

# ***Fam83h*** Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***Fam83h***

**Project type**

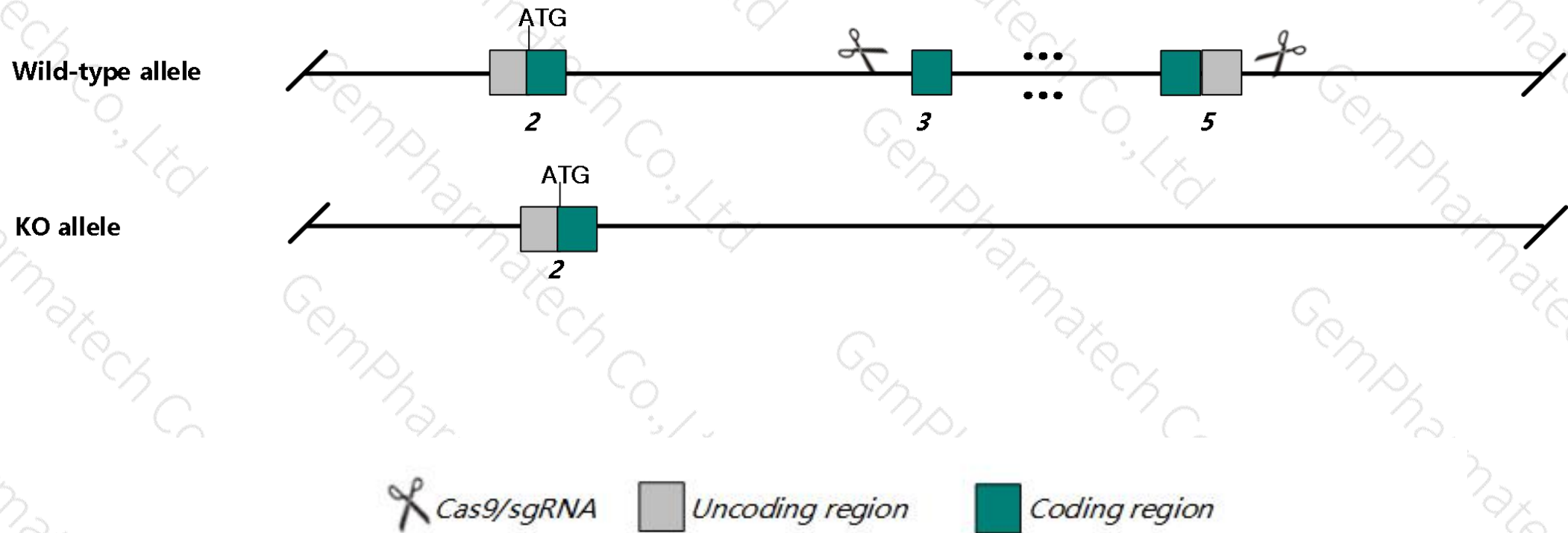
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fam83h* gene. The schematic diagram is as follows:



- The *Fam83h* gene has 3 transcripts. According to the structure of *Fam83h* gene, exon3-exon5 of *Fam83h*-202 (ENSMUST00000170153.1) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fam83h* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit decreased body size, sparse and scruffy coat, scaly skin, weakness, hypoactivity, delayed incisor eruption, periodontal pockets around incisors and molars with inserted coat hairs, partial postnatal lethality and premature death.
- The *Fam83h* gene is located on the Chr15. 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)

## Fam83h family with sequence similarity 83, member H [ *Mus musculus* (house mouse) ]

Gene ID: 105732, updated on 13-Mar-2020

### Summary

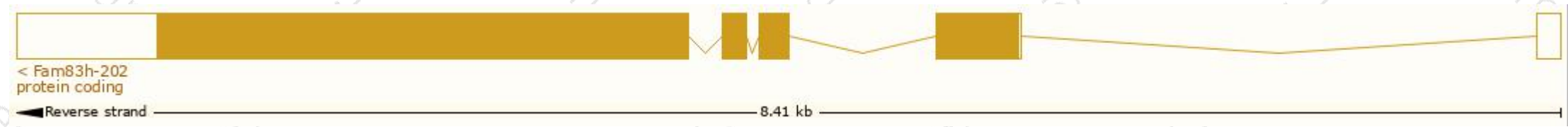
Official Symbol	Fam83h provided by <a href="#">MGI</a>
Official Full Name	family with sequence similarity 83, member H provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:2145900</a>
See related	<a href="#">Ensembl:ENSMUSG00000046761</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA409316
Expression	Broad expression in colon adult (RPKM 22.6), small intestine adult (RPKM 16.0) and 16 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

