Fut8 Cas9-KO Strategy

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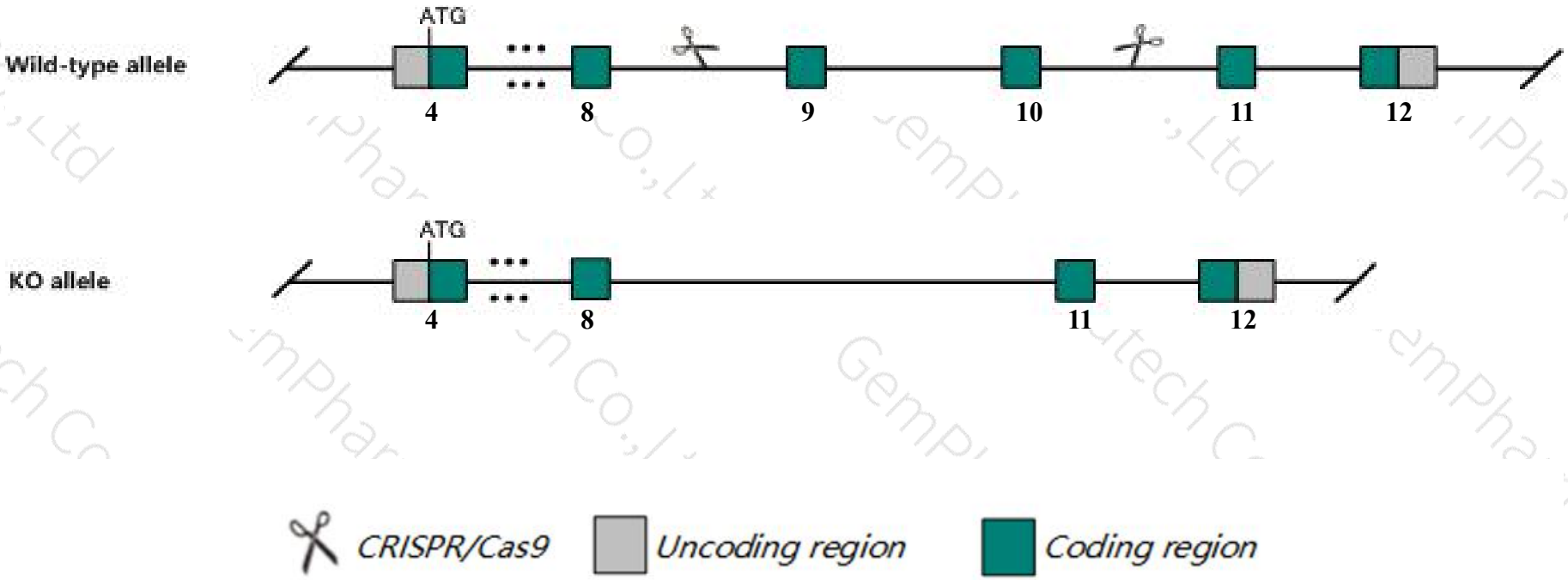
Project Overview

Project Name	***Fut8***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fut8* gene. The schematic diagram is as follows:



Technical routes

➢ The *Fut8* gene has 7 transcripts. According to the structure of *Fut8* gene, exon9-exon10 of *Fut8-201* (ENSMUST00000062804.7) transcript is recommended as the knockout region.The region contains 424bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Fut8* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

- According to the existing MGI data,Homozygous null mutation of this gene results in partial postnatal lethality, growth retardation, and progressive emphysema-like changes that include enlarged alveoli, increased lung capacity and compliance, and alveolar cell apoptosis. Postnatal survival is sensitive to genetic background.

