

Zmym2 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Zmym2

Project type

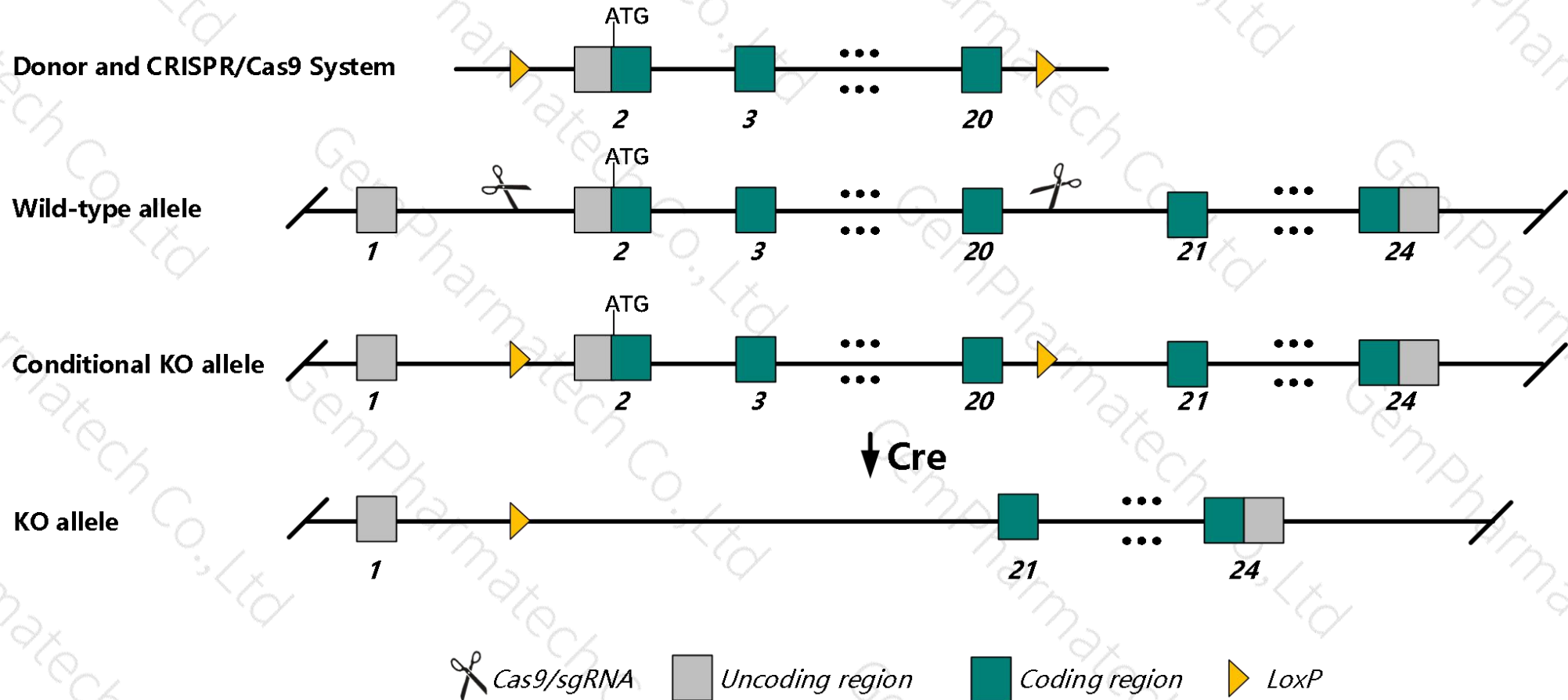
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zmym2* gene. The schematic diagram is as follows:



- The *Zmym2* gene has 7 transcripts. According to the structure of *Zmym2* gene, exon2-exon20 of *Zmym2-201* (ENSMUST00000022511.9) transcript is recommended as the knockout region. The region contains start codon ATG and most of coding region. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zmym2* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA 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.

- According to the existing MGI data, Mice homozygous for an ENU-induced mutation exhibit prenatal lethality.
- The *Zmym2* gene is located on the Chr14. 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)

Zmym2 zinc finger, MYM-type 2 [Mus musculus (house mouse)]

Gene ID: 76007, updated on 31-Jan-2019

Summary



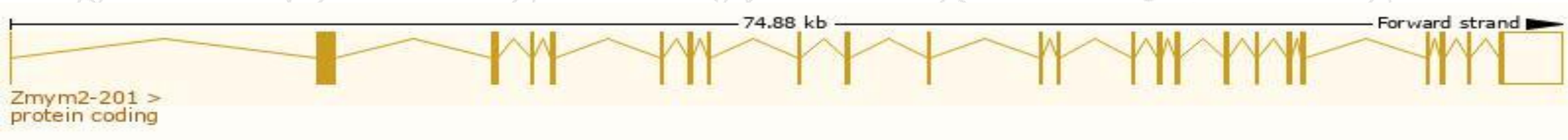
Official Symbol	Zmym2 provided by MGI
Official Full Name	zinc finger, MYM-type 2 provided by MGI
Primary source	MGI:MGI:1923257
See related	Ensembl:ENSMUSG000000021945
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5830413P05Rik, FIM, MYM, RAMP, SCLL, Zfp198, Znf198
Summary	This gene encodes a protein that contains nine MYM-type zinc finger motifs. Expression of this gene may mediate the inhibition of hematopoietic cell development during ontogeny, and the encoded protein may also play a role in transforming growth factor-beta signaling as a Smad binding protein. [provided by RefSeq, Feb 2011]
Expression	Broad expression in CNS E11.5 (RPKM 12.5), CNS E14 (RPKM 11.4) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zmym2-201	ENSMUST00000022511.9	6974	1376aa	Protein coding	CCDS49506	Q9CU65	TSL:1 GENCODE basic APPRIS P1
Zmym2-202	ENSMUST000000223669.1	1281	290aa	Protein coding	-	A0A286YCD5	GENCODE basic
Zmym2-204	ENSMUST000000224922.1	2829	No protein	Processed transcript	-	-	
Zmym2-205	ENSMUST000000225282.1	741	No protein	Processed transcript	-	-	
Zmym2-203	ENSMUST000000223965.1	772	No protein	Retained intron	-	-	
Zmym2-207	ENSMUST000000226025.1	607	No protein	Retained intron	-	-	
Zmym2-206	ENSMUST000000225393.1	332	No protein	Retained intron	-	-	

