Fut9 Cas9-CKO Strategy

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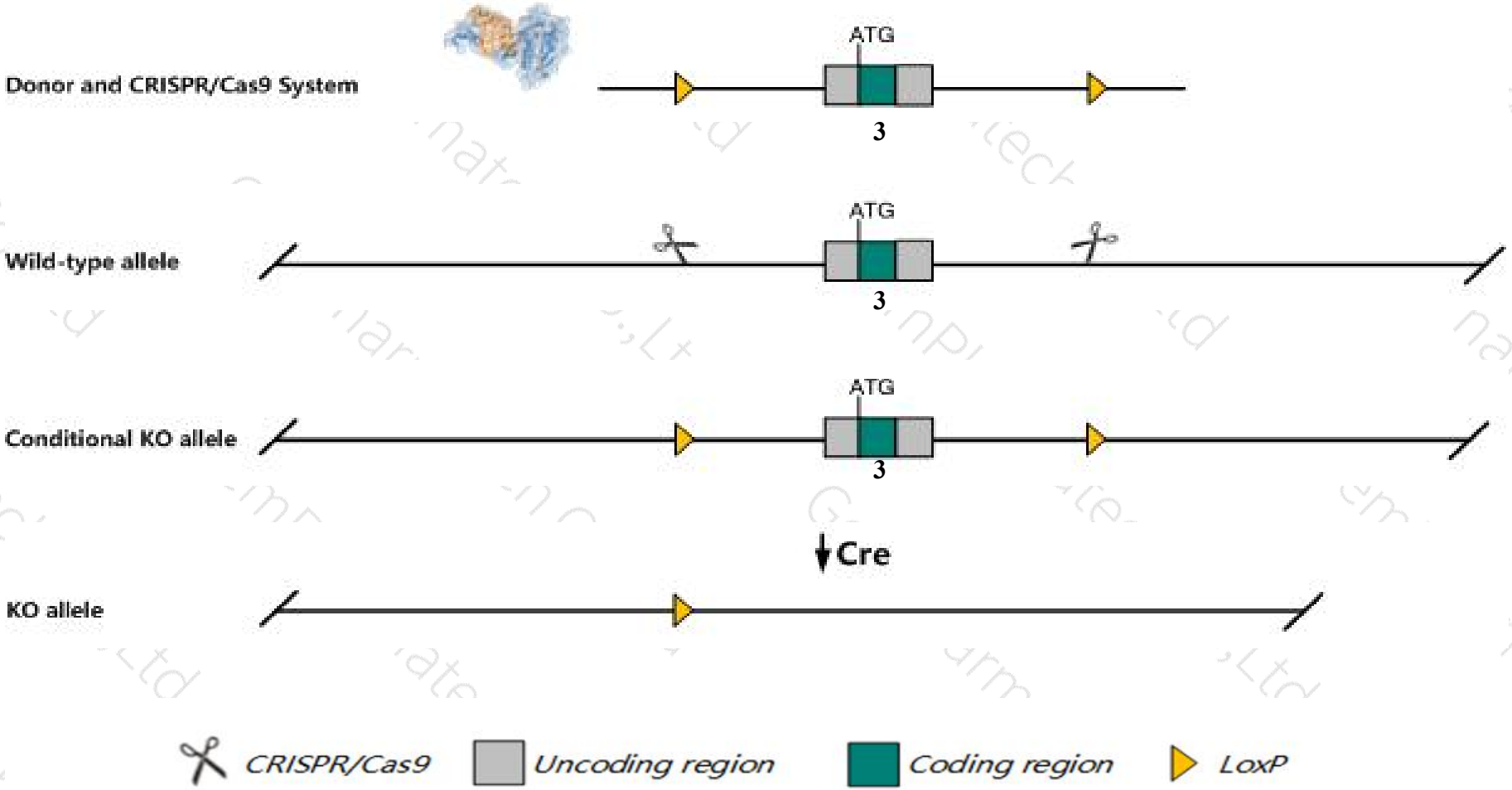
Project Overview

Project Name	***Fut9***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fut9* gene. The schematic diagram is as follows:



Technical routes

- The *Fut9* gene has 3 transcripts. According to the structure of *Fut9* gene, exon3 of *Fut9-201* (ENSMUST00000084770.4) transcript is recommended as the knockout region.The region contains all 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 *Fut9* 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 increased number of neuronal stem cells with increased self-renewal capacity.

➢ The *Fut9* gene is located on the Chr4. 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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Fut9 fucosyltransferase 9 [Mus musculus (house mouse)]

Gene ID: 14348, updated on 19-Mar-2019

Summary

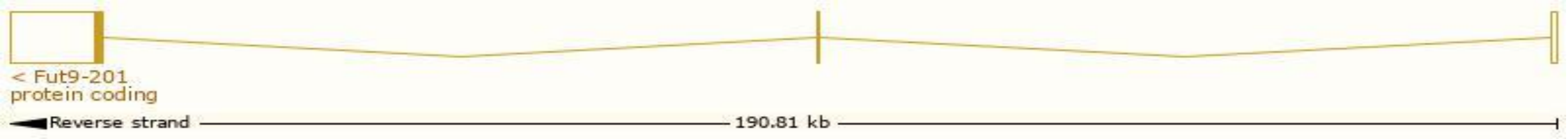
Official Symbol	Fut9 provided by MGI
Official Full Name	fucosyltransferase 9 provided by MGI
Primary source	MGI:MGI:1330859
See related	Ensembl:ENSMUSG00000055373
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI746471, AU067636, mFUT9, mFuc-TIX
Expression	Biased expression in kidney adult (RPKM 6.6), cerebellum adult (RPKM 5.7) and 7 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

