

# *Zfp36l1* Cas9-CKO Strategy

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**Reviewer: Xueting Zhang**

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# Project Overview

**Project Name**

***Zfp36l1***

**Project type**

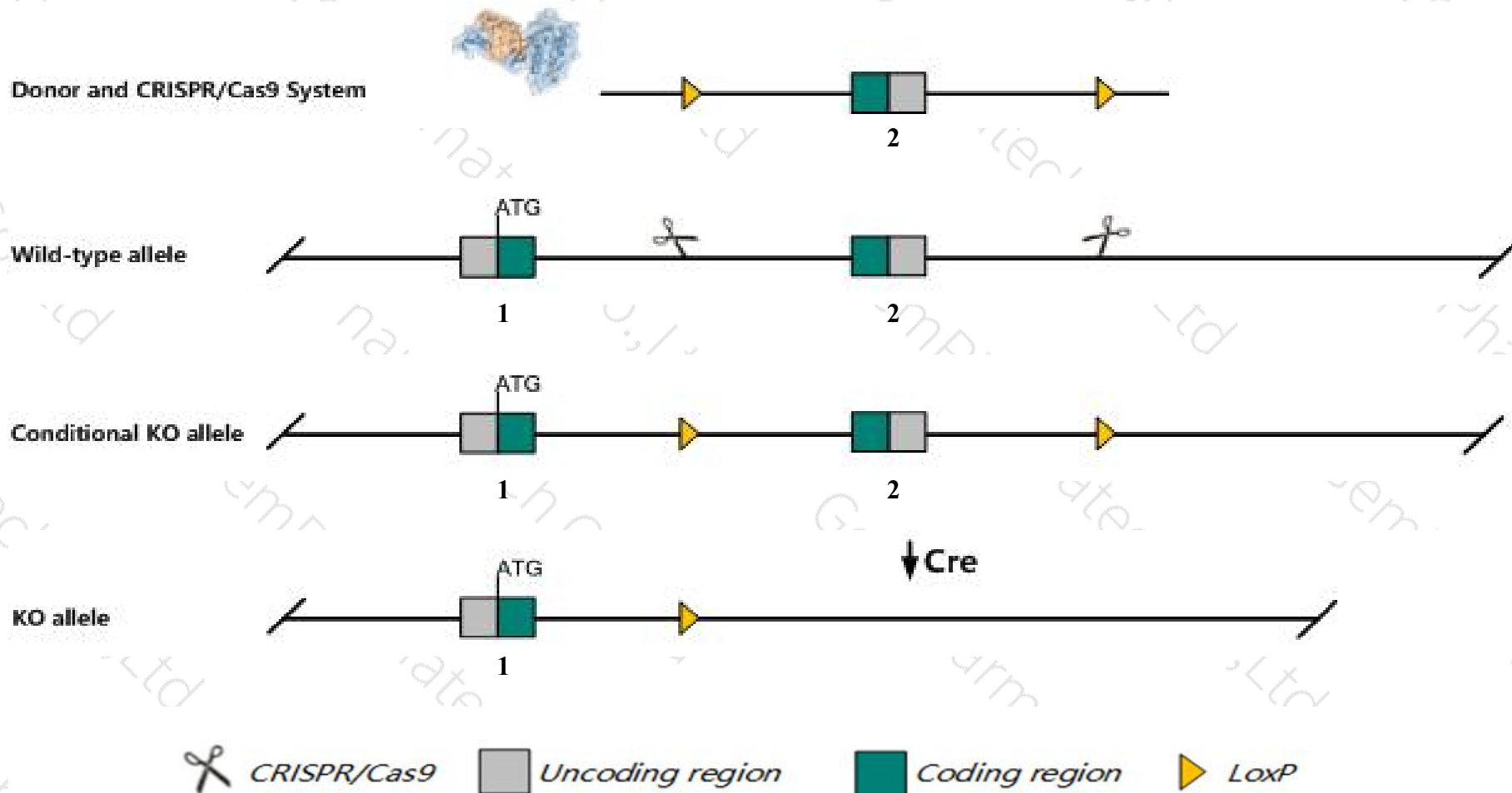
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp3611* gene. The schematic diagram is as follows:



