Ggt5 Cas9-KO Strategy

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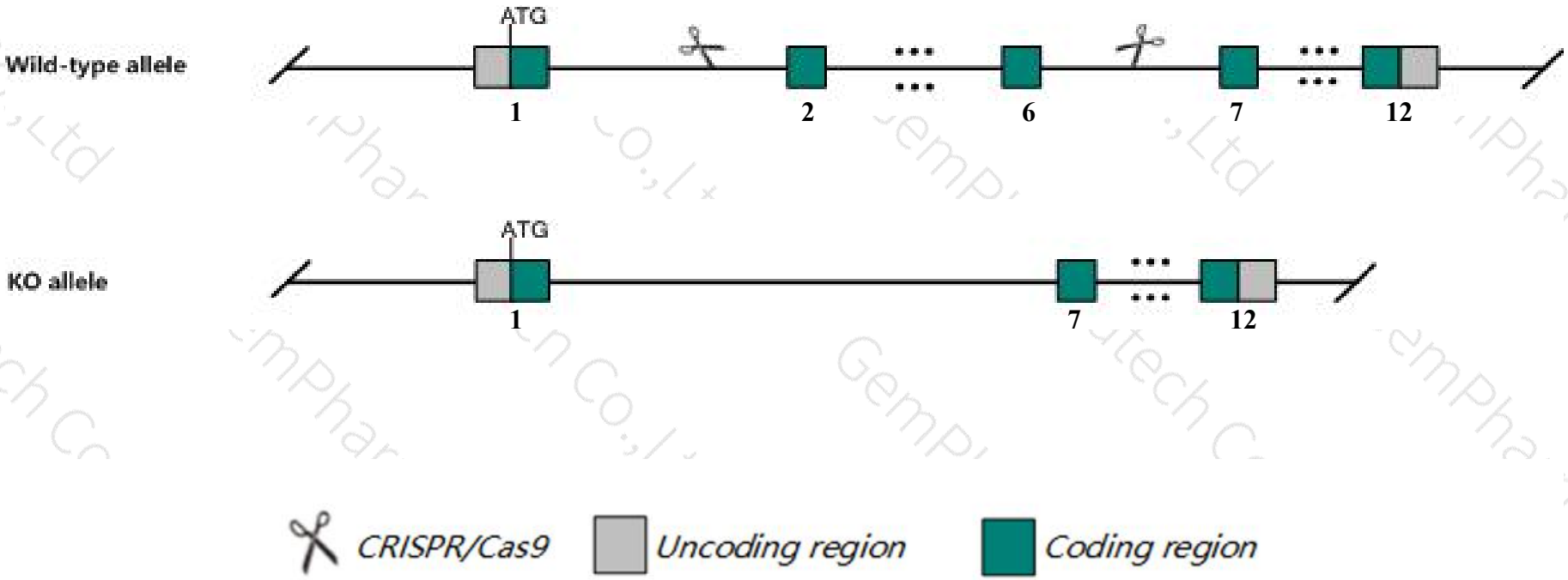
Design Date: 2019-7-29

Project Overview

Project Name	***Ggt5***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ggt5* gene. The schematic diagram is as follows:



Technical routes

➢ The *Ggt5* gene has 7 transcripts. According to the structure of *Ggt5* gene, exon2-exon6 of *Ggt5-201* (ENSMUST00000072217.8) transcript is recommended as the knockout region.The region contains 728bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ggt5* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

- According to the existing MGI data,Homozygous mutants show an attenuation in neutrophil recruitment in an experimental model of peritonitis.

- The *Ggt5* gene is located on the Chr10. 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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Ggt5 gamma-glutamyltransferase 5 [Mus musculus (house mouse)]

Gene ID: 23887, updated on 31-Jan-2019

Summary

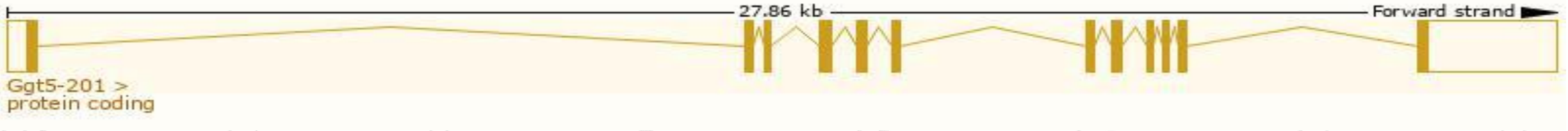
Official Symbol	Ggt5 provided by MGI
Official Full Name	gamma-glutamyltransferase 5 provided by MGI
Primary source	MGI:MGI:1346063
See related	Ensembl:ENSMUSG00000006344
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI551243, GGL, GGT-REL, Ggtla1
Expression	Broad expression in ovary adult (RPKM 21.4), mammary gland adult (RPKM 16.4) and 15 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

