

Fat2 Cas9-KO Strategy

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Project Overview

Project Name

Fat2

Project type

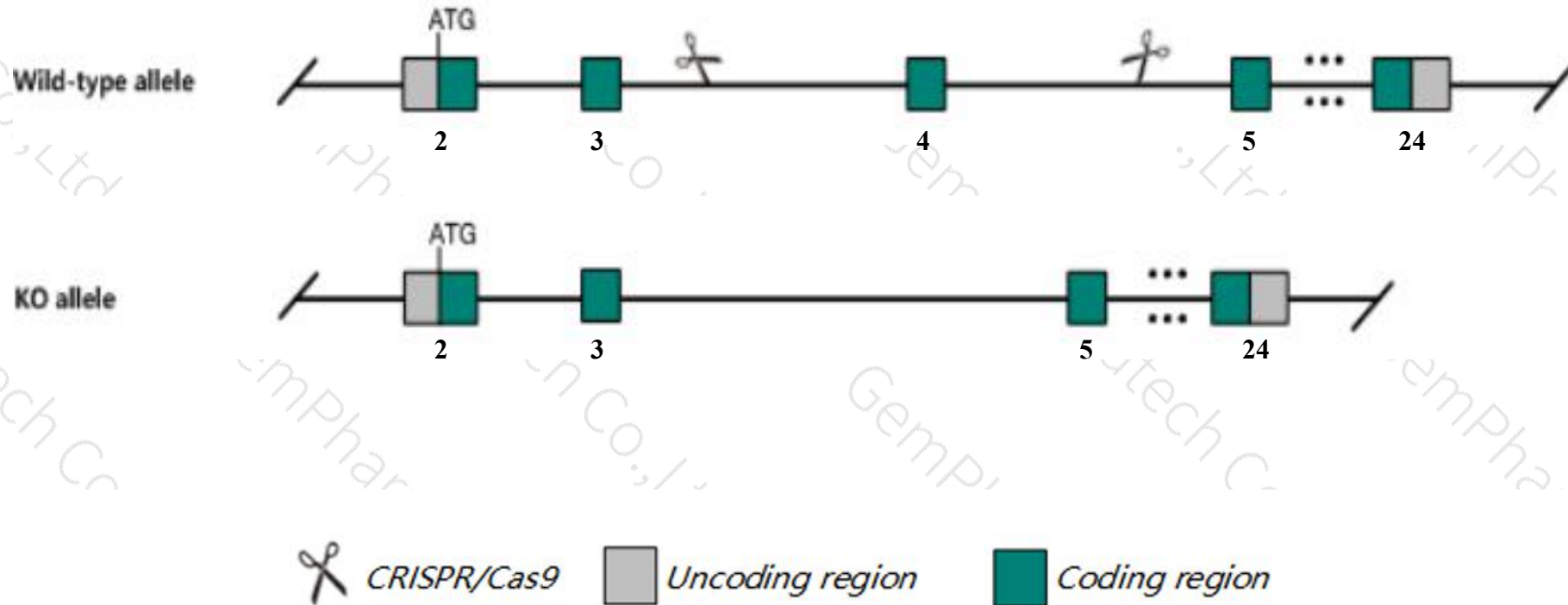
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fat2* gene. The schematic diagram is as follows:



- The *Fat2* gene has 2 transcripts. According to the structure of *Fat2* gene, exon4 of *Fat2-201*(ENSMUST00000068853.12) transcript is recommended as the knockout region. The region contains 59bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fat2* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for a knock-out allele are healthy, fertile and overtly normal, with no apparent defects in the development of red blood cells or platelets.
- The *Fat2* 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)

Fat2 FAT atypical cadherin 2 [Mus musculus (house mouse)]

Gene ID: 245827, updated on 13-Mar-2020

Summary



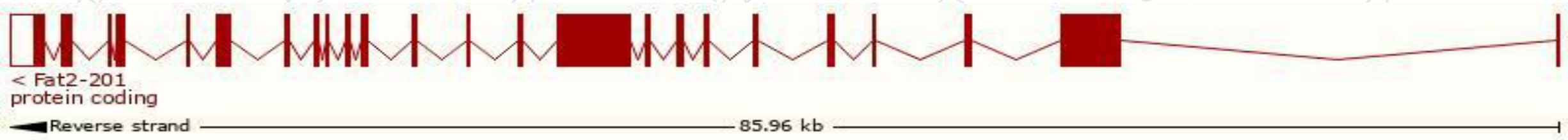
Official Symbol	Fat2 provided by MGI
Official Full Name	FAT atypical cadherin 2 provided by MGI
Primary source	MGI:MGI:2685369
See related	Ensembl:ENSMUSG00000055333
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	EMI2, Fath2, Gm523, mKIAA0811
Expression	Biased expression in cerebellum adult (RPKM 20.8) and bladder adult (RPKM 3.4) See more
Orthologs	human all

