Mfng Cas9-KO Strategy

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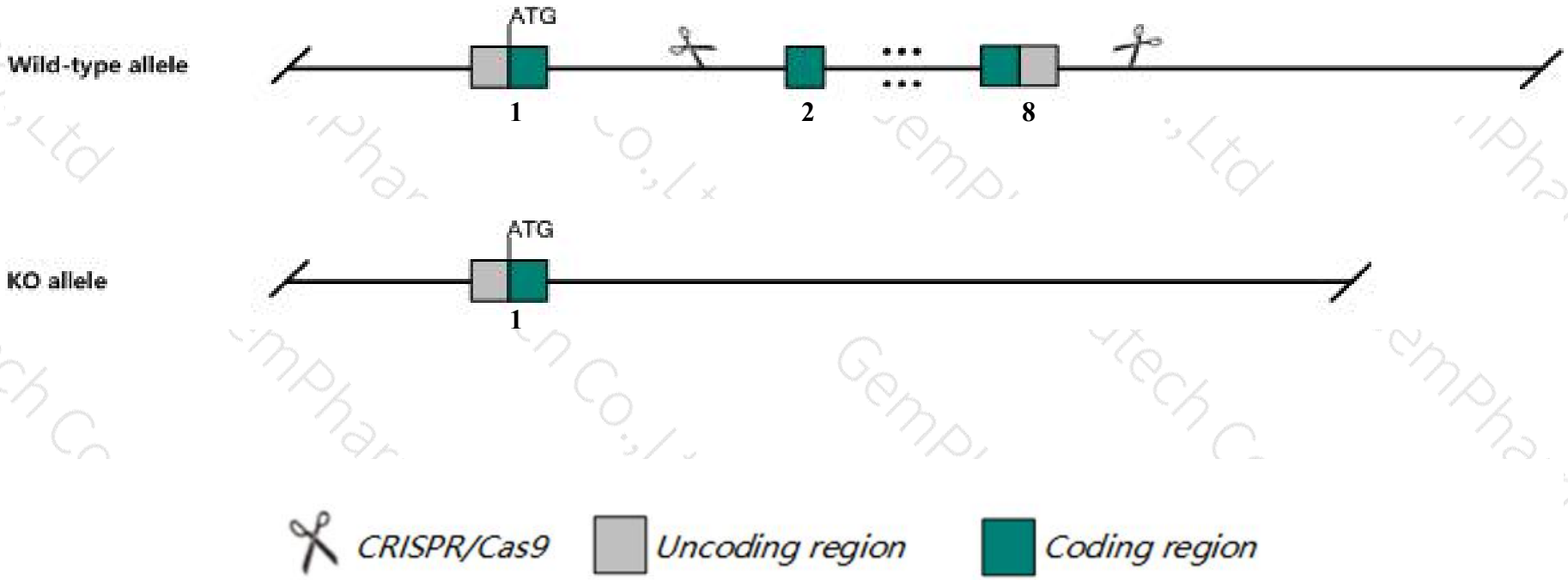
Project Overview

Project Name	***Mfng***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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



Technical routes

➢ The *Mfng* gene has 4 transcripts. According to the structure of *Mfng* gene, exon2-exon8 of *Mfng-201* (ENSMUST00000018313.5) 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 *Mfng* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a null mutation exhibit normal pancreatic development, morphology and physiology. Mice homozygous for a different knock-out allele exhibit altered lymphocyte numbers, abnormal circulating factors II, VII, IX and XI, and decreased prothrombin and partial thromboplastin time.

- The N-terminal of *Mfng* gene will remain several amino acids ,it may remain the partial function of *Mfng* gene.

- The *Mfng* 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）

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Mfng MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase [*Mus musculus* (house mouse)]

Gene ID: 17305, updated on 10-Oct-2019

Summary

Official Symbol	Mfng provided by MGI
Official Full Name	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase provided by MGI
Primary source	MGI:MGI:1095404
See related	Ensembl:ENSMUSG00000018169
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	AW546563
Expression	Broad expression in subcutaneous fat pad adult (RPKM 50.0), mammary gland adult (RPKM 49.8) and 17 other tissues See more
Orthologs	human all

Genomic context

Location: 15 E1; 15 37.69 cM

See Mfng in Genome Data Viewer

Exon count: 11

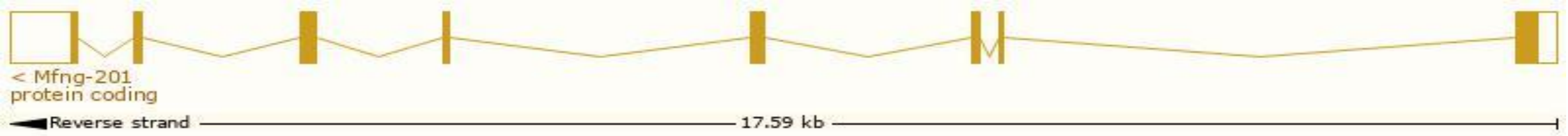
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	15	NC_000081.6 (78755882..78773516, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	15	NC_000081.5 (78586313..78603875, complement)