- The *Fut8* gene is located on the Chr12. 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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Fut8 fucosyltransferase 8 [Mus musculus (house mouse)]

Gene ID: 53618, updated on 31-Jan-2019

Summary

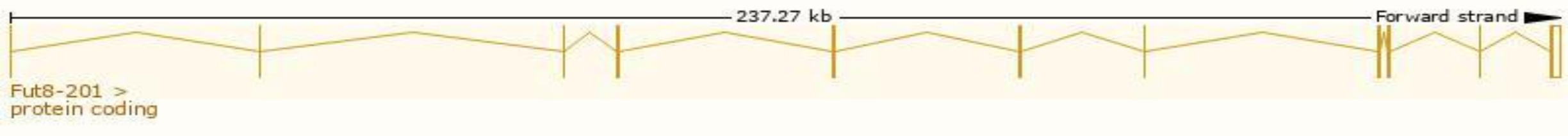
Official Symbol	Fut8 provided by MGI
Official Full Name	fucosyltransferase 8 provided by MGI
Primary source	MGI:MGI:1858901
See related	Ensembl:ENSMUSG00000021065
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Ubiquitous expression in adrenal adult (RPKM 7.1), cerebellum adult (RPKM 6.8) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

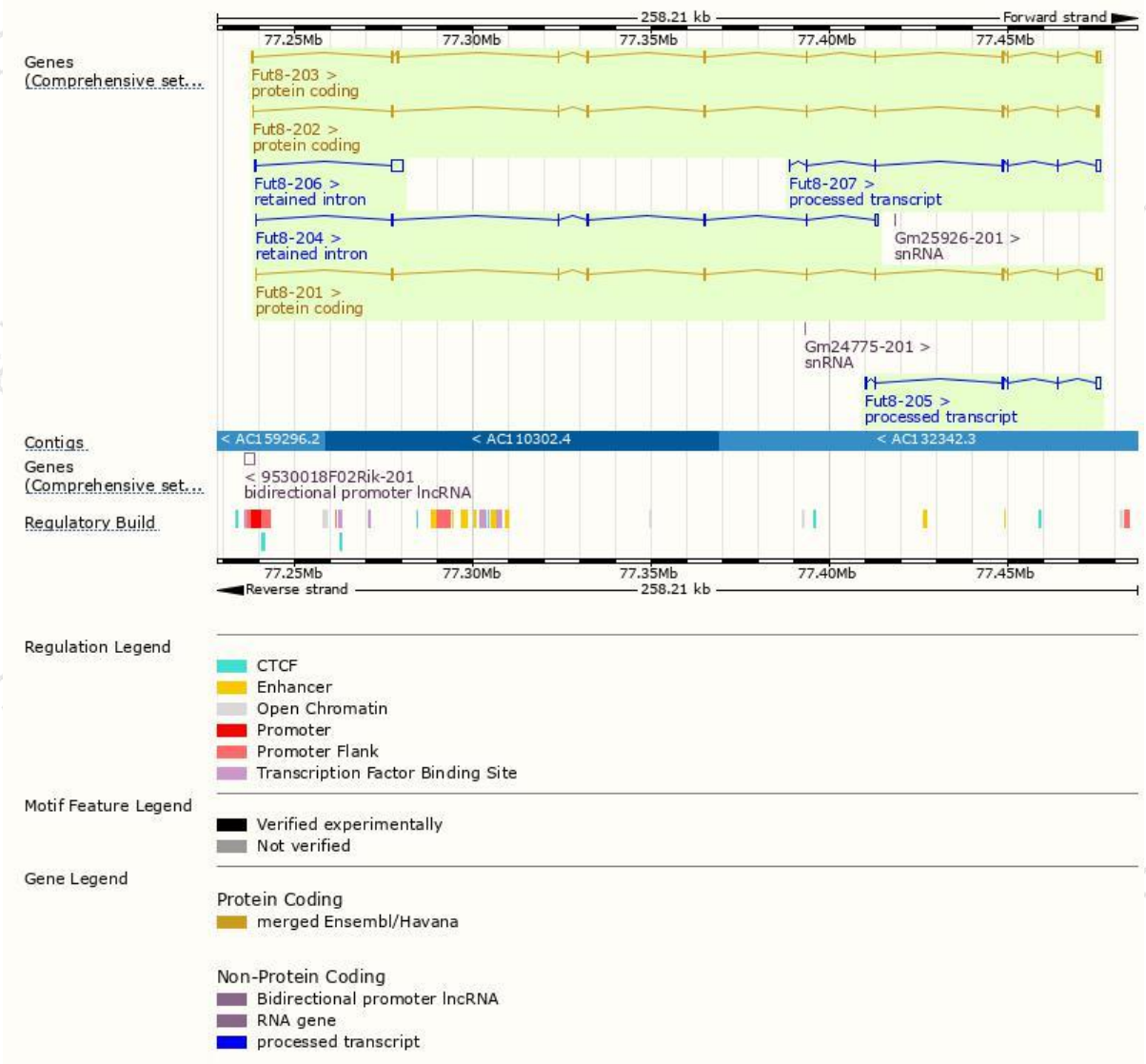
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fut8-201	ENSMUST00000062804.7	3358	575aa	Protein coding	CCDS25999	Q9WTS2	TSL:1 GENCODE basic APPRIS P1
Fut8-203	ENSMUST00000177595.8	2980	575aa	Protein coding	CCDS25999	Q9WTS2	TSL:1 GENCODE basic APPRIS P1
Fut8-202	ENSMUST00000171770.9	2765	575aa	Protein coding	CCDS25999	Q9WTS2	TSL:1 GENCODE basic APPRIS P1
Fut8-205	ENSMUST00000218851.1	2099	No protein	Processed transcript	-	-	TSL:1
Fut8-207	ENSMUST00000219299.1	2079	No protein	Processed transcript	-	-	TSL:1
Fut8-206	ENSMUST00000219289.1	3554	No protein	Retained intron	-	-	TSL:1
Fut8-204	ENSMUST00000217879.1	2209	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Fut8-201* transcript,The transcription is shown below