# Technical routes

- The *Zfp3611* gene has 4 transcripts. According to the structure of *Zfp3611* gene, exon2 of *Zfp3611*-201(ENSMUST00000021552.2) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp3611* 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, homozygous null mice display embryonic lethality with failure of chorioallantoic fusion.
- The *Zfp361l* gene is located on the Chr12. 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)

## Zfp36l1 zinc finger protein 36, C3H type-like 1 [Mus musculus (house mouse)]

Gene ID: 12192, updated on 13-Mar-2020

### Summary

**Official Symbol** Zfp36l1 provided by [MGI](#)

**Official Full Name** zinc finger protein 36, C3H type-like 1 provided by [MGI](#)

**Primary source** [MGI:MGI:107946](#)

**See related** [Ensembl:ENSMUSG00000021127](#)

**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** AW742437, AW743212, Berg36, Brf1, D530020L18Rik, ERF1, TIS11b, cMG1

**Expression** Ubiquitous expression in adrenal adult (RPKM 144.4), ovary adult (RPKM 112.7) and 25 other tissues [See more](#)

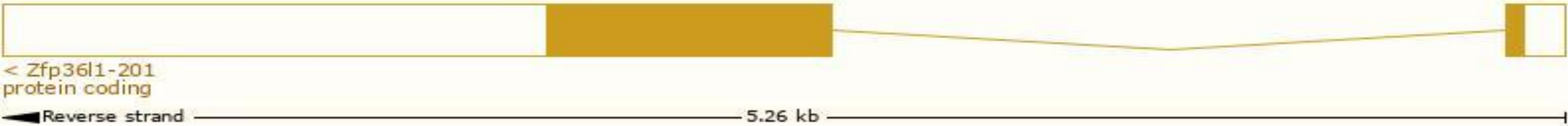
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

