

***Fat4* Cas9-KO Strategy**

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Project Overview

Project Name

Fat4

Project type

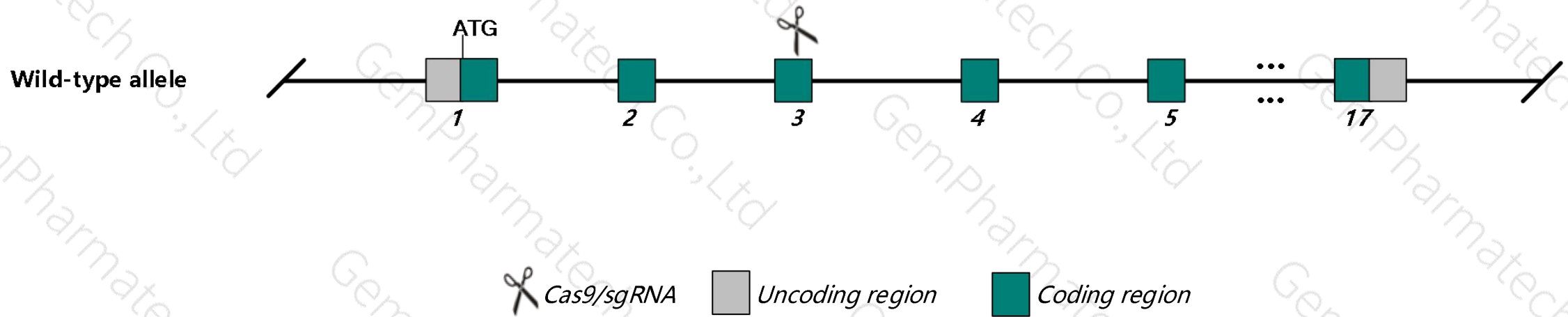
Cas9-KO

Strain background

C57BL/6N

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fat4* gene. The schematic diagram is as follows:



- In this project we use CRISPR/Cas9 technology to modify *Fat4* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6N 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/6N mice.

- According to the existing MGI data, Homozygous inactivation of this gene leads to neonatal lethality, reduced birth body size, curly tails, kyphosis, small lungs, renal cysts, and defects in sternum and vertebrae morphology, neural tube width, cochlear elongation, stereocilia orientation, kidney development, and intestinal elongation.
- The *Fat4* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Fat4 FAT atypical cadherin 4 [*Mus musculus* (house mouse)]

Gene ID: 329628, updated on 21-Sep-2019

Summary



Official Symbol Fat4 provided by [MGI](#)

Official Full Name FAT atypical cadherin 4 provided by [MGI](#)

Primary source [MGI:MGI:3045256](#)

See related [Ensembl:ENSMUSG00000046743](#)

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 9430004M15; 6030410K14Rik

Expression Broad expression in limb E14.5 (RPKM 8.9), CNS E14 (RPKM 5.9) and 19 other tissues [See more](#)

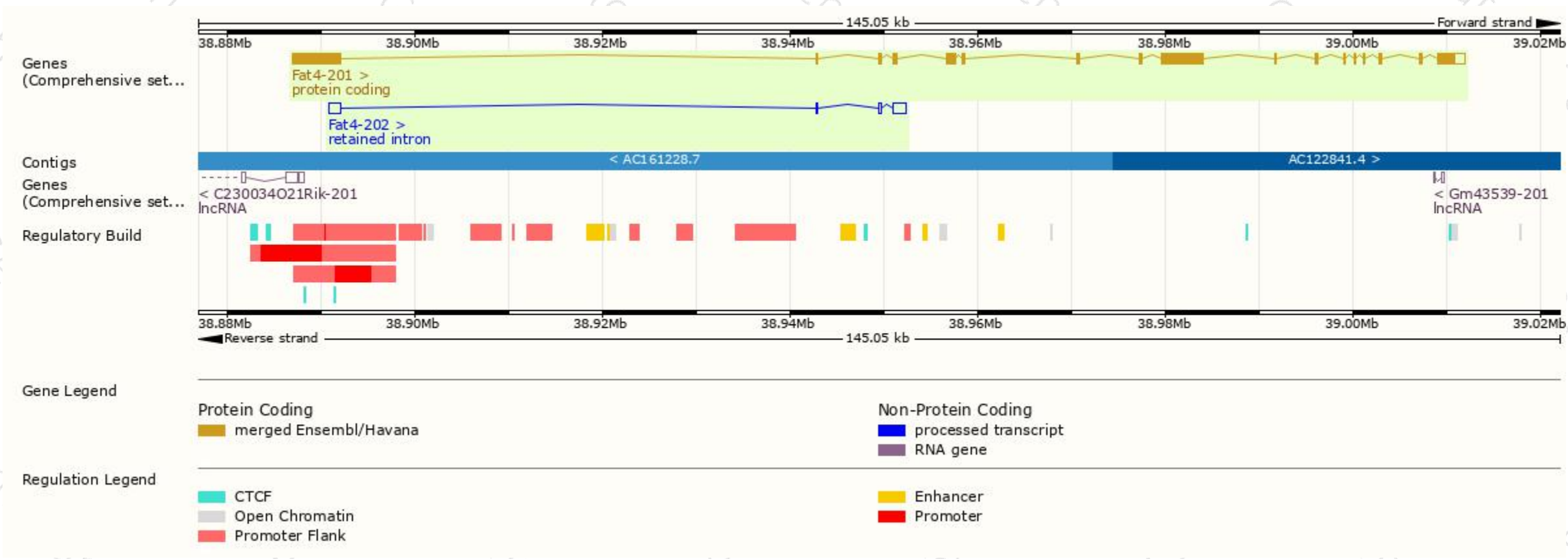
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