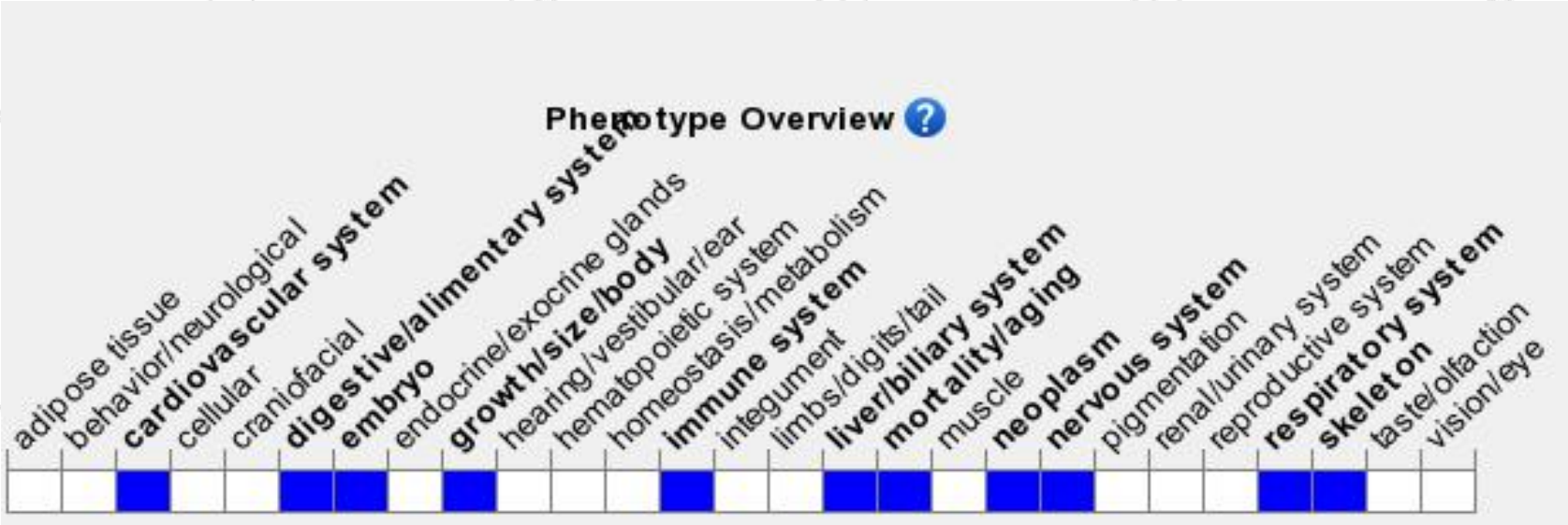


Genomic location distribution



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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