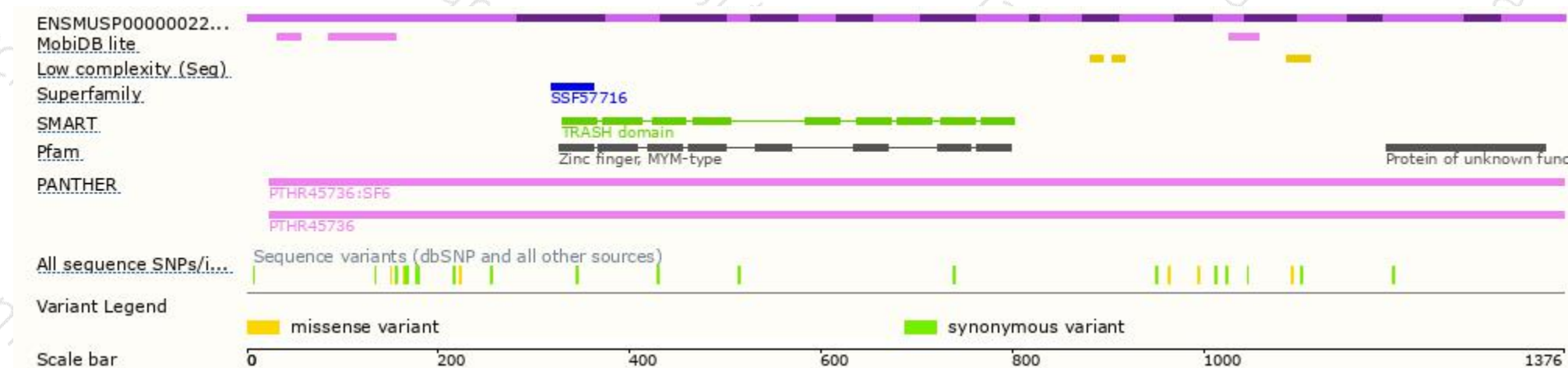
The strategy is based on the design of *Zmym2-201* transcript,The transcription is shown below



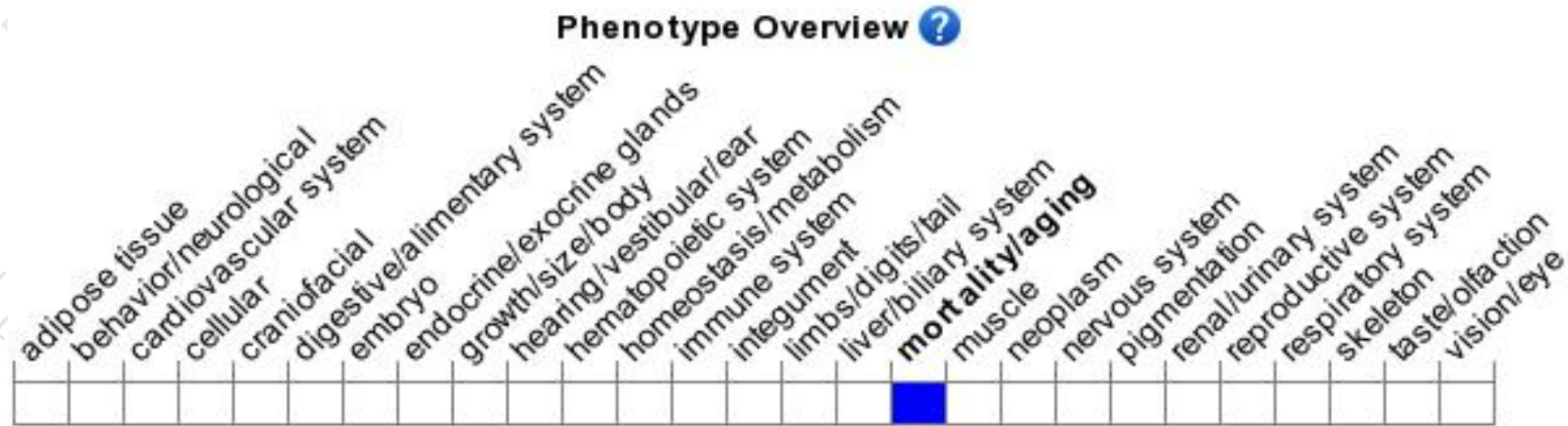
Genomic location distribution



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, Mice homozygous for an ENU-induced mutation exhibit prenatal lethality.

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

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