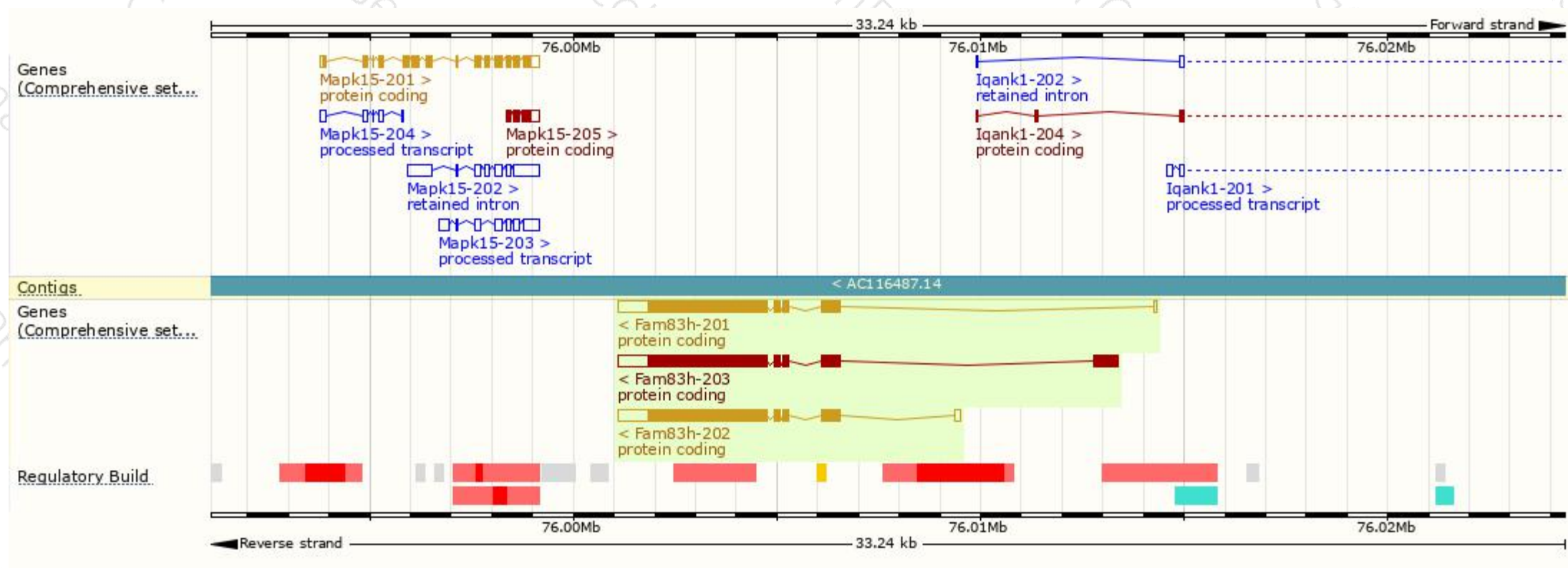
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fam83h-202	<a href="#">ENSMUST00000170153.1</a>	4534	<a href="#">1209aa</a>	Protein coding	<a href="#">CCDS27559</a>	<a href="#">Q148V8</a>	TSL:1 GENCODE basic APPRIS P2
Fam83h-201	<a href="#">ENSMUST00000060807.11</a>	4502	<a href="#">1209aa</a>	Protein coding	<a href="#">CCDS27559</a>	<a href="#">Q148V8</a>	TSL:1 GENCODE basic APPRIS P2
Fam83h-203	<a href="#">ENSMUST00000238313.1</a>	4994	<a href="#">1409aa</a>	Protein coding	-	-	GENCODE basic APPRIS ALT2

The strategy is based on the design of *Fam83h-202* transcript,The transcription is shown below

