

Fut2 Cas9-CKO Strategy

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Project Overview

Project Name

Fut2

Project type

Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fut2* gene. The schematic diagram is as follows:

The *Fut2* gene has 5 transcripts. According to the structure of *Fut2* gene, exon2 of *Fut2-201* (ENSMUST00000069800.5) 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 *Fut2* 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.

According to the existing MGI data, Mice homozygous for disruptions in this gene display an essentially normal phenotype. Females are somewhat more susceptible to infections with *Candida albicans*.

The *Fut2* gene is located on the Chr7. 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.

Fut2 fucosyltransferase 2 [Mus musculus (house mouse)]

Gene ID: 14344, updated on 31-Jan-2019

Summary



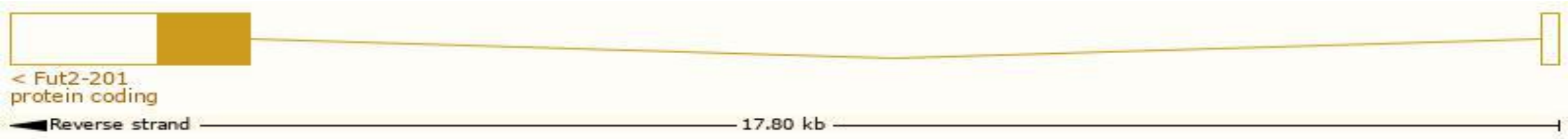
Official Symbol	Fut2 provided by MGI
Official Full Name	fucosyltransferase 2 provided by MGI
Primary source	MGI:MGI:109374
See related	Ensembl:ENSMUSG00000055978
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Summary	<p>This gene is one of three genes in mouse which encode a galactoside 2-L-fucosyltransferase. These genes differ in their developmental- and tissue-specific expression. The encoded type II membrane protein is anchored in the Golgi apparatus and controls the final step in the creation of alpha (1,2) fucosylated carbohydrates by the addition of a terminal fucose in an alpha (1,2) linkage. This enzyme is involved in the synthesis of the Lewis antigen as well as the H-antigen, a precursor of the A and B antigens of the ABH histo-blood group. The biological function of the fucosylated carbohydrate products is thought to involve cell-adhesion and interactions with microorganisms. Disruption of this gene results in altered glycosylation of gastric mucosa and uterine epithelia. Alternative splicing results in multiple transcript variants.</p> <p>[provided by RefSeq, Dec 2012]</p>
Expression	Biased expression in colon adult (RPKM 53.5), stomach adult (RPKM 21.9) and 4 other tissues See more
Orthologs	human all

