

***Fabp12* Cas9-CKO Strategy**

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Project Overview

Project Name

Fabp12

Project type

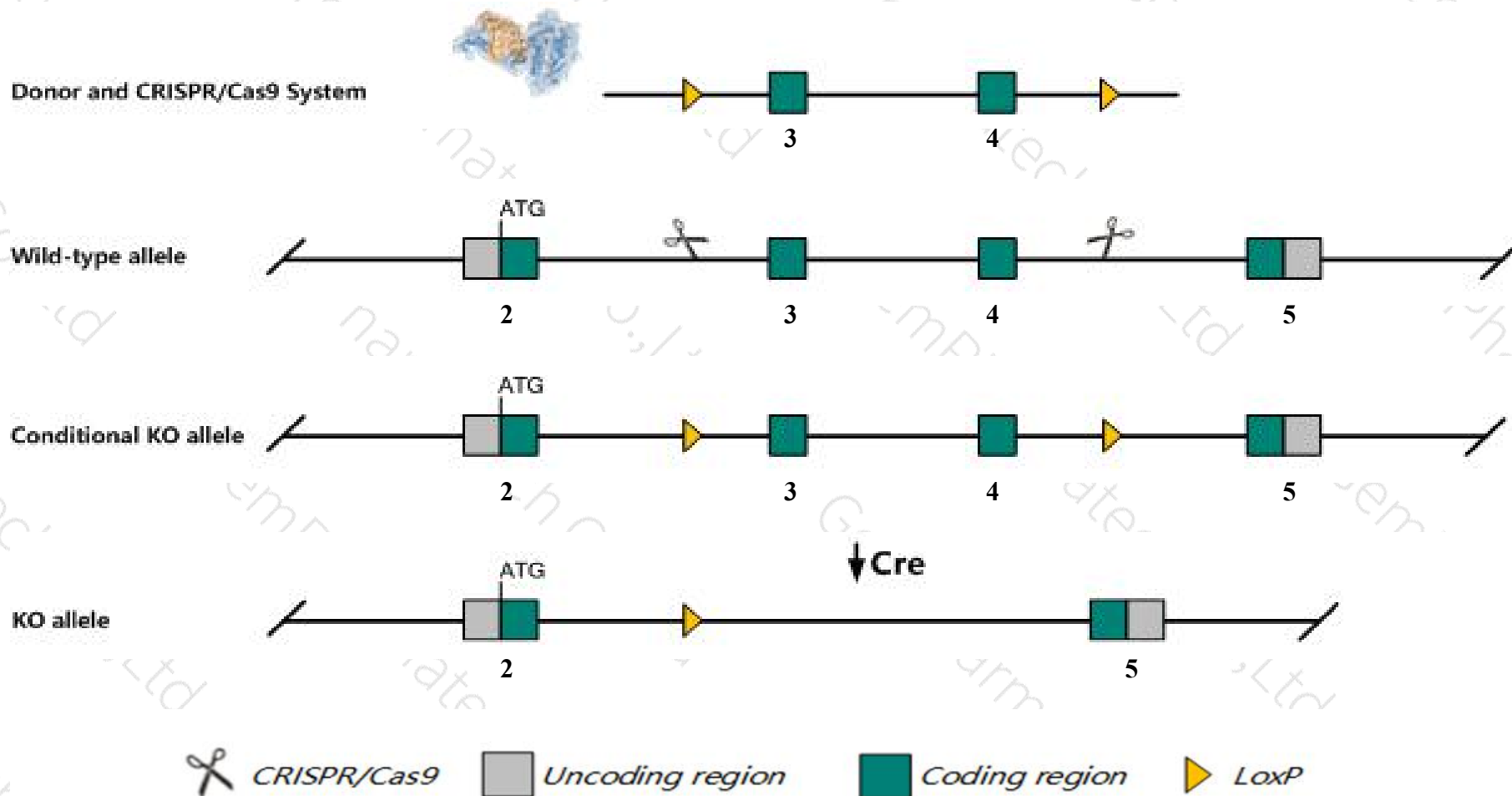
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fabp12* gene. The schematic diagram is as follows:



Technical routes

- The *Fabp12* gene has 4 transcripts. According to the structure of *Fabp12* gene, exon3-exon4 of *Fabp12*-204 (ENSMUST00000172126.7) transcript is recommended as the knockout region. The region contains 275bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fabp12* 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

- The *Fabp12* gene is located on the Chr3. 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)

Fabp12 fatty acid binding protein 12 [Mus musculus (house mouse)]

Gene ID: 75497, updated on 13-Mar-2020

Summary



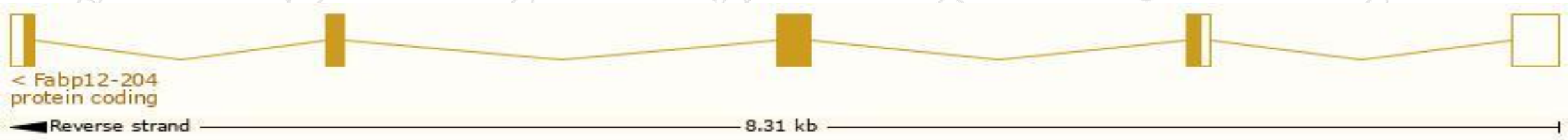
Official Symbol	Fabp12 provided by MGI
Official Full Name	fatty acid binding protein 12 provided by MGI
Primary source	MGI:MGI:1922747
See related	Ensembl:ENSMUSG00000027530
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1700008G05Rik
Expression	Biased expression in testis adult (RPKM 2.8), liver E18 (RPKM 0.8) and 2 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
Fabp12-201	ENSMUST00000029043.12	2512	132aa	Protein coding	CCDS17239	Q9DAK4	TSL:1 GENCODE basic APPRIS P1
Fabp12-204	ENSMUST00000172126.7	779	132aa	Protein coding	CCDS17239	Q9DAK4	TSL:1 GENCODE basic APPRIS P1
Fabp12-202	ENSMUST00000117917.7	648	132aa	Protein coding	CCDS17239	Q9DAK4	TSL:1 GENCODE basic APPRIS P1
Fabp12-203	ENSMUST00000119761.1	548	132aa	Protein coding	CCDS17239	Q9DAK4	TSL:3 GENCODE basic APPRIS P1

