

# ***Fut2*** Cas9-KO Strategy

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# Project Overview

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**Project Name**

***Fut2***

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**Project type**

**Cas9-KO**

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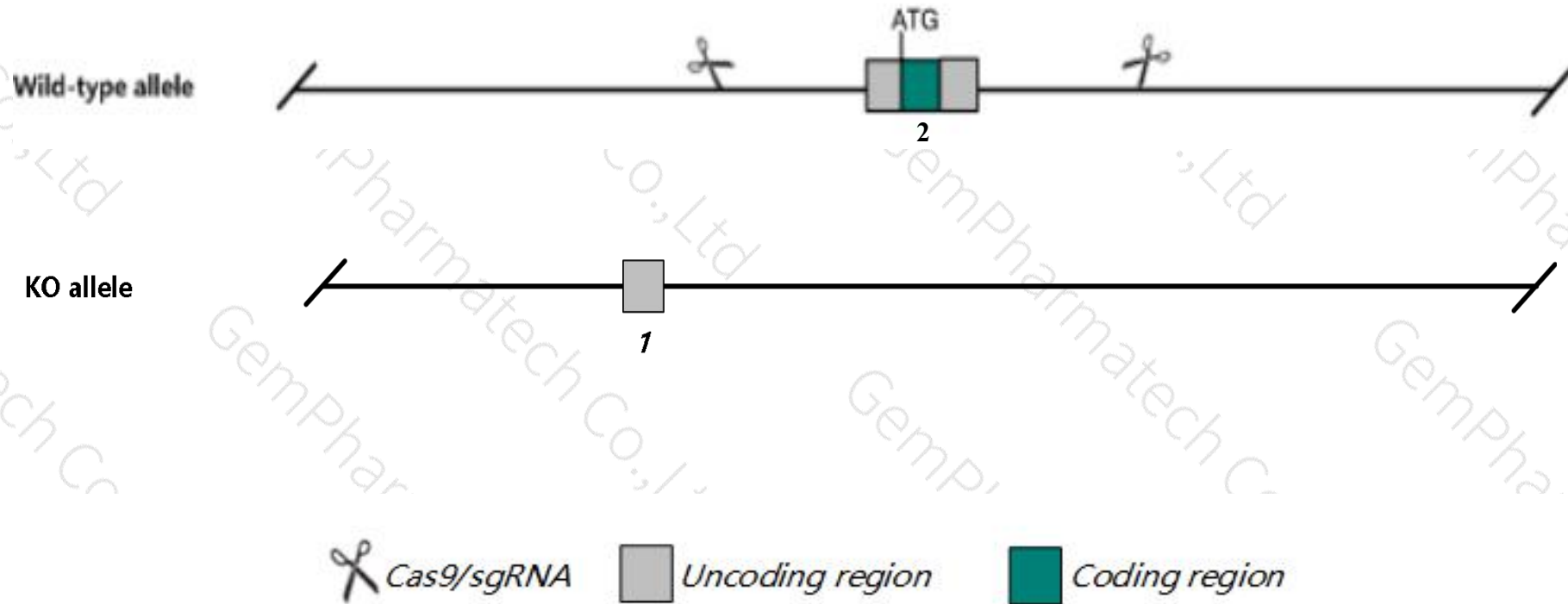
**Strain background**

**C57BL/6J**

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# 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: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## Fut2 fucosyltransferase 2 [Mus musculus (house mouse)]

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

### Summary



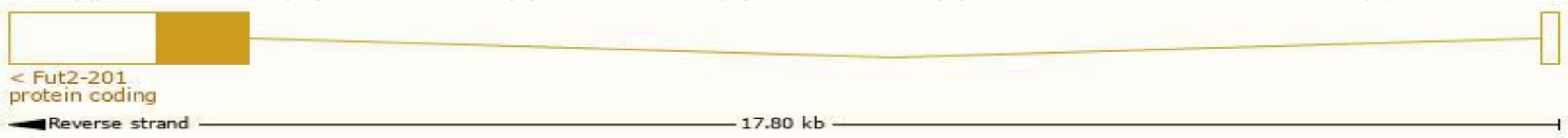
<b>Official Symbol</b>	Fut2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	fucosyltransferase 2 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:109374</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000055978</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	REVIEWED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Summary</b>	<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>
<b>Expression</b>	Biased expression in colon adult (RPKM 53.5), stomach adult (RPKM 21.9) and 4 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information（Ensembl）

