

# ***Tgm2*** Cas9-KO Strategy

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# Project Overview

**Project Name**

***Tgm2***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tgm2* gene. The schematic diagram is as follows:



- The *Tgm2* gene has 4 transcripts. According to the structure of *Tgm2* gene, exon2-exon4 of *Tgm2-201* (ENSMUST00000103122.9) transcript is recommended as the knockout region. The region contains 542bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tgm2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, A homozygous null mutation causes alterations in glucose and aerobic energy metabolism, tumor growth, and response to myocardial infarction, liver injury, and LPS-induced sepsis. A second null mutation confers resistance to renal injury, while a third one alters cell adhesion and T cell physiology.
- The *Tgm2* gene is located on the Chr2. 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)

## Tgm2 transglutaminase 2, C polypeptide [Mus musculus (house mouse)]

Gene ID: 21817, updated on 25-Mar-2019

### Summary



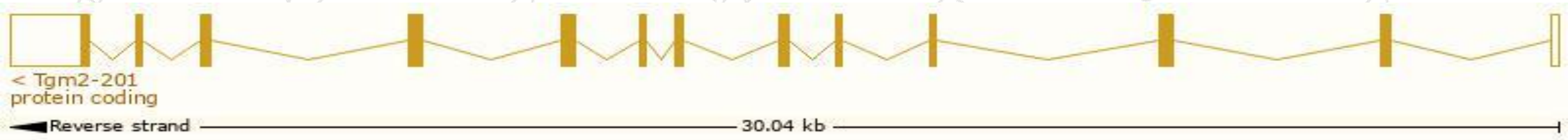
<b>Official Symbol</b>	Tgm2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	transglutaminase 2, C polypeptide provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:98731</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000037820</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	G[a]h, TG2, TGase2, tTG, tTGas
<b>Expression</b>	Broad expression in mammary gland adult (RPKM 134.3), lung adult (RPKM 130.8) and 19 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

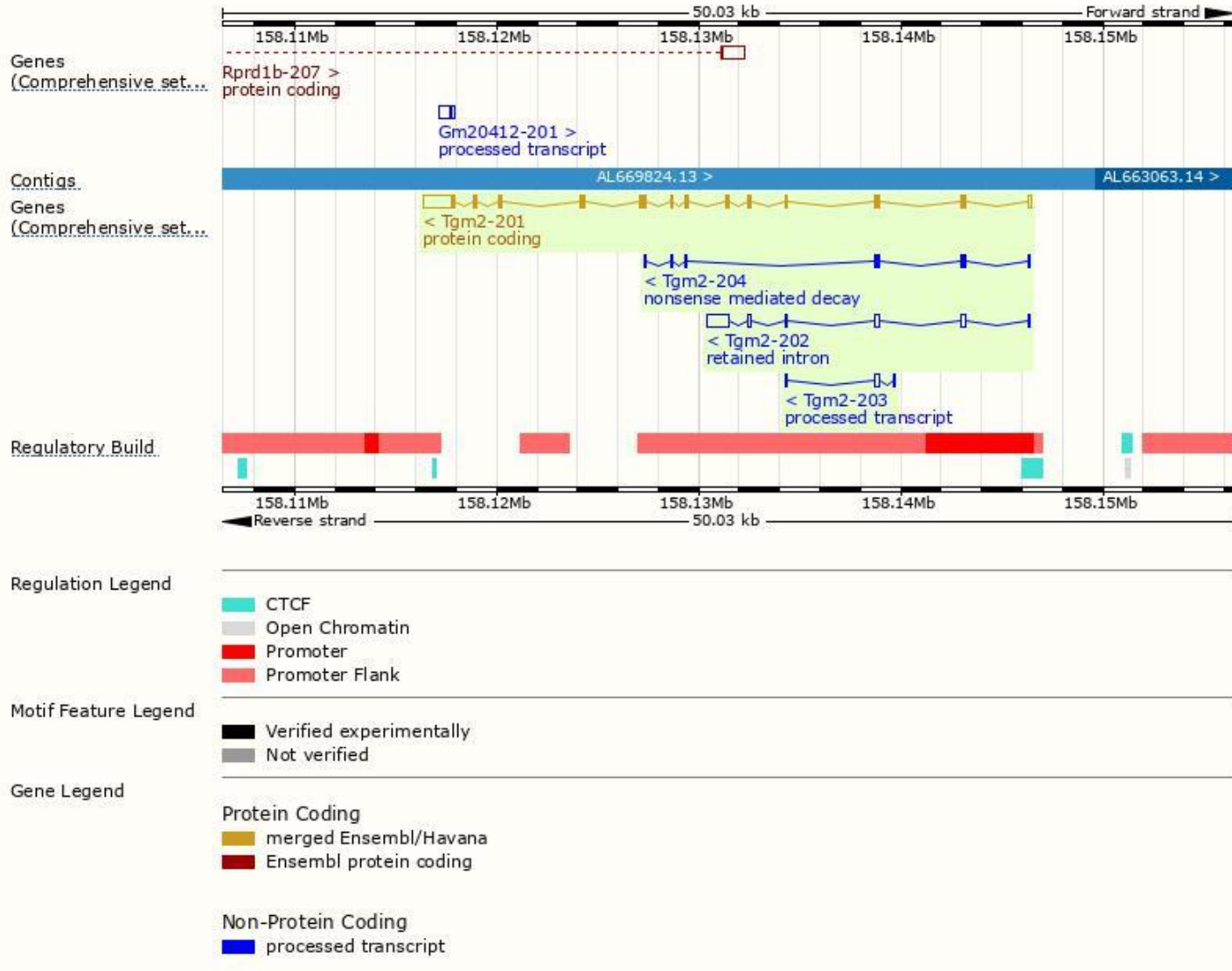
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tgm2-201	<a href="#">ENSMUST00000103122.9</a>	3596	<a href="#">686aa</a>	Protein coding	<a href="#">CCDS16985</a>	<a href="#">P21981</a>	TSL:1 GENCODE basic APPRIS P1
Tgm2-204	<a href="#">ENSMUST00000174718.1</a>	748	<a href="#">146aa</a>	Nonsense mediated decay	-	<a href="#">G3UXE8</a>	TSL:5
Tgm2-203	<a href="#">ENSMUST00000152690.1</a>	352	No protein	Processed transcript	-	-	TSL:3
Tgm2-202	<a href="#">ENSMUST00000140923.7</a>	1876	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Tgm2-201* transcript,The transcription is shown below

