Gpa33 Cas9-KO Strategy

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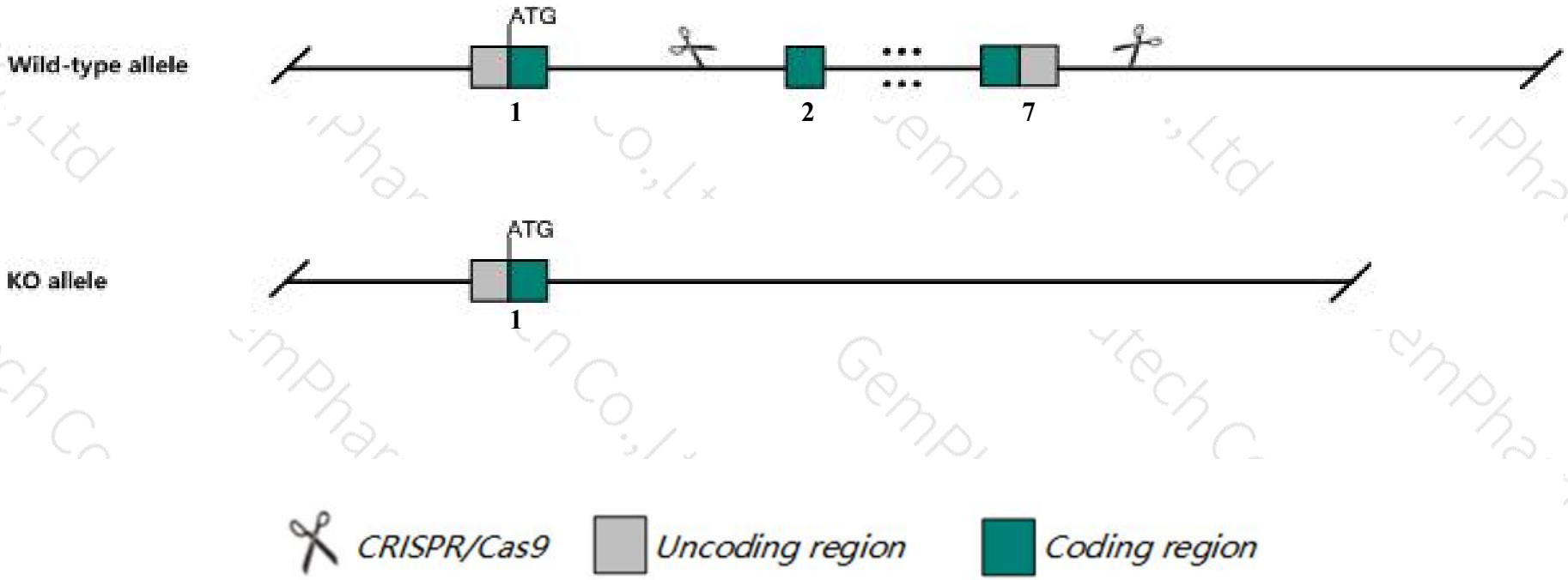
Project Overview

Project Name	***Gpa33***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gpa33* gene. The schematic diagram is as follows:



Technical routes

➢ The *Gpa33* gene has 4 transcripts. According to the structure of *Gpa33* gene, exon2-exon7 of *Gpa33-202* (ENSMUST00000060833.13) transcript is recommended as the knockout region.The region contains 917bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Gpa33* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a knock-out allele exhibit increased susceptibility to induced colitis and impaired oral tolerance to ovalbumin.