Transcript information (Ensembl)

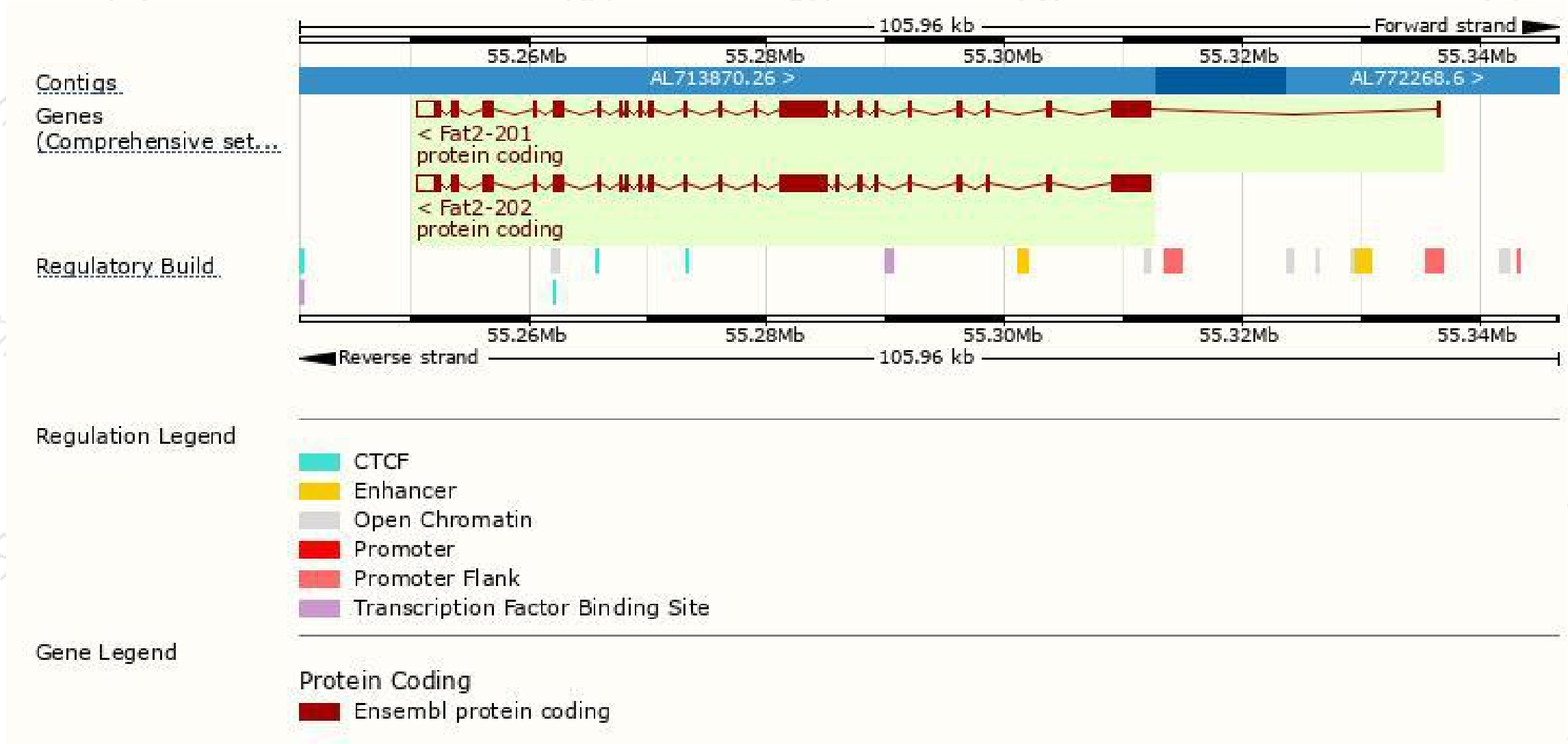
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fat2-201	ENSMUST00000068853.12	14528	4351aa	Protein coding	CCDS36157	Q5F226	TSL:5 GENCODE basic APPRIS P1
Fat2-202	ENSMUST00000108864.1	14423	4351aa	Protein coding	CCDS36157	Q5F226	TSL:5 GENCODE basic APPRIS P1

The strategy is based on the design of *Fat2-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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