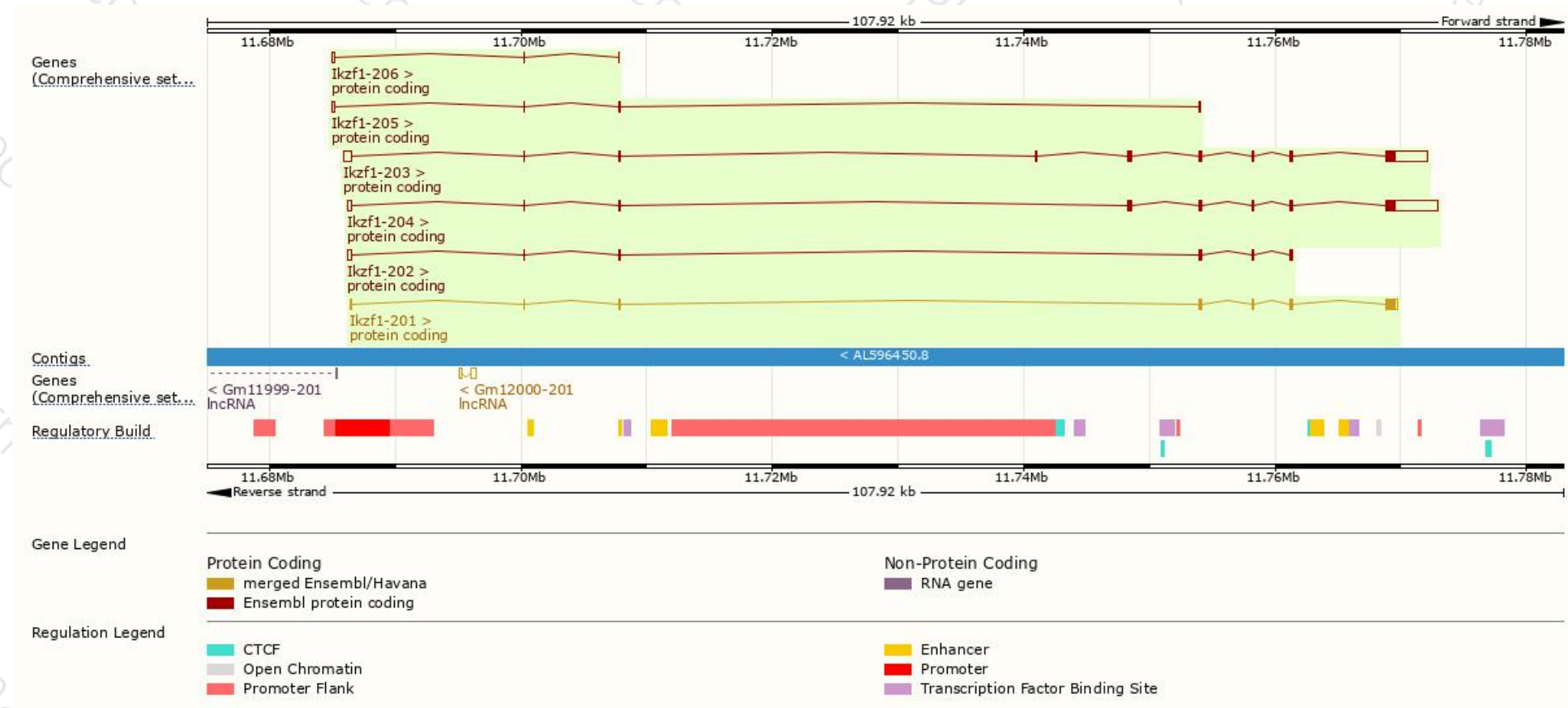
The gene has 6 transcripts,all transcripts are shown below:

