

# *Mgat5b* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***Mgat5b***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mgat5b* gene. The schematic diagram is as follows:



- The *Mgat5b* gene has 4 transcripts. According to the structure of *Mgat5b* gene, exon2 of *Mgat5b-201* (ENSMUST00000103027.9) transcript is recommended as the knockout region. The region contains 113bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mgat5b* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit low levels of O-man-linked beta1,6-branched glycans. Mice homozygous for a different knock-out allele exhibit decreased susceptibility to cuprizone induced injury.
- The *Mgat5b* gene is located on the Chr11. 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)

## Mgat5b mannoside acetylglucosaminyltransferase 5, isoenzyme B [Mus musculus (house mouse)]

Gene ID: 268510, updated on 31-Jan-2019

### Summary



|                           |   |
|---------------------------|---|
| <b>Official Symbol</b>    | Mgat5b provided by <a href="#">MGI</a>  |
| <b>Official Full Name</b> | mannoside acetylglucosaminyltransferase 5, isoenzyme B provided by <a href="#">MGI</a>  |
| <b>Primary source</b>     | <a href="#">MGI:MGI:3606200</a>   |
| <b>See related</b>        | <a href="#">Ensembl:ENSMUSG00000043857</a>  |
| <b>Gene type</b>          | protein coding  |
| <b>RefSeq status</b>      | PROVISIONAL   |
| <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>Also known as</b>      | C330018B01, GnT-IX, mGnTVB  |
| <b>Expression</b>         | Biased expression in whole brain E14.5 (RPKM 22.3), CNS E18 (RPKM 20.1) and 8 other tissues <a href="#">See more</a>  |
| <b>Orthologs</b>          | <a href="#">human</a> <a href="#">all</a>   |

# Transcript information (Ensembl)

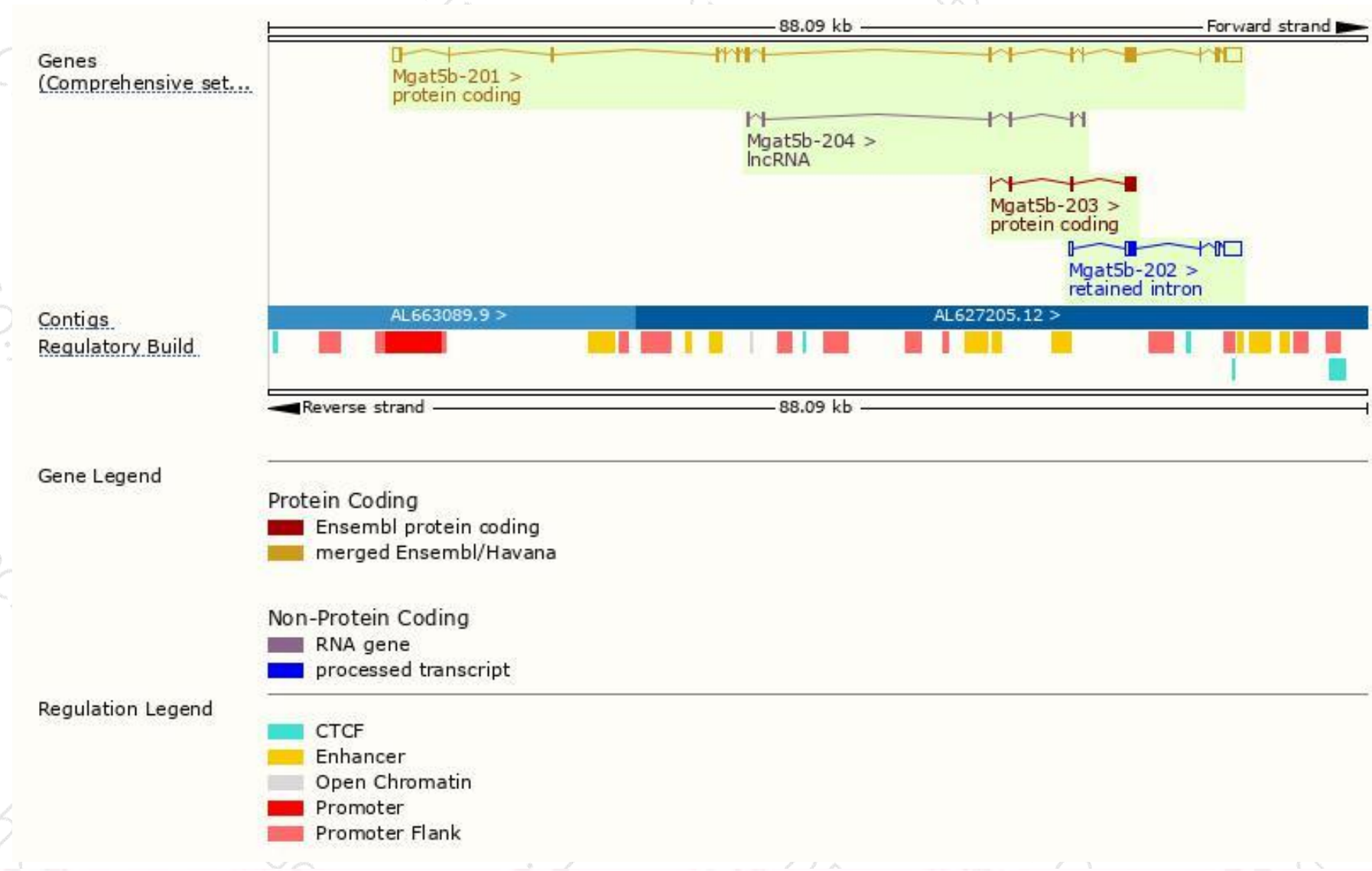
The gene has 4 transcripts,all transcripts are shown below:

| Name       | Transcript ID                        | bp   | Protein               | Biotype         | CCDS                      | UniProt                | Flags   |
|------------|--------------------------------------|------|-----------------------|-----------------|---------------------------|------------------------|---|
| Mgat5b-201 | <a href="#">ENSMUST00000103027.9</a> | 4258 | <a href="#">792aa</a> | Protein coding  | <a href="#">CCDS25682</a> | <a href="#">Q765H6</a> | TSL:5 GENCODE basic APPRIS P1   |
| Mgat5b-203 | <a href="#">ENSMUST00000136584.1</a> | 641  | <a href="#">214aa</a> | Protein coding  | -                         | <a href="#">F7BPB5</a> | 5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3 |
| Mgat5b-202 | <a href="#">ENSMUST00000126757.1</a> | 2568 | No protein            | Retained intron | -                         | -                      | TSL:1   |
| Mgat5b-204 | <a href="#">ENSMUST00000139905.1</a> | 725  | No protein            | lncRNA          | -                         | -                      | TSL:3   |

The strategy is based on the design of *Mgat5b-201* transcript,The transcription is shown below

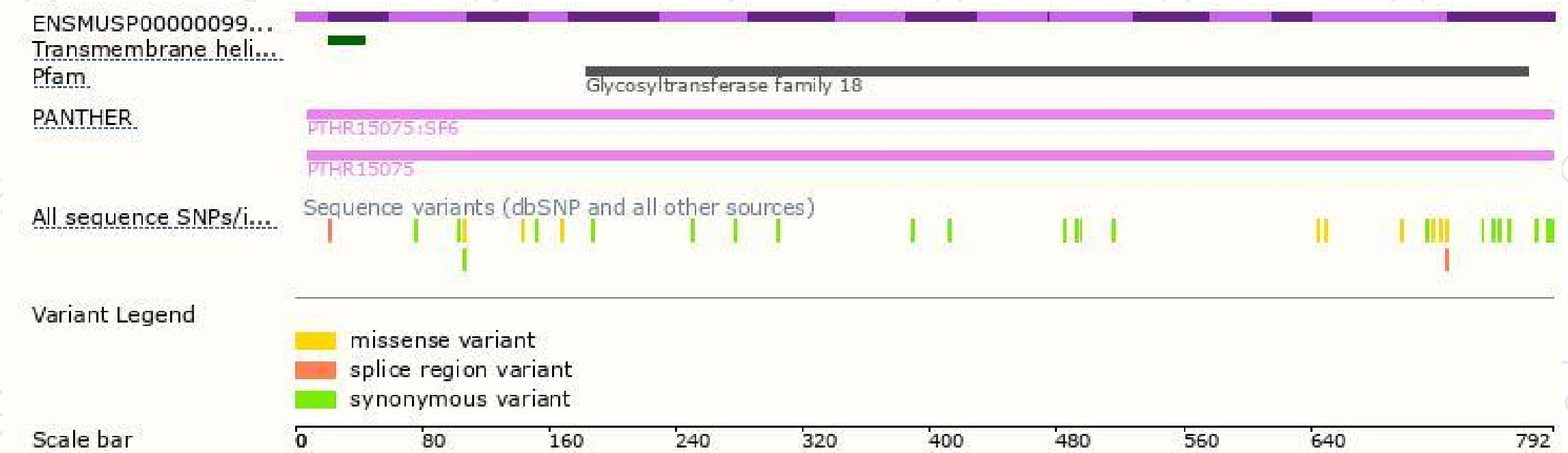


# Genomic location distribution

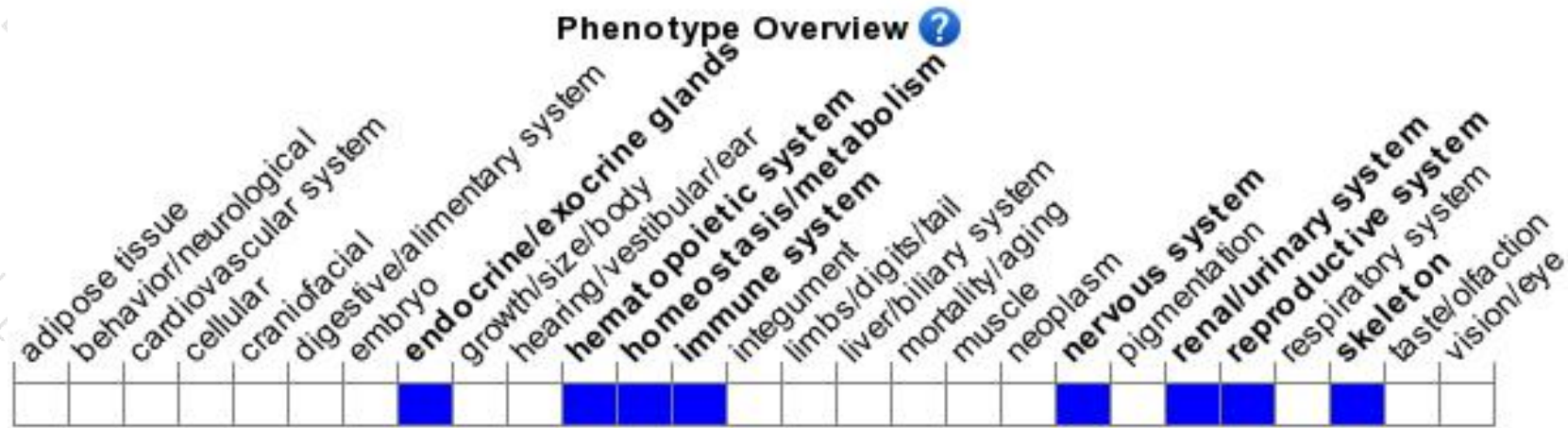




# Protein domain



# 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 low levels of O-man-linked beta1,6-branched glycans. Mice homozygous for a different knock-out allele exhibit decreased susceptibility to cuprizone induced injury.

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

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