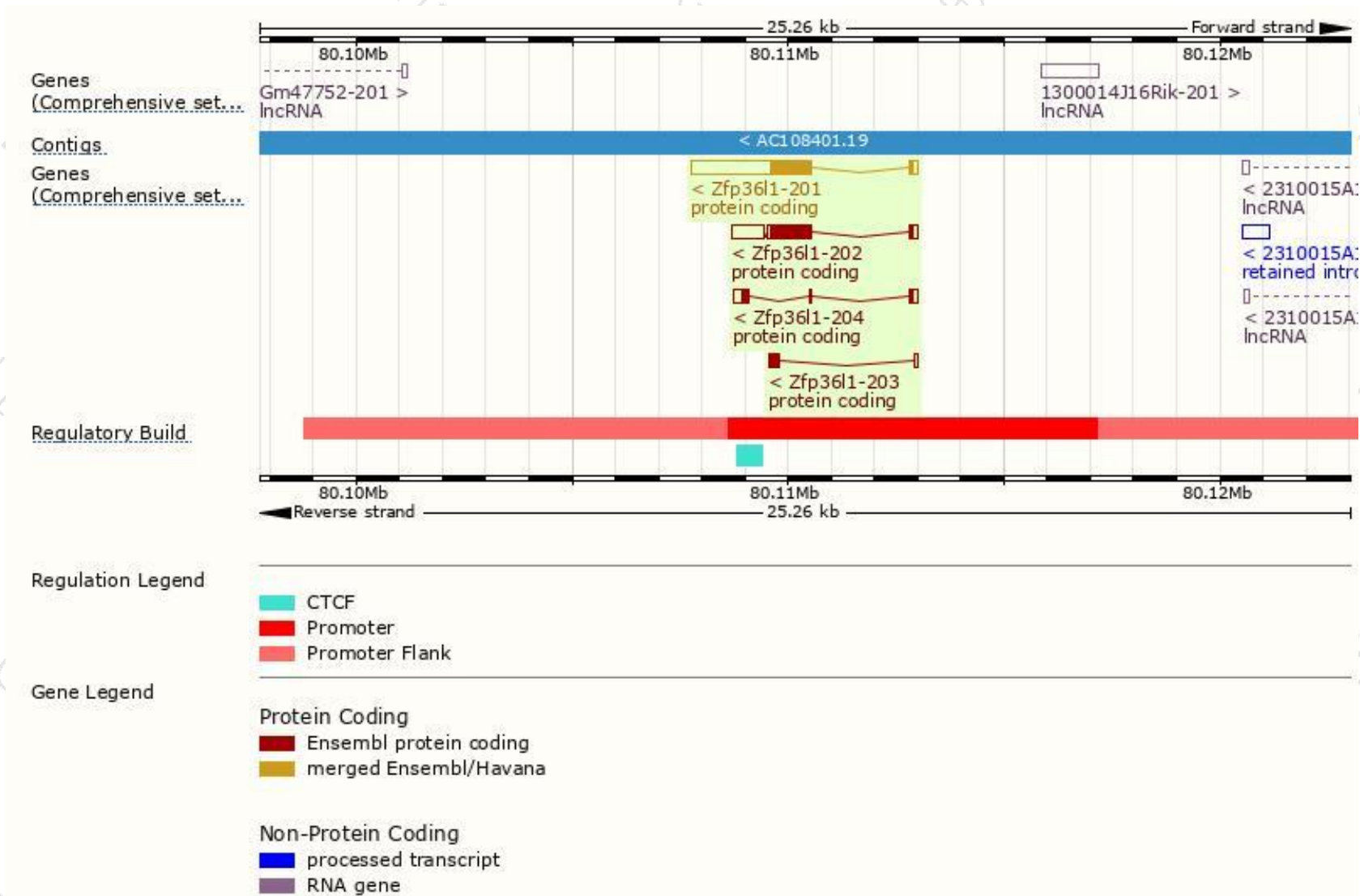
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp3611-201	<a href="#">ENSMUST00000021552.2</a>	2990	<a href="#">338aa</a>	Protein coding	<a href="#">CCDS26010</a>	<a href="#">P23950 Q543H2</a>	TSL:1 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 P1
Zfp3611-202	<a href="#">ENSMUST00000165114.1</a>	1934	<a href="#">338aa</a>	Protein coding	<a href="#">CCDS26010</a>	<a href="#">P23950 Q543H2</a>	TSL:5 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 P1
Zfp3611-204	<a href="#">ENSMUST00000219642.1</a>	545	<a href="#">84aa</a>	Protein coding	-	<a href="#">A0A1W2P7G3</a>	TSL:3 GENCODE basic
Zfp3611-203	<a href="#">ENSMUST00000218835.1</a>	292	<a href="#">57aa</a>	Protein coding	-	<a href="#">A0A1W2P6I1</a>	TSL:3 GENCODE basic

The strategy is based on the design of *Zfp3611-201* transcript,the transcription is shown below:



# Genomic location distribution





# Protein domain

ENSMUSP00000021...

MobiDB lite

Low complexity (Seq)