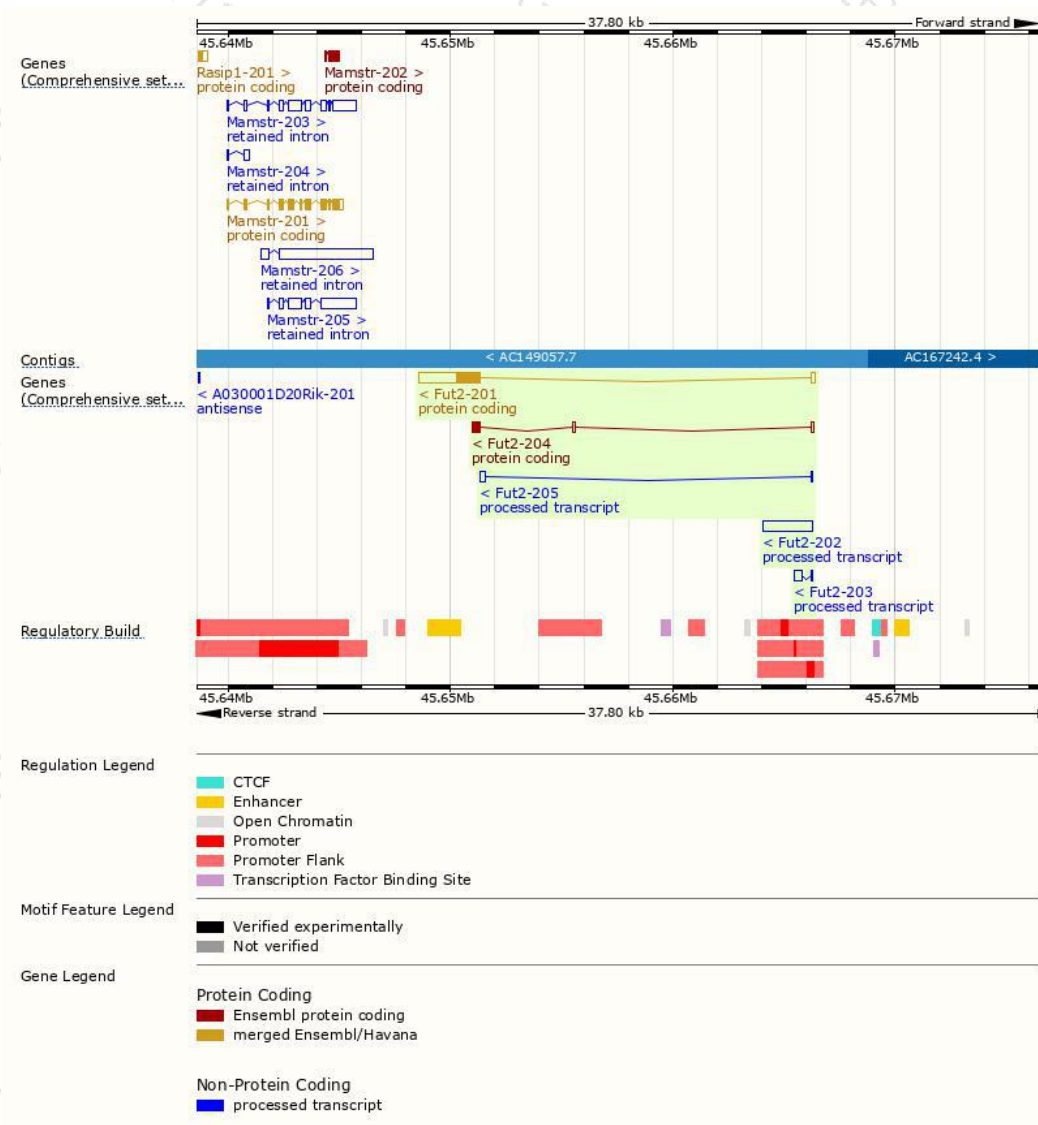
The gene has 5 transcripts,all transcripts are shown below:

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

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

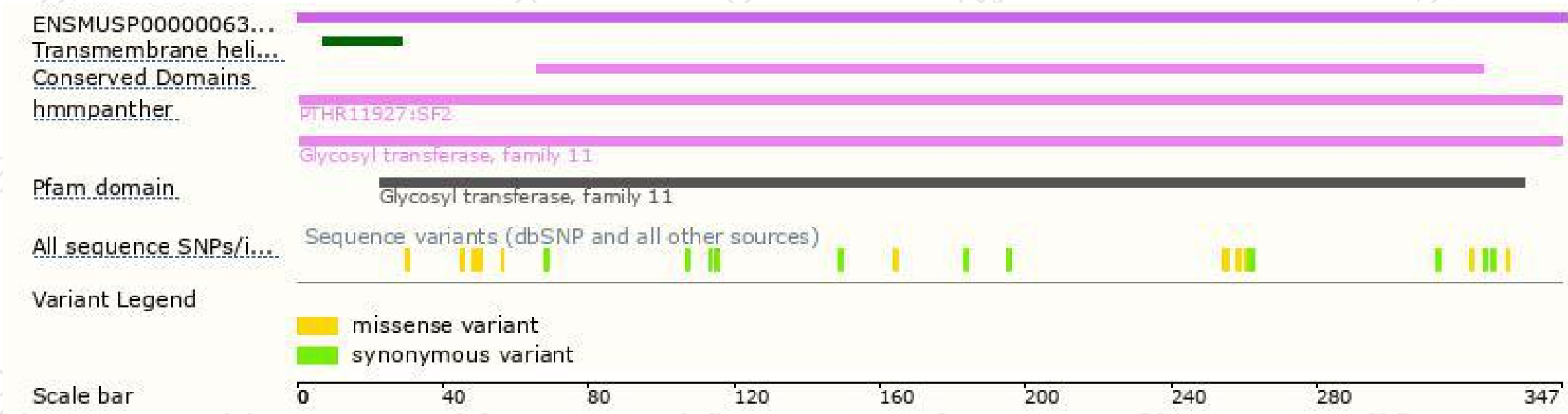


# Genomic location distribution

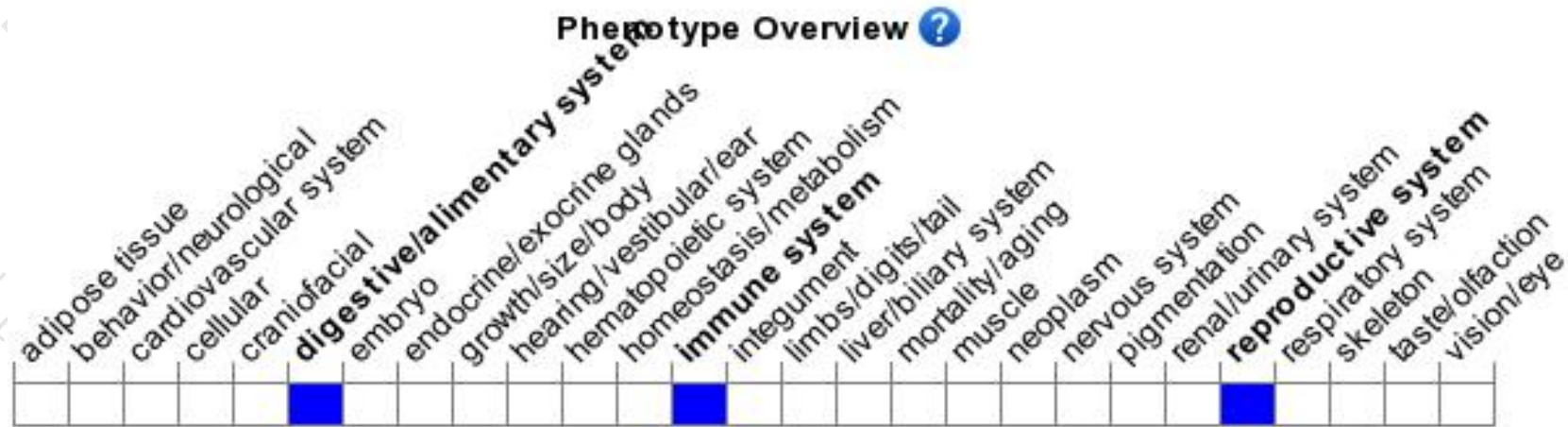




# Protein domain



# 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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