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

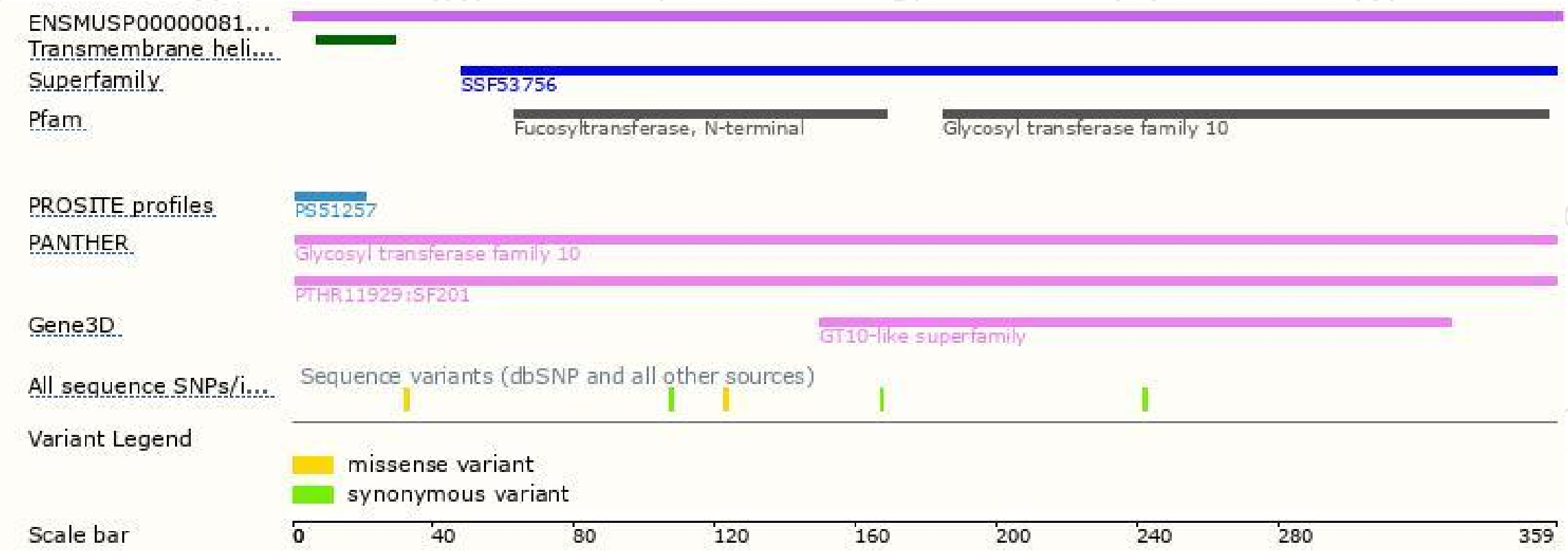
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fut9-201	ENSMUST00000084770.4	12134	359aa	Protein coding	CCDS18011	O88819 Q14AE3	TSL:1 GENCODE basic APPRIS P1
Fut9-202	ENSMUST00000108199.1	2579	359aa	Protein coding	CCDS18011	O88819 Q14AE3	TSL:1 GENCODE basic APPRIS P1
Fut9-203	ENSMUST00000149875.1	1859	No protein	lncRNA	-	-	TSL:1

The strategy is based on the design of *Fut9-201* transcript,The transcription is shown below

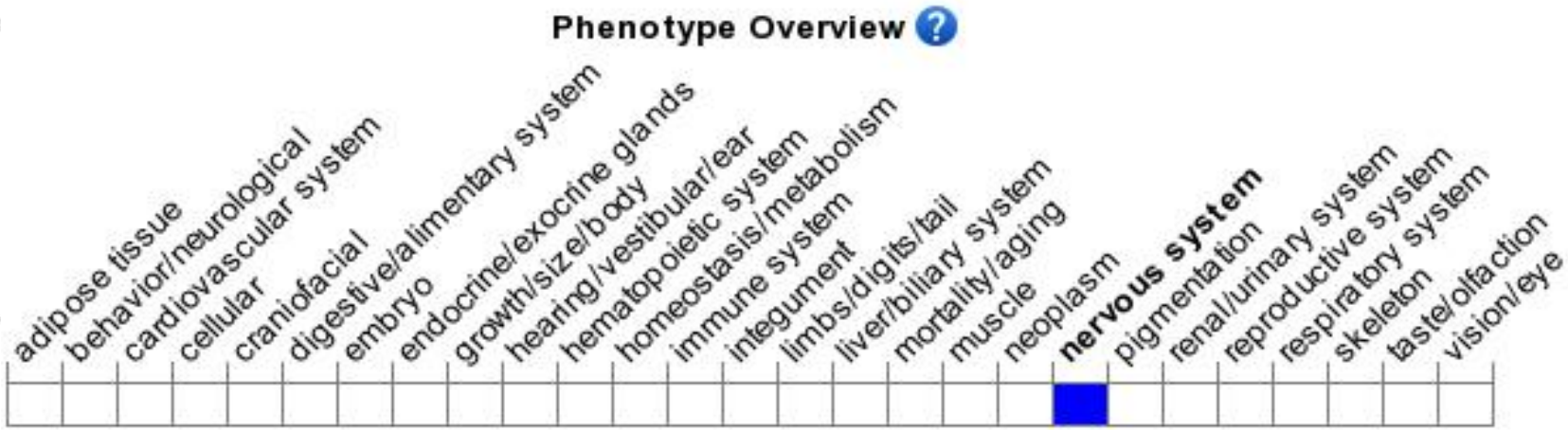


Genomic location distribution

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/).

According to the existing MGI data,Mice homozygous for a knock-out allele exhibit increased number of neuronal stem cells with increased self-renewal capacity.

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

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