

***Fam126a* Cas9-KO Strategy**

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Project Overview

Project Name

Fam126a

Project type

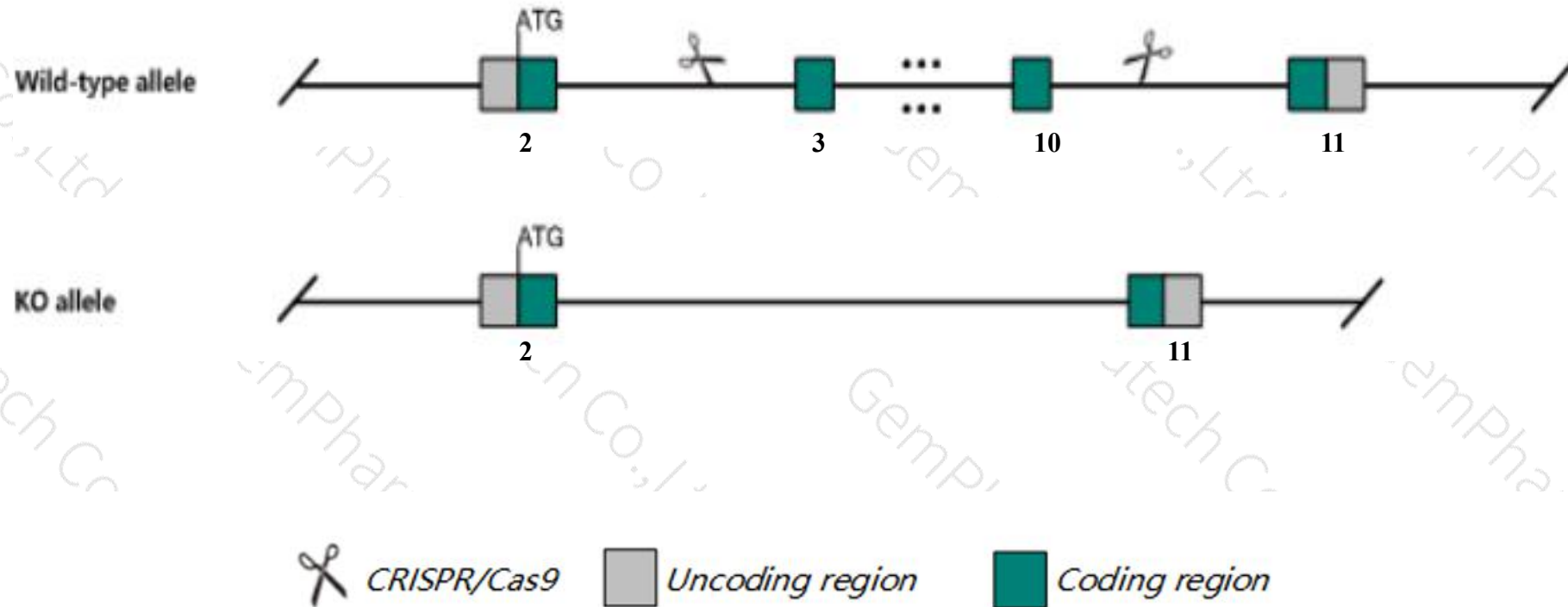
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fam126a* gene. The schematic diagram is as follows:



- The *Fam126a* gene has 7 transcripts. According to the structure of *Fam126a* gene, exon3-exon10 of *Fam126a-201*(ENSMUST00000030849.12) transcript is recommended as the knockout region. The region contains 940bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fam126a* 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 targeted null mutation not exhibit an obvious abnormal phenotype or specific defects in myelination as evaluated by light and electron microscopy analysis, unlike human patients.
- Transcript *Fam126a*-204 may not be affected.
- The *Fam126a* gene is located on the Chr5. 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)

Fam126a family with sequence similarity 126, member A [Mus musculus (house mouse)]

Gene ID: 84652, updated on 13-Mar-2020

Summary



Official Symbol Fam126a provided by [MGI](#)

Official Full Name family with sequence similarity 126, member A provided by [MGI](#)

Primary source [MGI:MGI:2149839](#)