Transcript information（Ensembl）

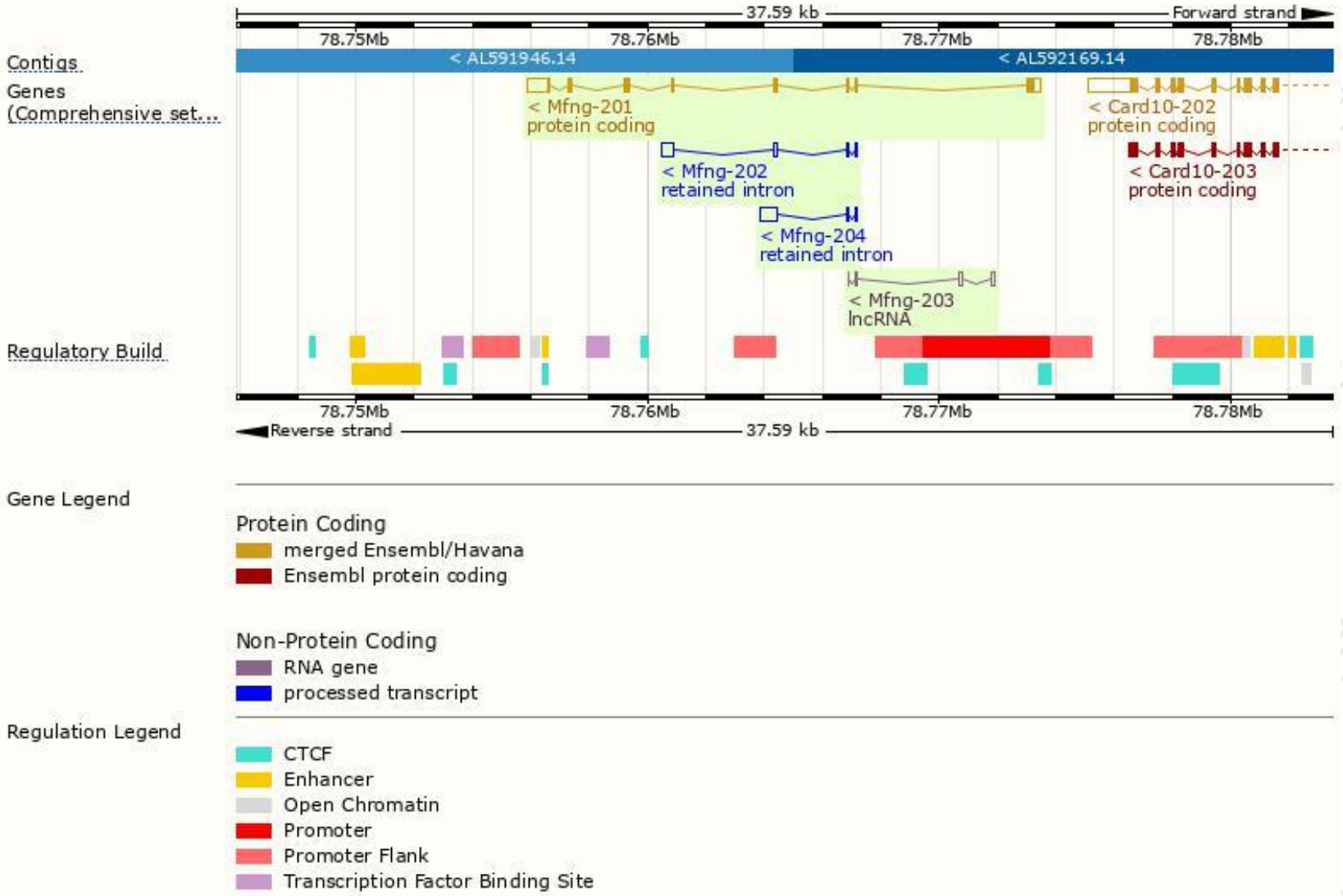
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mfng-201	ENSMUST00000018313.5	1865	321aa	Protein coding	CCDS27622	O09008 Q3UPI0	TSL:1 GENCODE basic APPRIS P1
Mfng-204	ENSMUST00000136795.1	717	No protein	Retained intron	-	-	TSL:5
Mfng-202	ENSMUST00000123518.7	706	No protein	Retained intron	-	-	TSL:3
Mfng-203	ENSMUST00000128389.1	319	No protein	lncRNA	-	-	TSL:3

