

# Fgf15 Cas9-CKO Strategy

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**Reviewer:** 

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# **Project Overview**



**Project Name** 

Fgf15

**Project type** 

Cas9-CKO

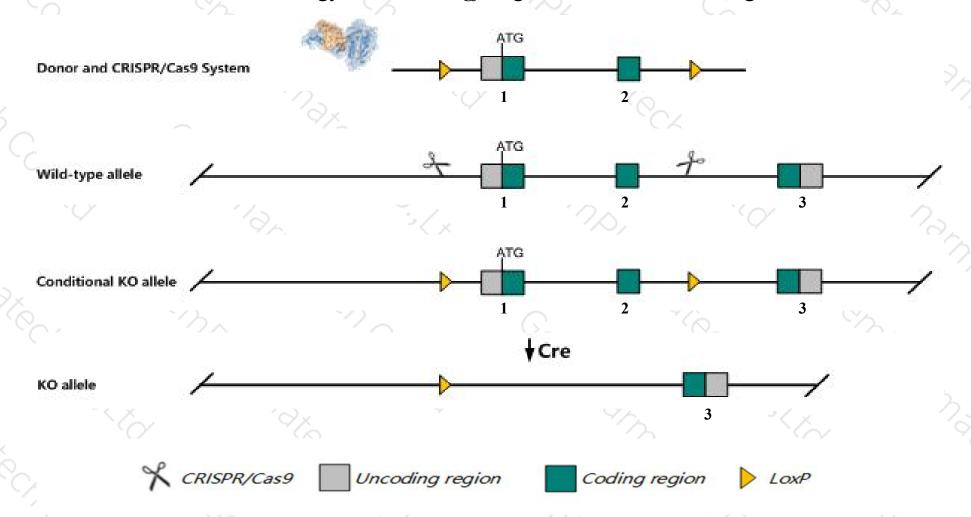
Strain background

C57BL/6JGpt

## Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Fgf15 gene. The schematic diagram is as follows:



### Technical routes



- The Fgf15 gene has 5 transcripts. According to the structure of Fgf15 gene, exon1-exon2 of Fgf15-201 (ENSMUST00000033389.6) 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 *Fgf15* 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, Targeted inactivation of this gene leads to a severe underrepresentation of homozygotes at weaning as well as highly penetrant ventricular septal defects and malalignment of the aorta and pulmonary trunk. No abnormalities in otic induction or otic vesicle formation are observed.
- The KO region contains functional region of the *Gm26793* gene. Knockout the region may affect the function of *Gm26793* gene.
- > The *Fgf15* gene is located on the Chr7. 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)



#### Fgf15 fibroblast growth factor 15 [ Mus musculus (house mouse) ]

Gene ID: 14170, updated on 11-Sep-2019

#### Summary



Official Symbol Fgf15 provided by MGI

Official Full Name fibroblast growth factor 15 provided by MGI

Primary source MGI:MGI:1096383

See related Ensembl:ENSMUSG00000031073

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 FGF19

Expression Biased expression in CNS E11.5 (RPKM 7.5), large intestine adult (RPKM 6.2) and 3 other tissues See more

Orthologs <u>human</u> <u>all</u>

# Transcript information (Ensembl)



The gene has 5 transcripts, all transcripts are shown below:

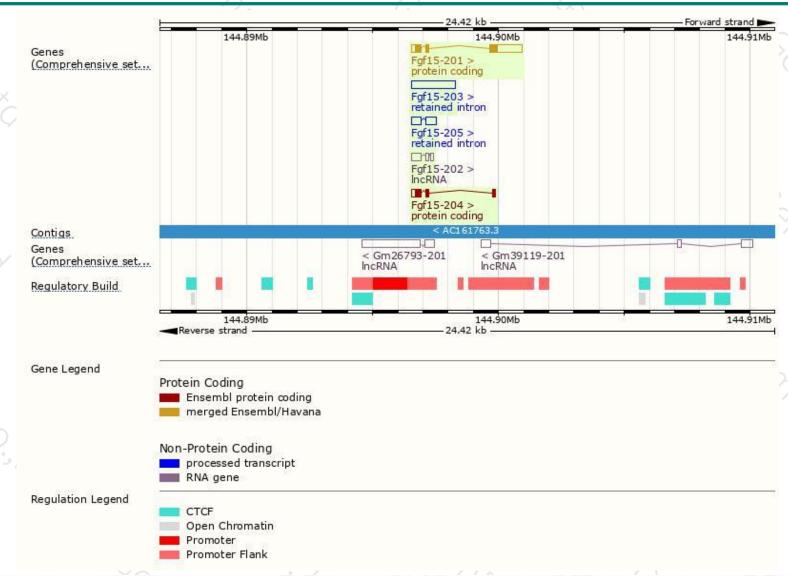
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fgf15-201	ENSMUST00000033389.6	1810	218aa	Protein coding	CCDS22053₽	<u>O35622</u> @ <u>Q790L8</u> @	TSL:1 GENCODE basic APPRIS P1
Fgf15-204	ENSMUST00000207229.1	600	<u>161aa</u>	Protein coding	\$ <b>2</b> 8	A0A140LIL5₽	CDS 3' incomplete TSL:3
Fgf15-203	ENSMUST00000207040.1	1753	No protein	Retained intron	170	<u> </u>	TSL:NA
Fgf15-205	ENSMUST00000208515.1	809	No protein	Retained intron	\$ <b>=</b> 8	-	TSL:2
Fgf15-202	ENSMUST00000207033.1	600	No protein	IncRNA	17.1	-	TSL:2

The strategy is based on the design of *Fgf15-201* transcript, The transcription is shown below



### Genomic location distribution





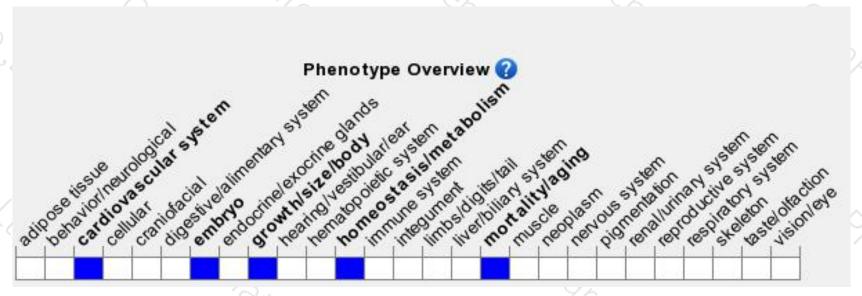
### Protein domain





# 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, Targeted inactivation of this gene leads to a severe underrepresentation of homozygotes at weaning as well as highly penetrant ventricular septal defects and malalignment of the aorta and pulmonary trunk. No abnormalities in otic induction or otic vesicle formation are observed.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