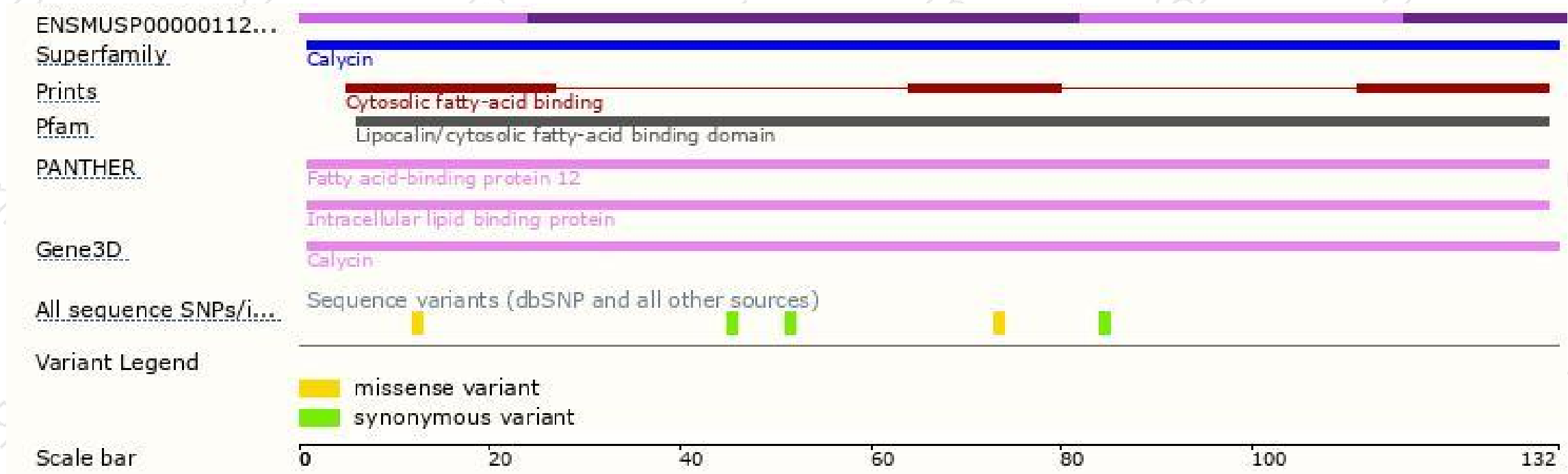
The strategy is based on the design of *Fabp12-204* transcript,the transcription is shown below:



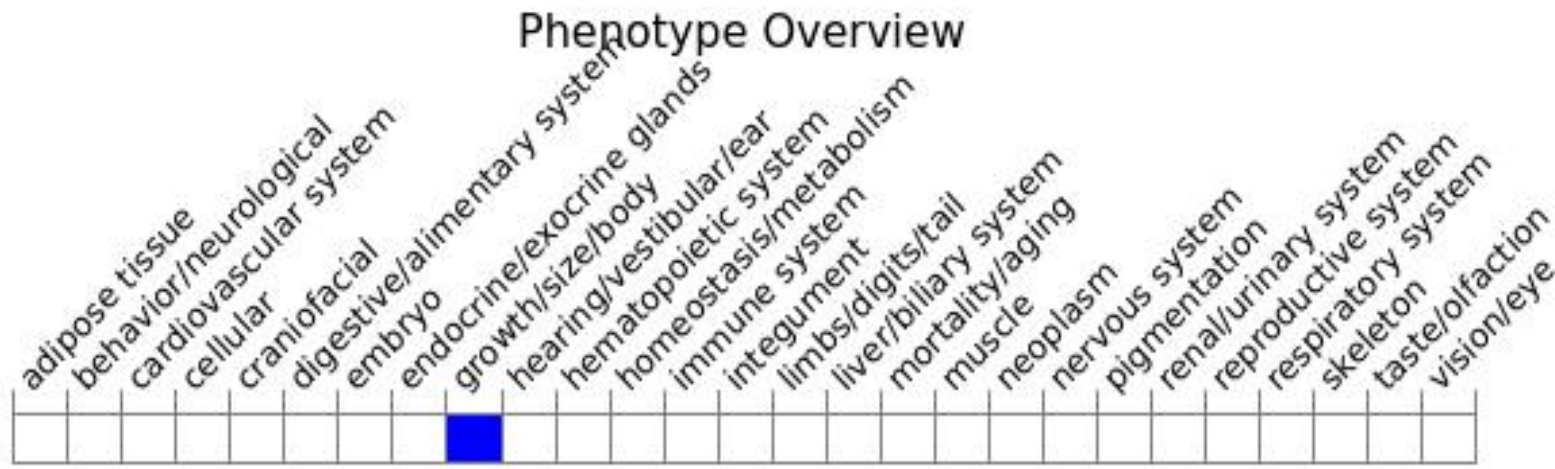
Genomic location distribution



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/>).

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

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