See related [Ensembl:ENSMUSG00000028995](#)

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 AB030242, Drctnnb1a

Expression Ubiquitous expression in liver E14 (RPKM 8.2), testis adult (RPKM 8.1) and 25 other tissues [See more](#)

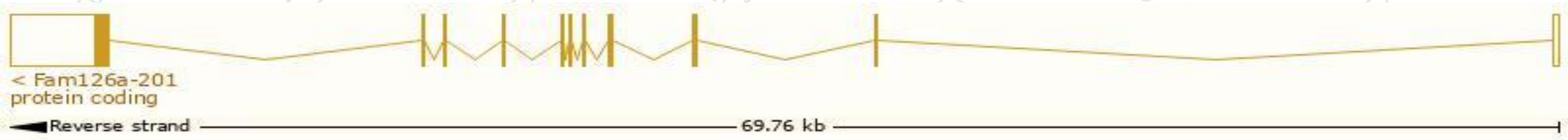
Orthologs [human all](#)

Transcript information (Ensembl)

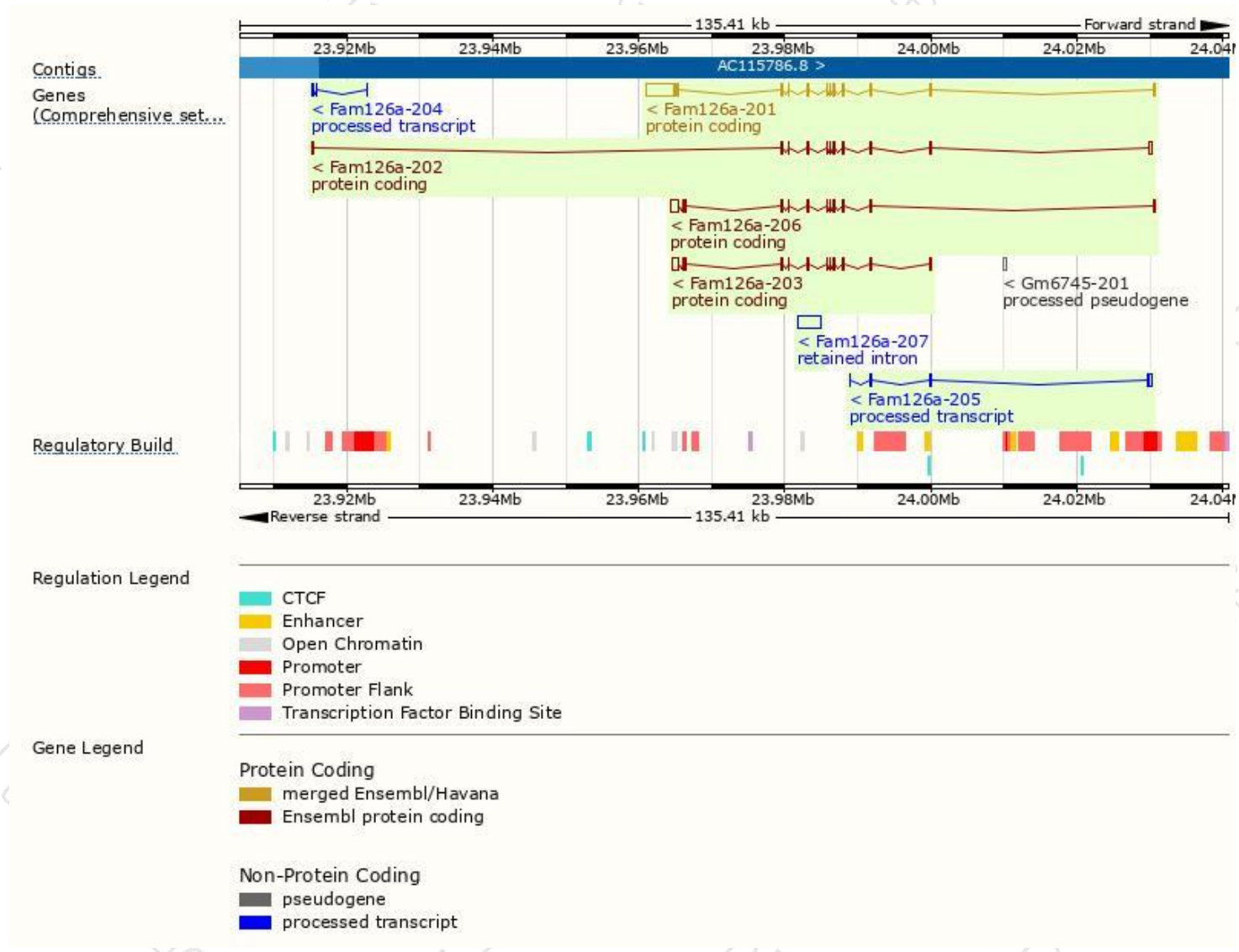
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fam126a-201	ENSMUST00000030849.12	5659	521aa	Protein coding	CCDS19113	Q6P9N1	TSL:1 GENCODE basic APPRIS P1
Fam126a-202	ENSMUST00000101513.8	1679	370aa	Protein coding	CCDS80221	Q6P9N1	TSL:1 GENCODE basic
Fam126a-206	ENSMUST00000197617.4	2288	338aa	Protein coding	-	A0A0G2JH12	TSL:5 GENCODE basic
Fam126a-203	ENSMUST00000115109.1	2195	420aa	Protein coding	-	Q6P9N1	TSL:5 GENCODE basic
Fam126a-205	ENSMUST00000147179.1	823	No protein	Processed transcript	-	-	TSL:1
Fam126a-204	ENSMUST00000126828.1	501	No protein	Processed transcript	-	-	TSL:2
Fam126a-207	ENSMUST00000198867.1	3127	No protein	Retained intron	-	-	TSL:NA

