Fam83h Cas9-CKO Strategy

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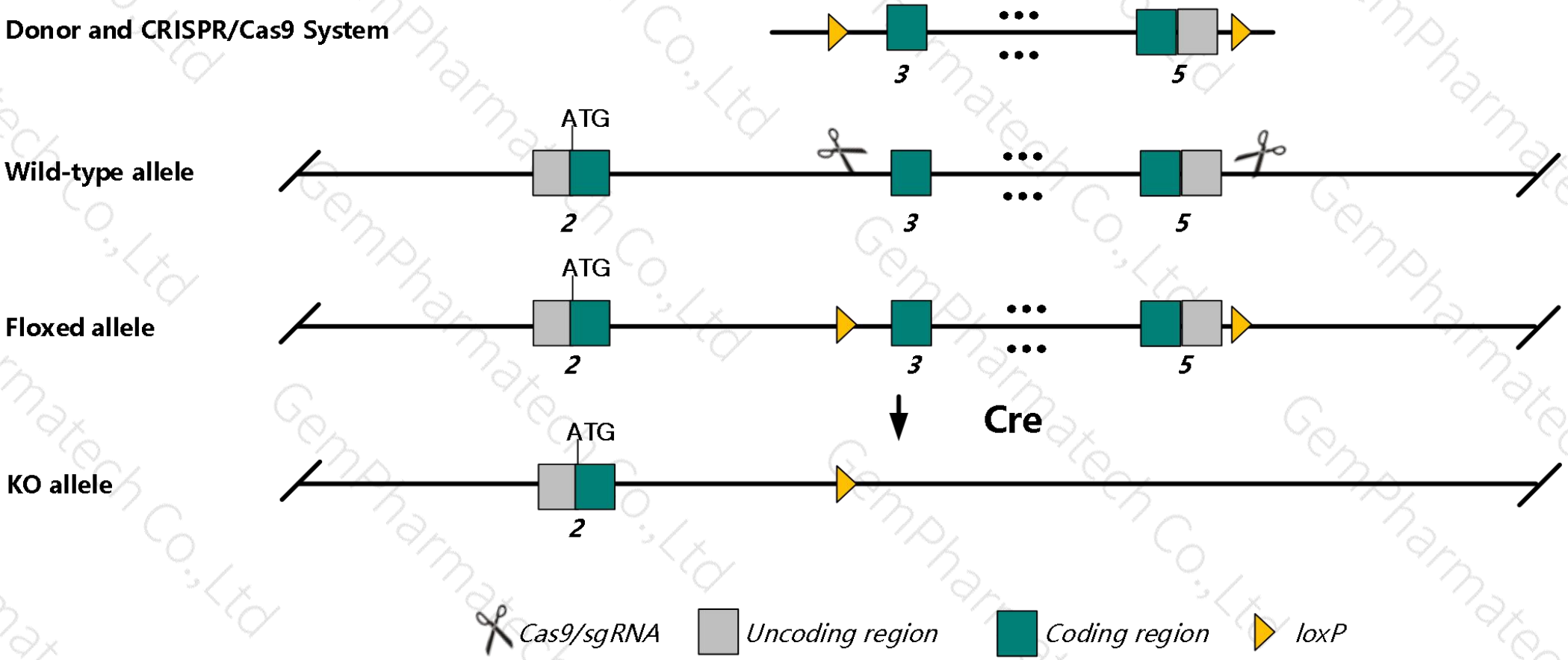
Project Overview

Project Name	***Fam83h***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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



Technical routes

- 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 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

➢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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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

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

Summary

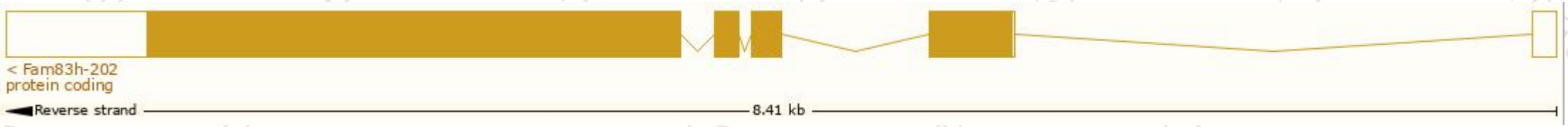
Official Symbol	Fam83h provided by MGI
Official Full Name	family with sequence similarity 83, member H provided by MGI
Primary source	MGI:MGI:2145900
See related	Ensembl:ENSMUSG00000046761
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata;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