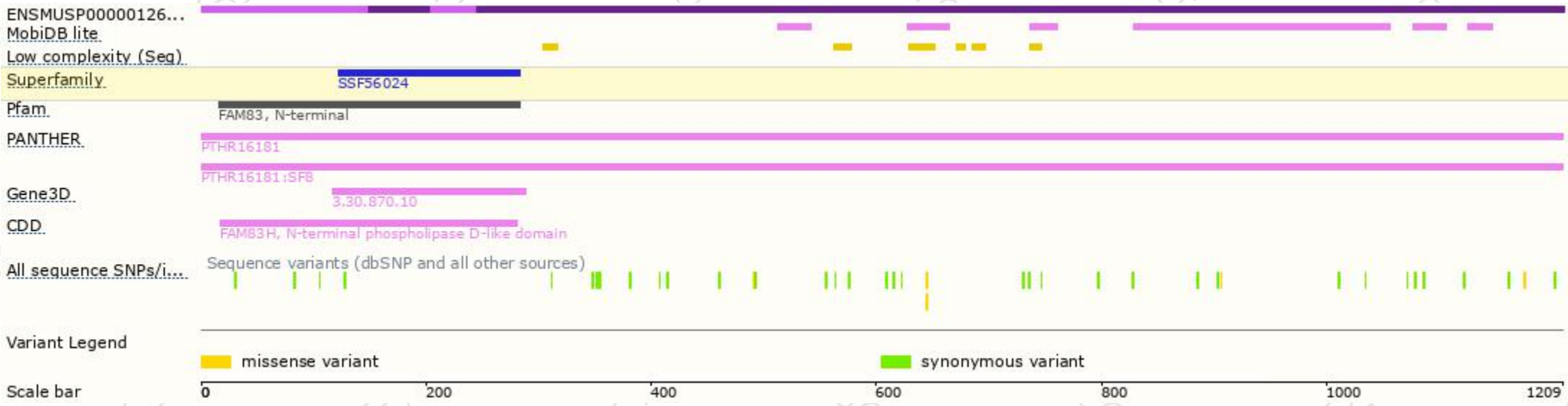


# Genomic location distribution

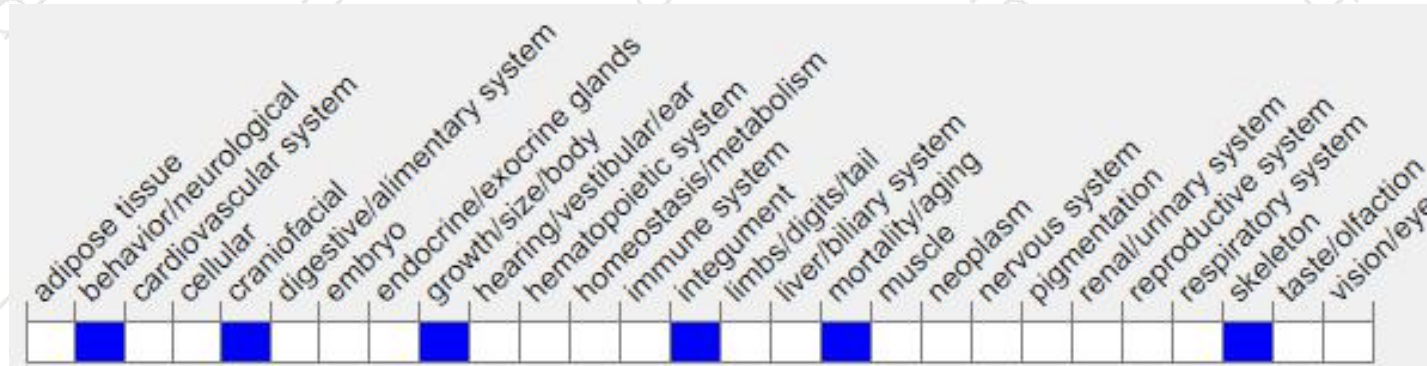




# Protein domain



# 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, Mice homozygous for a knock-out allele exhibit decreased body size, sparse and scruffy coat, scaly skin, weakness, hypoactivity, delayed incisor eruption, periodontal pockets around incisors and molars with inserted coat hairs, partial postnatal lethality and premature death.

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

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