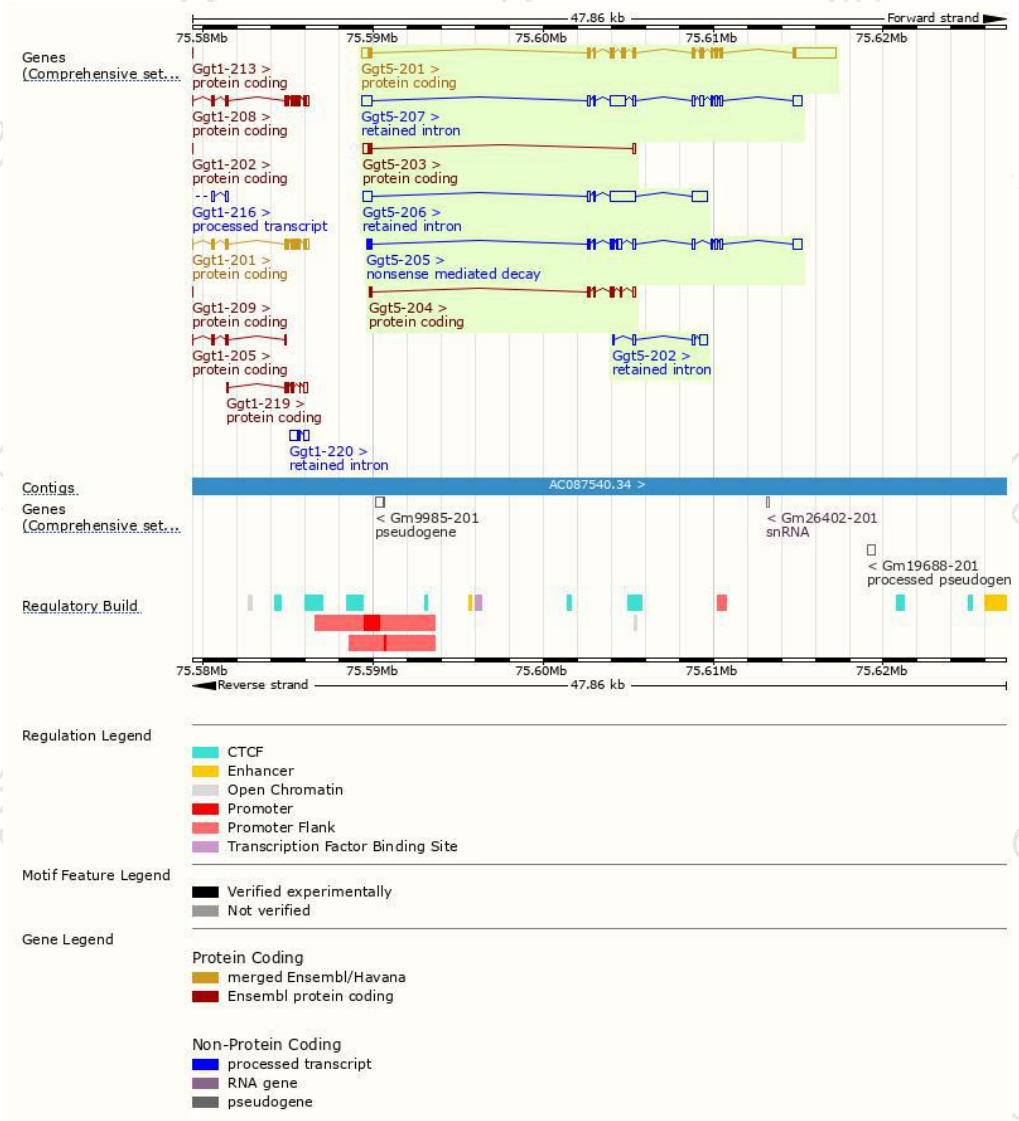
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ggt5-201	ENSMUST00000072217.8	4410	573aa	Protein coding	CCDS23928	Q9Z2A9	TSL:1 GENCODE basic APPRIS P1
Ggt5-204	ENSMUST00000189991.1	722	205aa	Protein coding	-	A0A087WSM3	CDS 5' incomplete TSL:3
Ggt5-203	ENSMUST00000189972.1	648	71aa	Protein coding	-	A0A087WNR3	TSL:3 GENCODE basic
Ggt5-205	ENSMUST00000218807.1	2051	230aa	Nonsense mediated decay	-	Q80WV0	TSL:1
Ggt5-206	ENSMUST00000219214.1	3071	No protein	Retained intron	-	-	TSL:1
Ggt5-207	ENSMUST00000219247.1	2875	No protein	Retained intron	-	-	TSL:1
Ggt5-202	ENSMUST00000188444.1	825	No protein	Retained intron	-	-	TSL:3