Superfamily

SMART

Pfam

PROSITE profiles

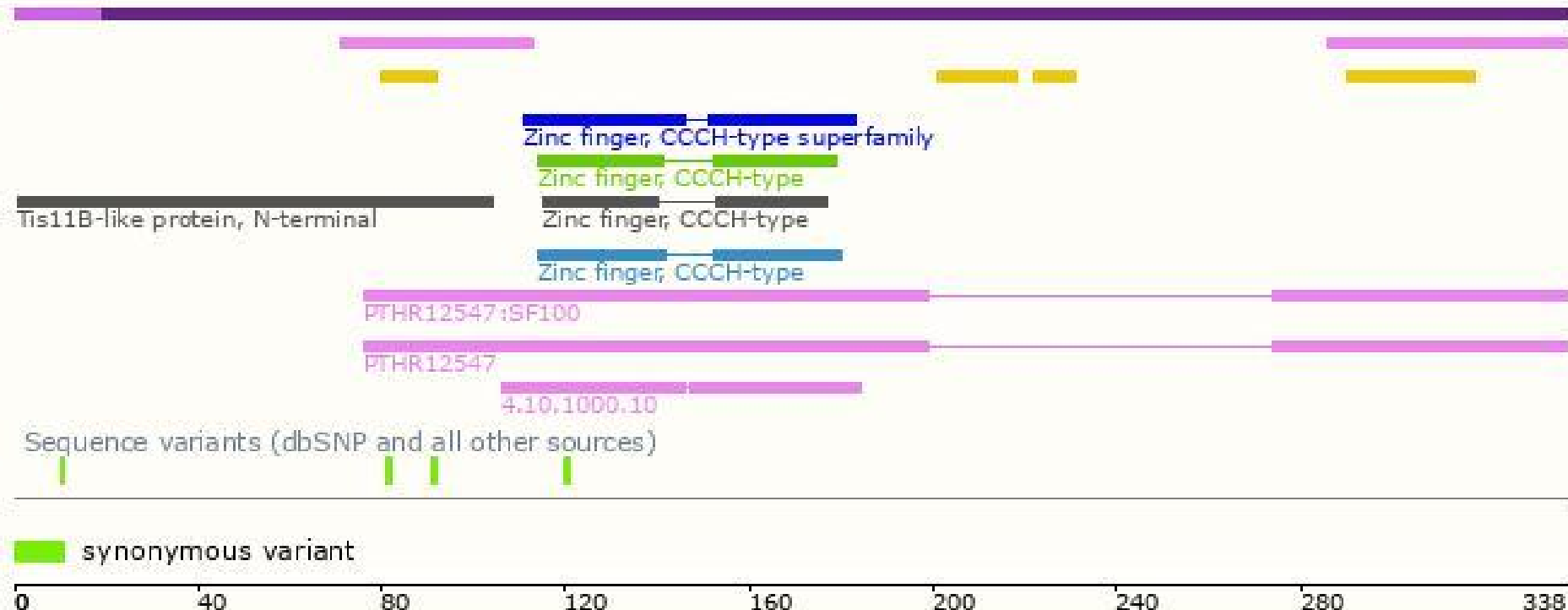
PANTHER

Gene3D

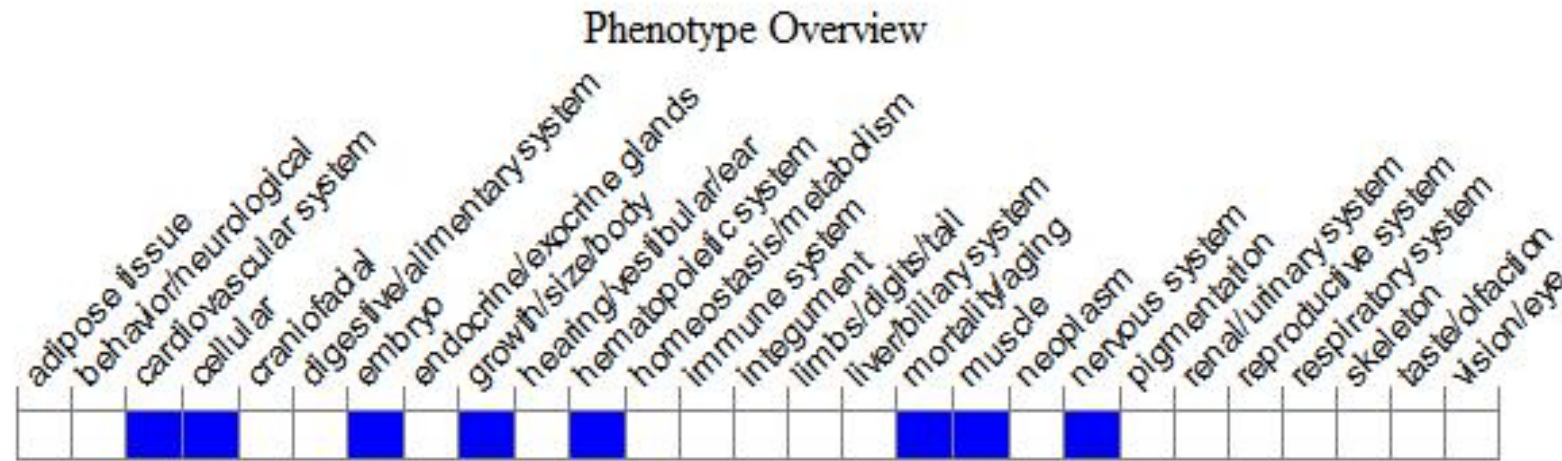
All sequence SNPs/i....

Variant Legend

Scale bar



# 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 null mice display embryonic lethality with failure of chorioallantoic fusion.

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

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