Transcript information（Ensembl）

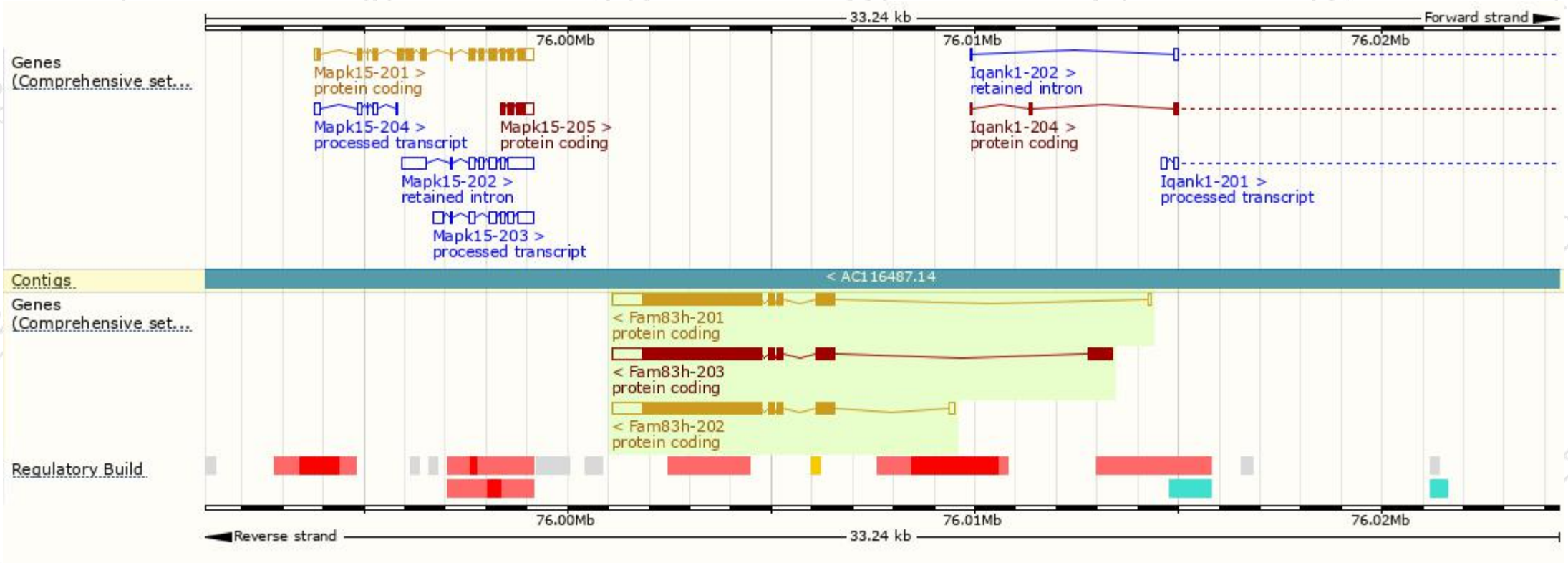
The gene has 3 transcripts,all transcripts are shown below:

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

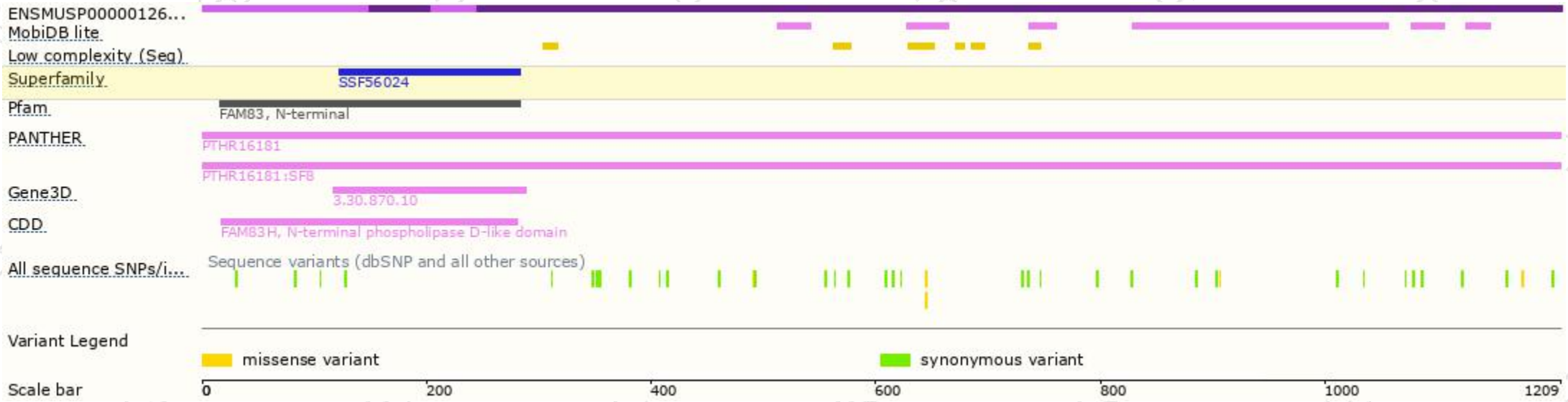
The strategy is based on the design of *Fam83h-202* transcript,The transcription is shown below



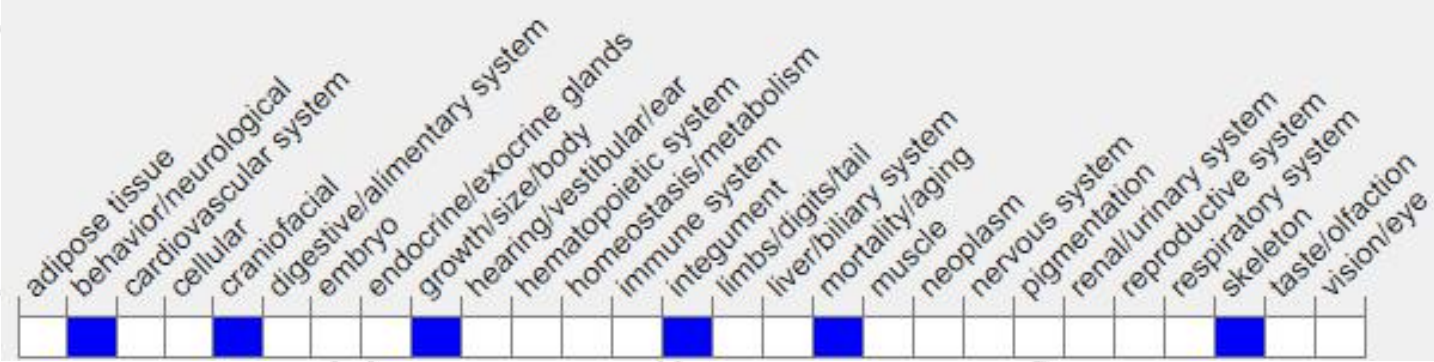
Genomic location distribution



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/).

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

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