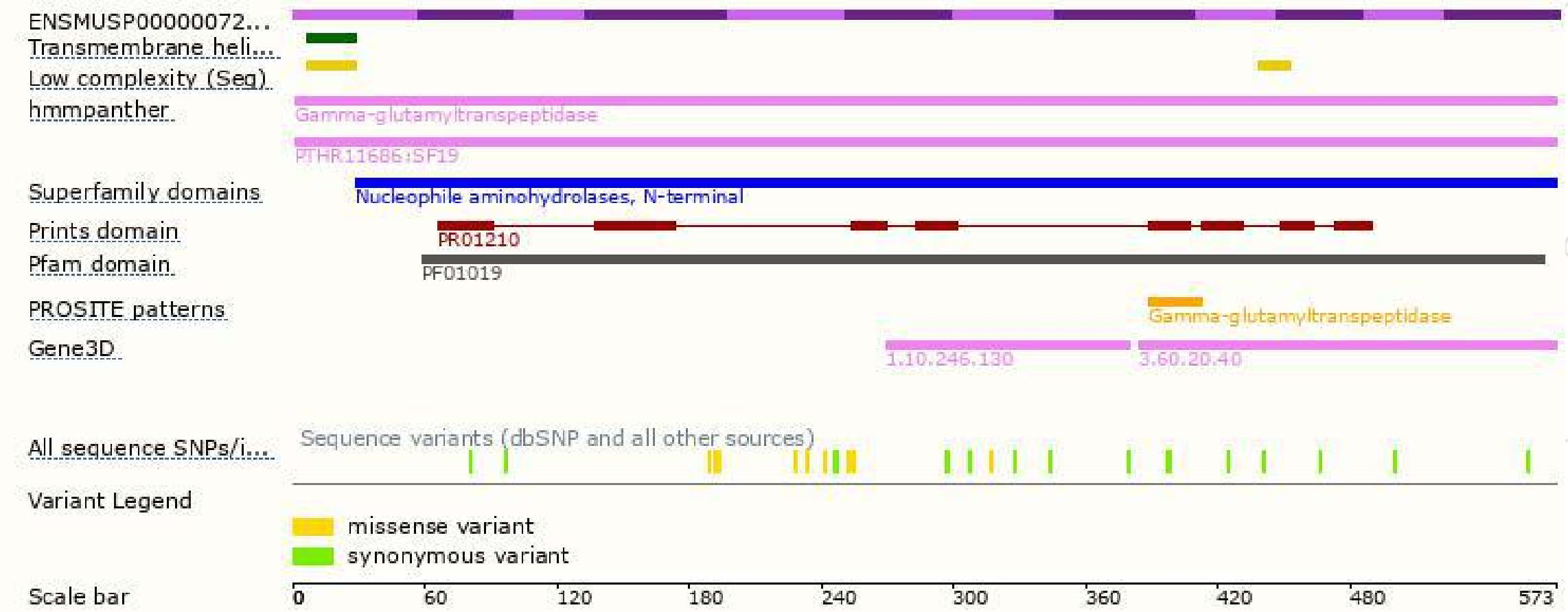
The strategy is based on the design of *Ggt5-201* transcript,The transcription is shown below



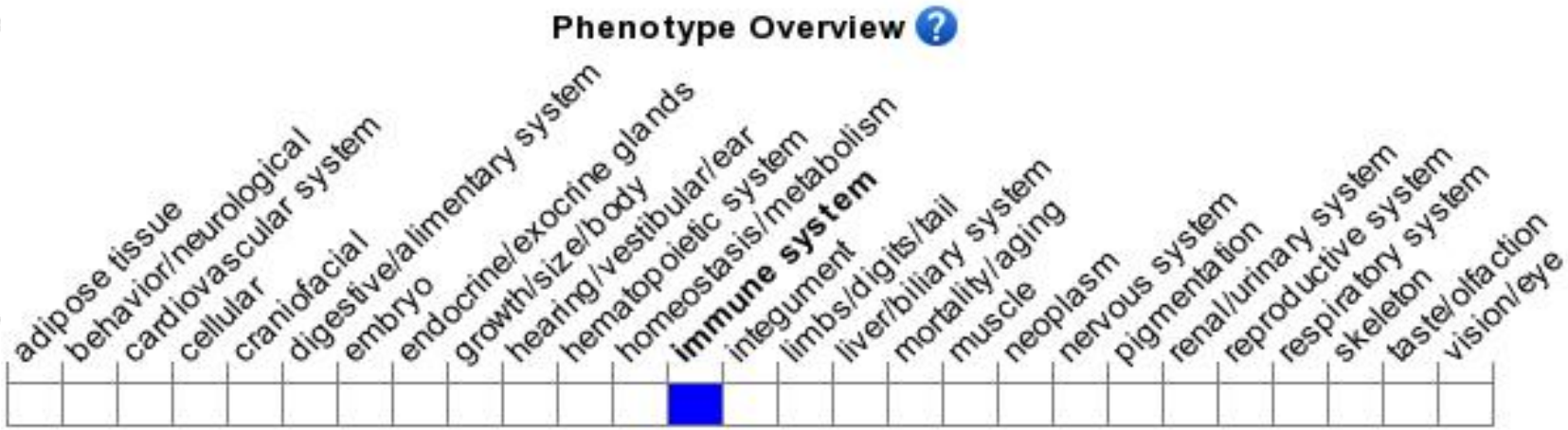
Genomic location distribution



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,Homozygous mutants show an attenuation in neutrophil recruitment in an experimental model of peritonitis.

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

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