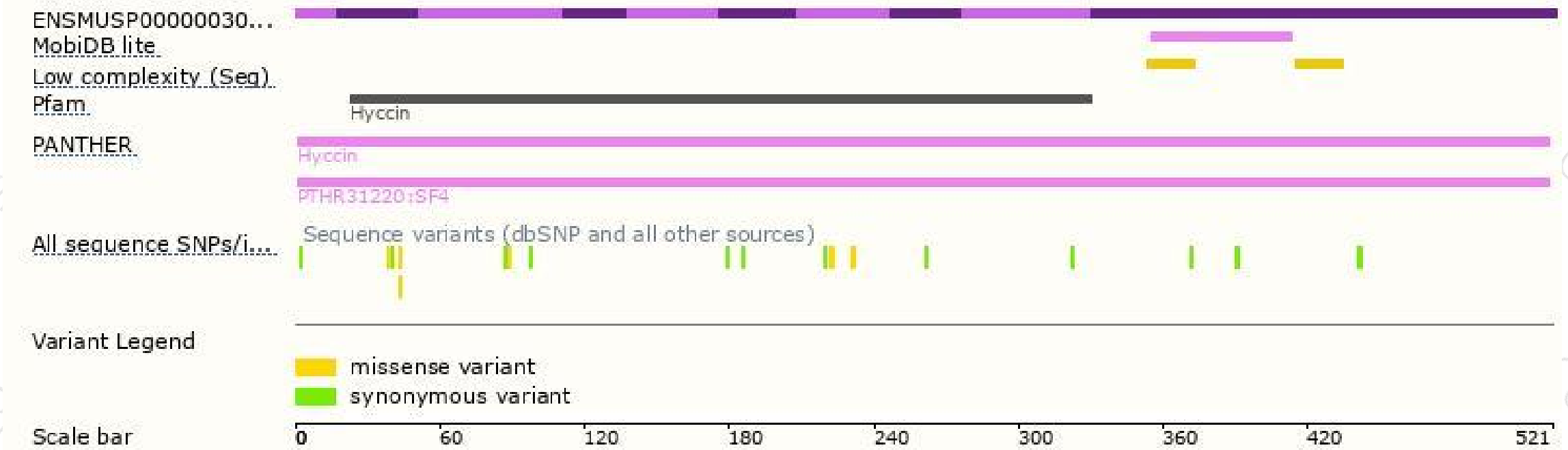
The strategy is based on the design of *Fam126a-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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