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

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

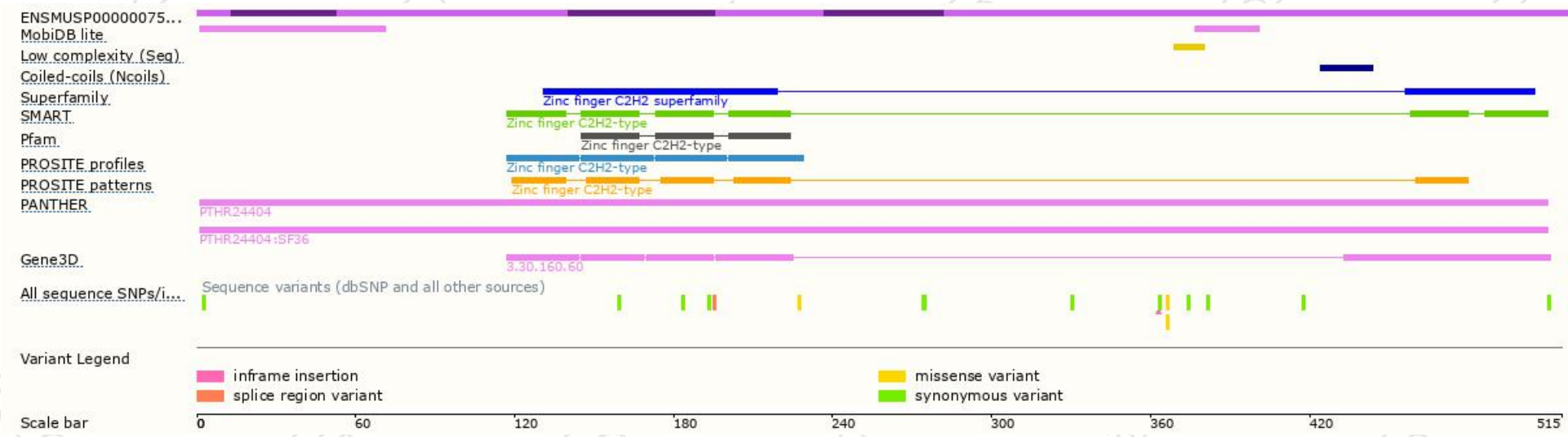


# Genomic location distribution

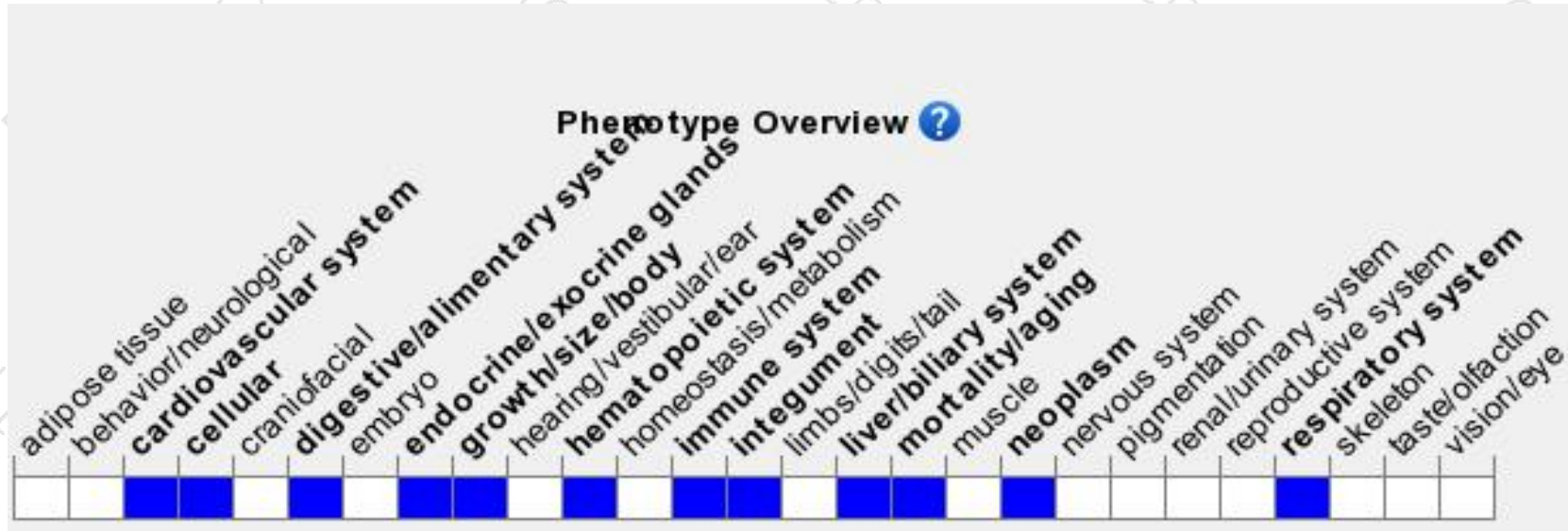




# Protein domain



# 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 hematopoietic cell maturation defects. Heterozygotes for one allele exhibit dominant negative effects and mice develop lymphoproliferative disorders.

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

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