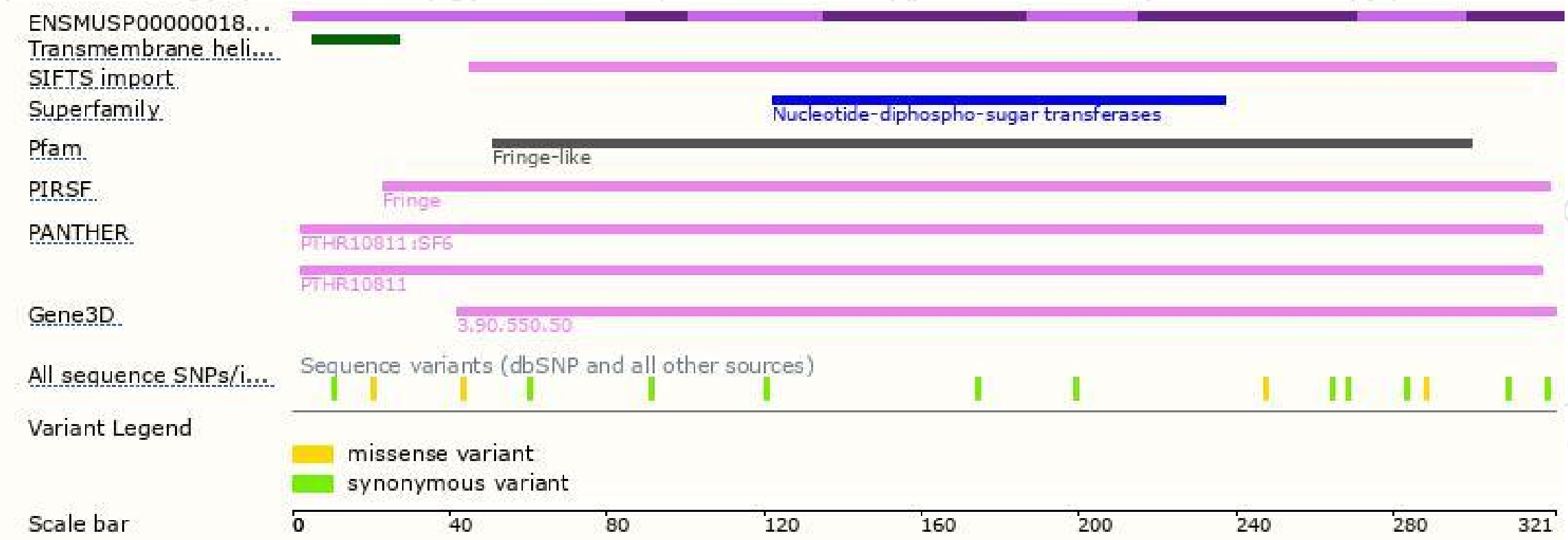
The strategy is based on the design of *Mfng-201* transcript,The transcription is shown below



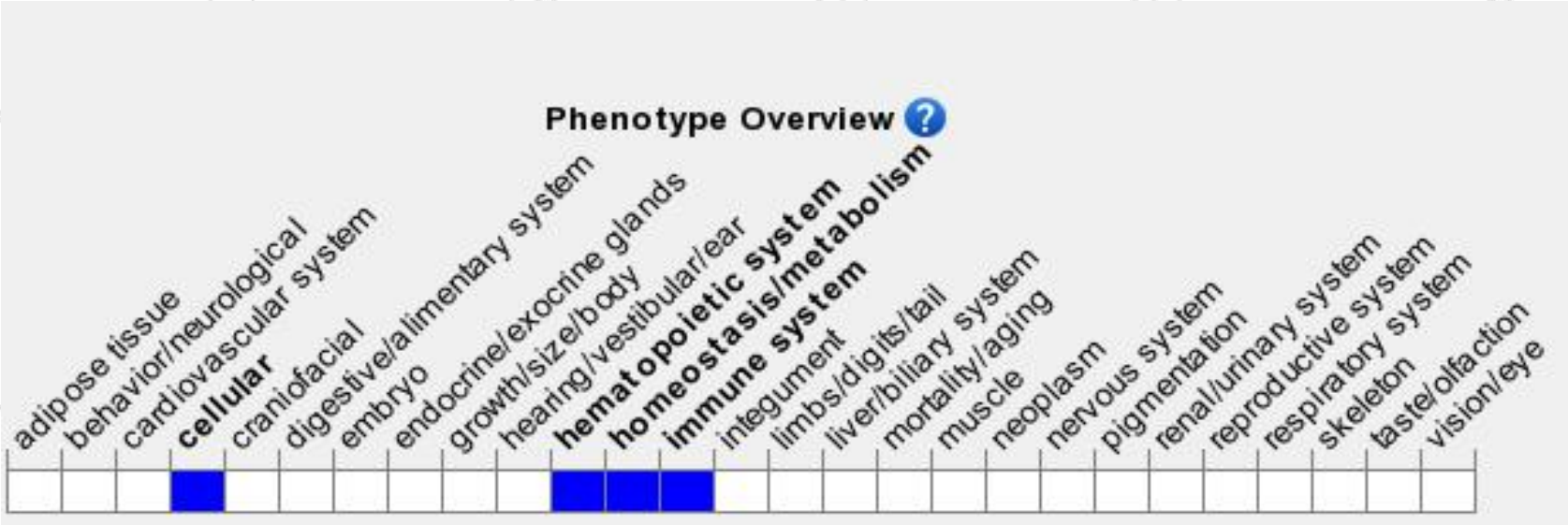
Genomic location distribution



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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