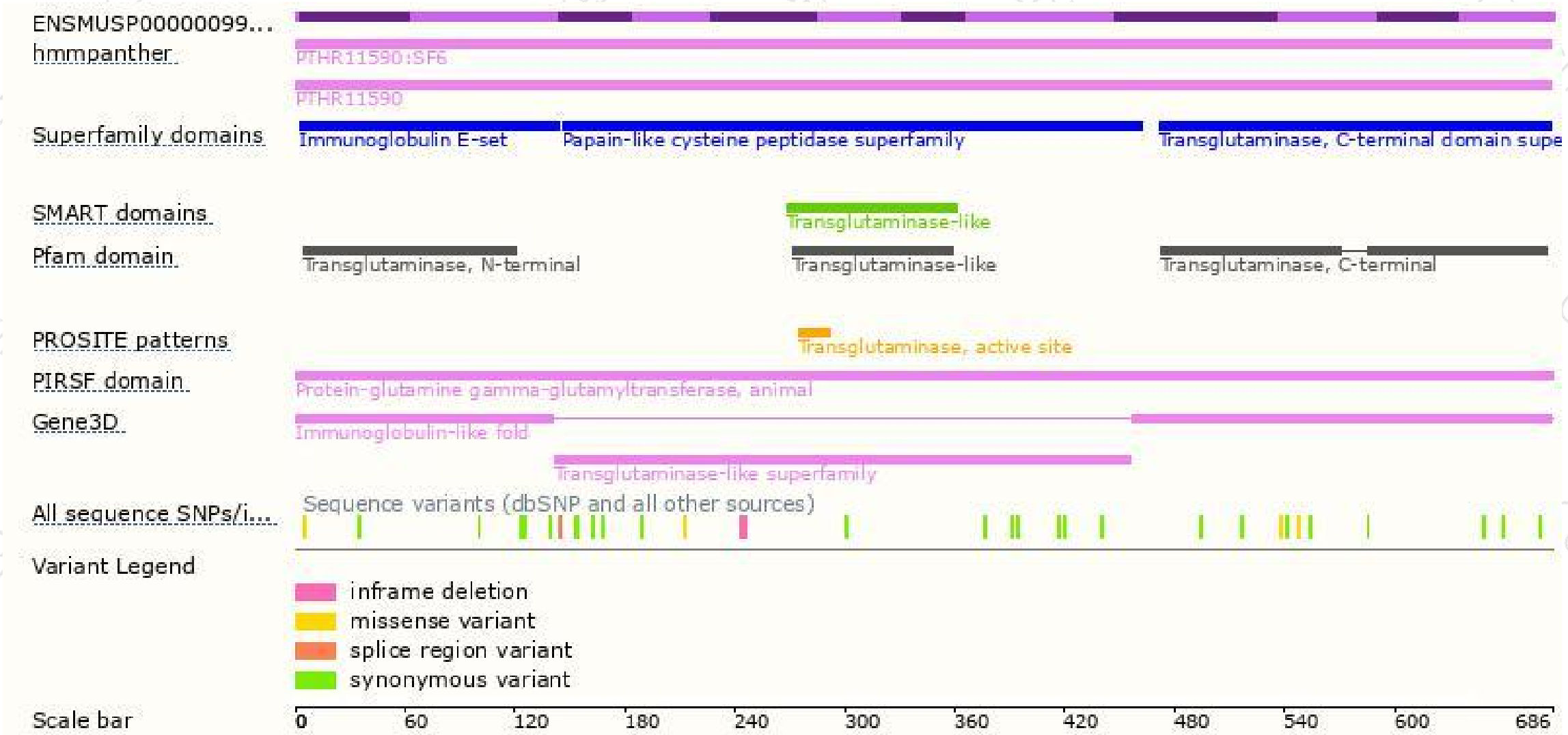


# Genomic location distribution

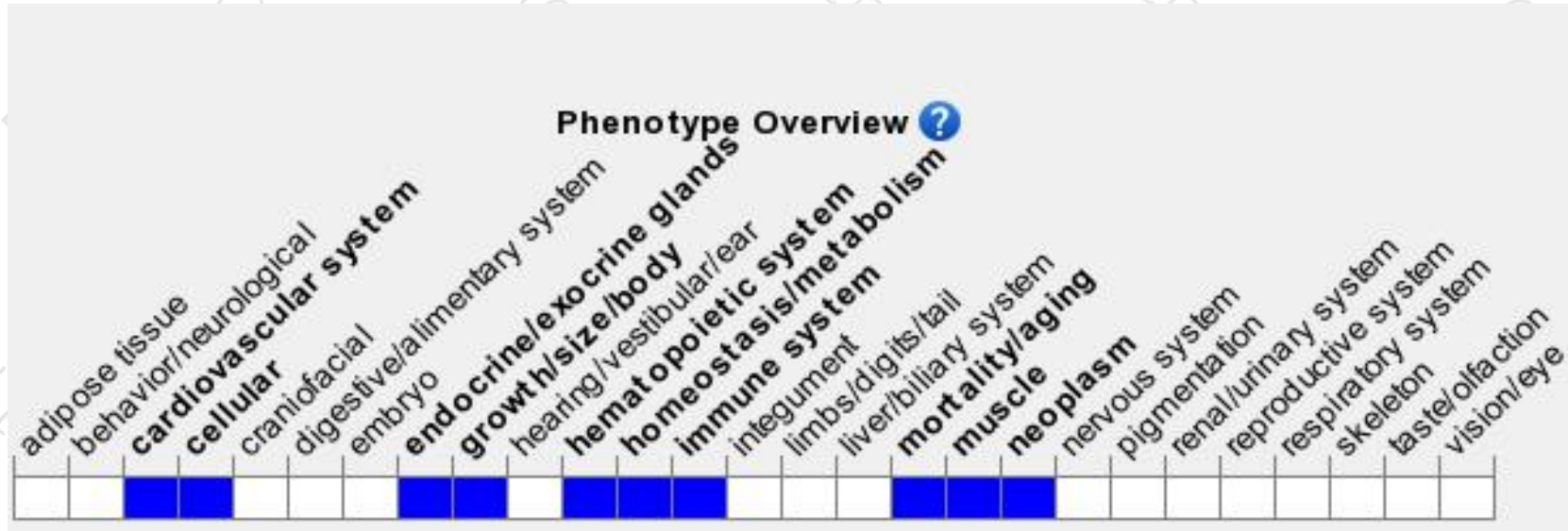




# Protein domain



# 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, A homozygous null mutation causes alterations in glucose and aerobic energy metabolism, tumor growth, and response to myocardial infarction, liver injury, and LPS-induced sepsis. A second null mutation confers resistance to renal injury, while a third one alters cell adhesion and T cell physiology.

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

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