Transcript information Ensembl

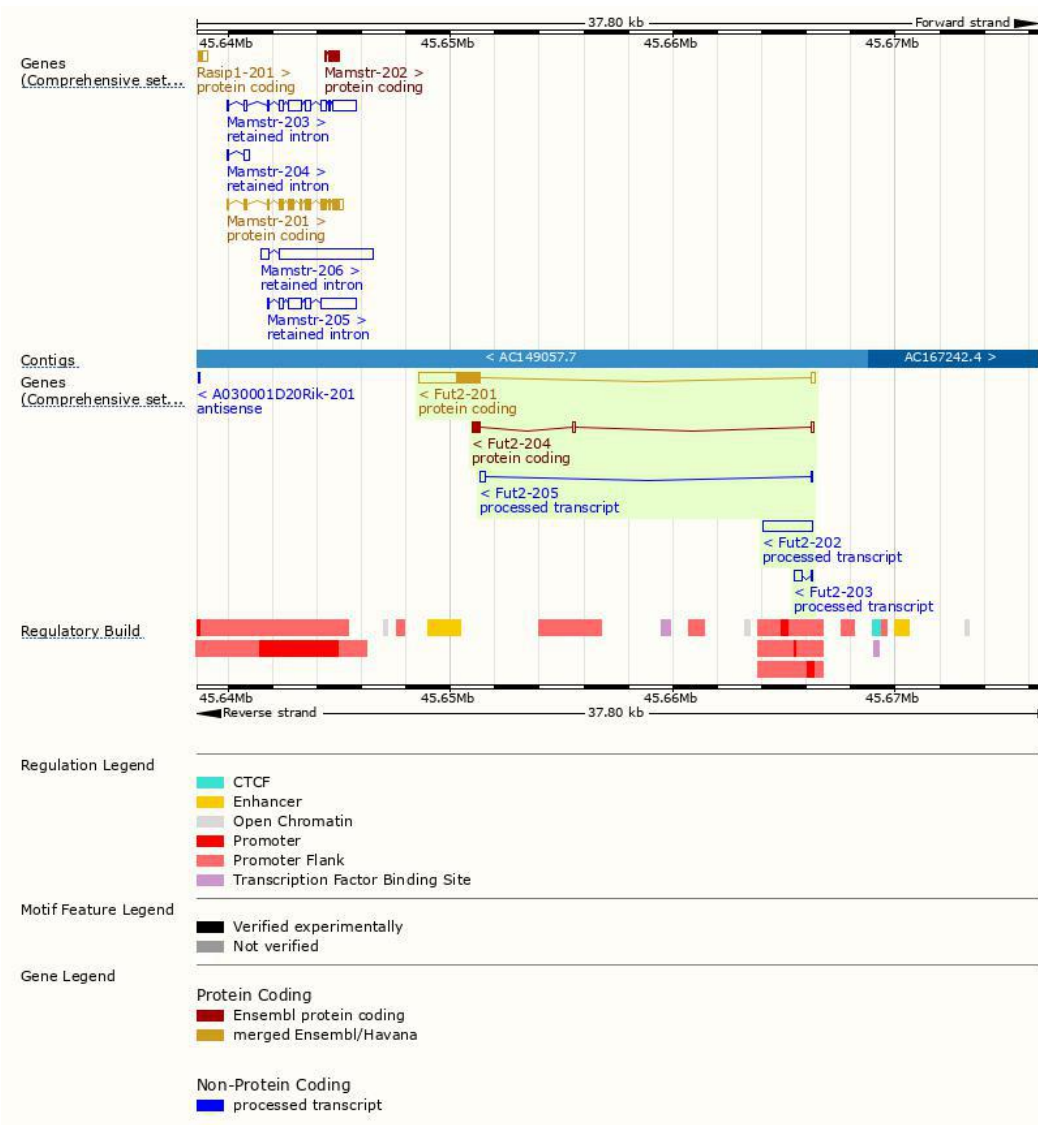
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fut2-201	ENSMUST00000069800.5	2955	347aa	Protein coding	CCDS21258	A6H6C9 Q9JL27	TSL:1 GENCODE basic APPRIS P1
Fut2-204	ENSMUST00000210620.1	606	118aa	Protein coding	-	A0A1B0GRD2	CDS 3' incomplete TSL:2
Fut2-202	ENSMUST00000209759.1	2234	No protein	Processed transcript	-	-	TSL:NA
Fut2-203	ENSMUST00000210470.1	417	No protein	Processed transcript	-	-	TSL:3
Fut2-205	ENSMUST00000211324.1	357	No protein	Processed transcript	-	-	TSL:5

The strategy is based on the design of *Fut2-201* transcript,The transcription is shown below



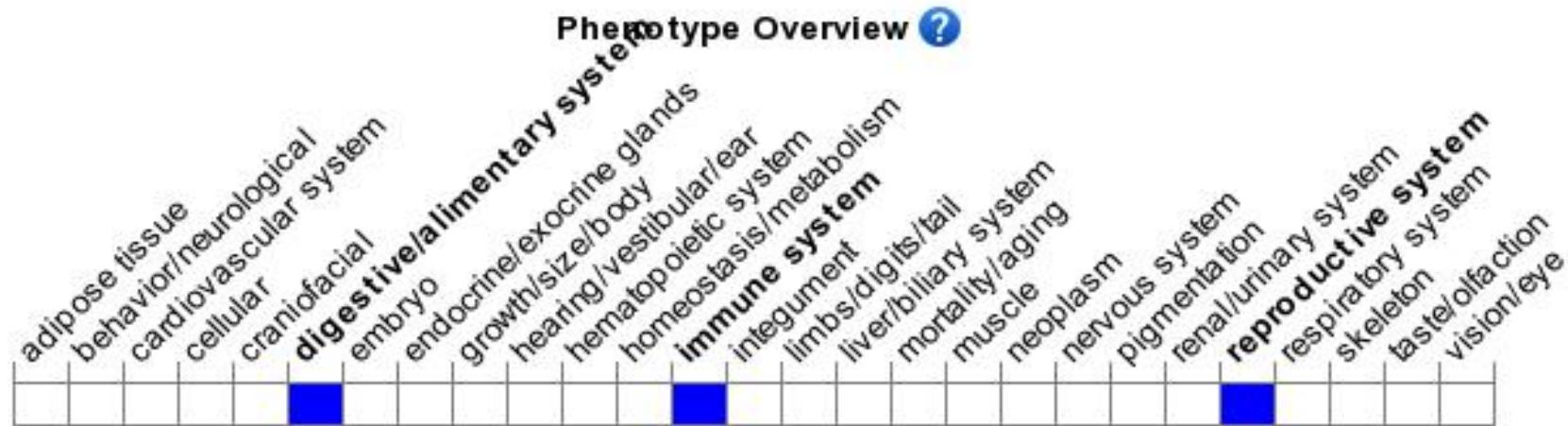
Genomic location distribution



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 disruptions in this gene display an essentially normal phenotype. Females are somewhat more susceptible to infections with *Candida albicans*.

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