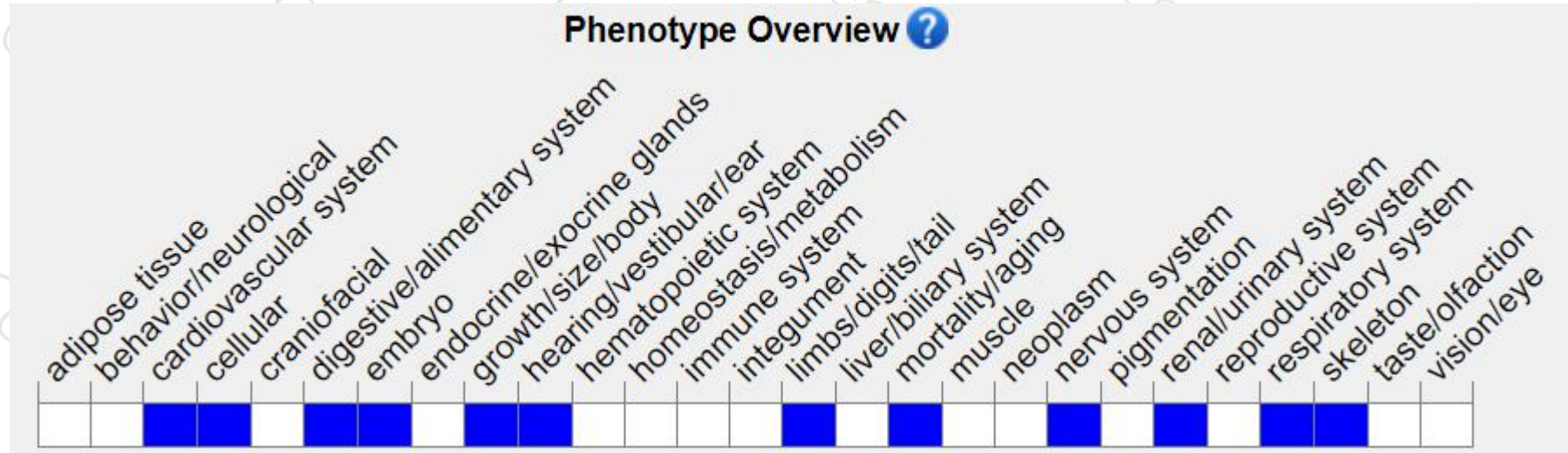
The gene has 2 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fat4-201	ENSMUST00000061260.7	16109	4981aa	Protein coding	CCDS17325	Q2PZL6	TSL:1 Gencode basic APPRIS P1
Fat4-202	ENSMUST00000129182.1	2994	No protein	Retained intron	-	-	TSL:1

Genomic location distribution



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

Homozygous inactivation of this gene leads to neonatal lethality, reduced birth body size, curly tails, kyphosis, small lungs, renal cysts, and defects in sternum and vertebrae morphology, neural tube width, cochlear elongation, stereocilia orientation, kidney development, and intestinal elongation.

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

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