- The *Gpa33* gene is located on the Chr1. 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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Gpa33 glycoprotein A33 (transmembrane) [Mus musculus (house mouse)]

Gene ID: 59290, updated on 31-Jan-2019

Summary

Official Symbol	Gpa33 provided by MGI
Official Full Name	glycoprotein A33 (transmembrane) provided by MGI
Primary source	MGI:MGI:1891703
See related	Ensembl:ENSMUSG00000000544
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	2010310L10Rik, 2210401D16Rik, BB116197, mA33
Expression	Biased expression in colon adult (RPKM 349.7), large intestine adult (RPKM 252.6) and 3 other tissues See more
Orthologs	human all

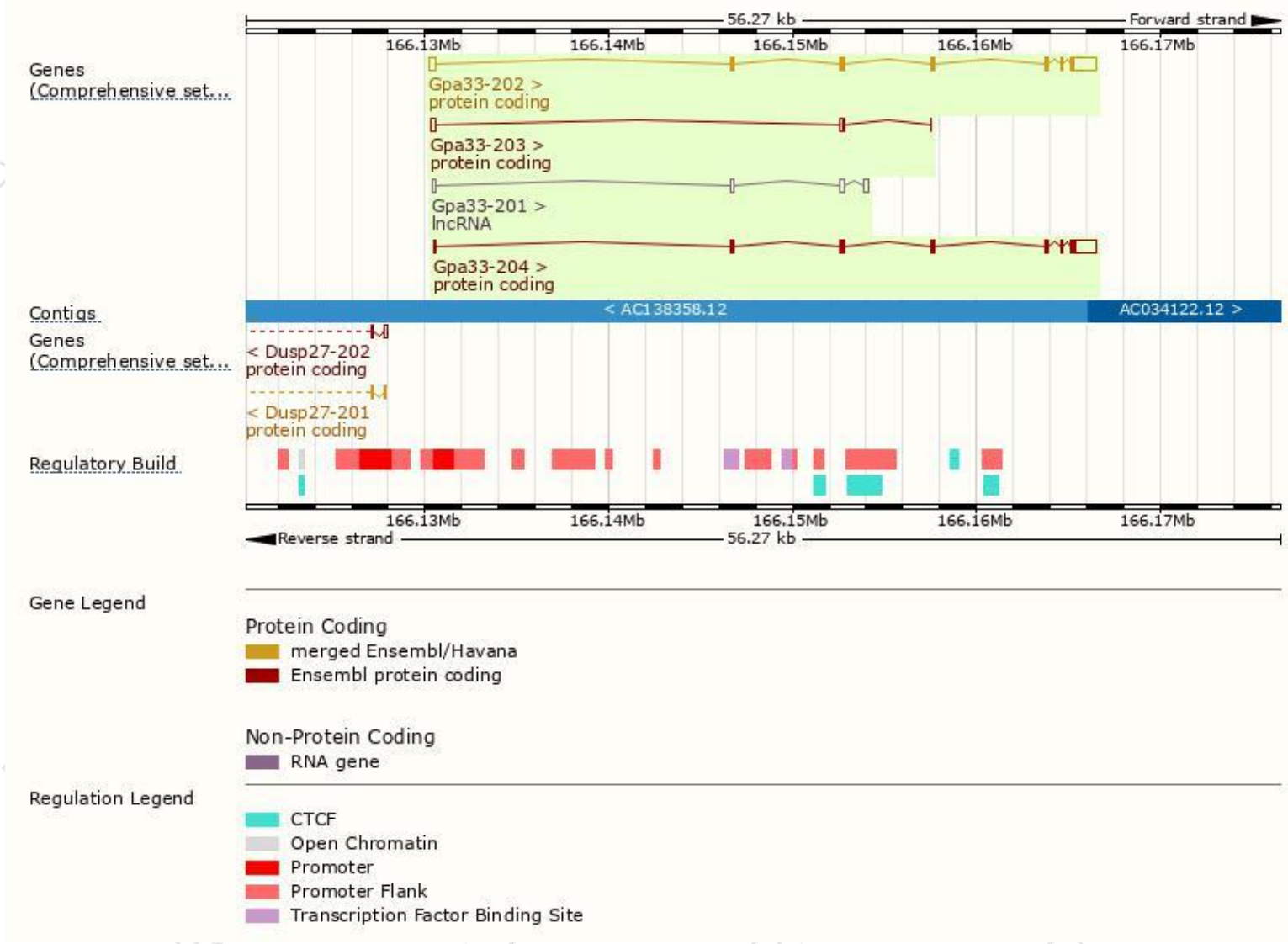
Transcript information（Ensembl）

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

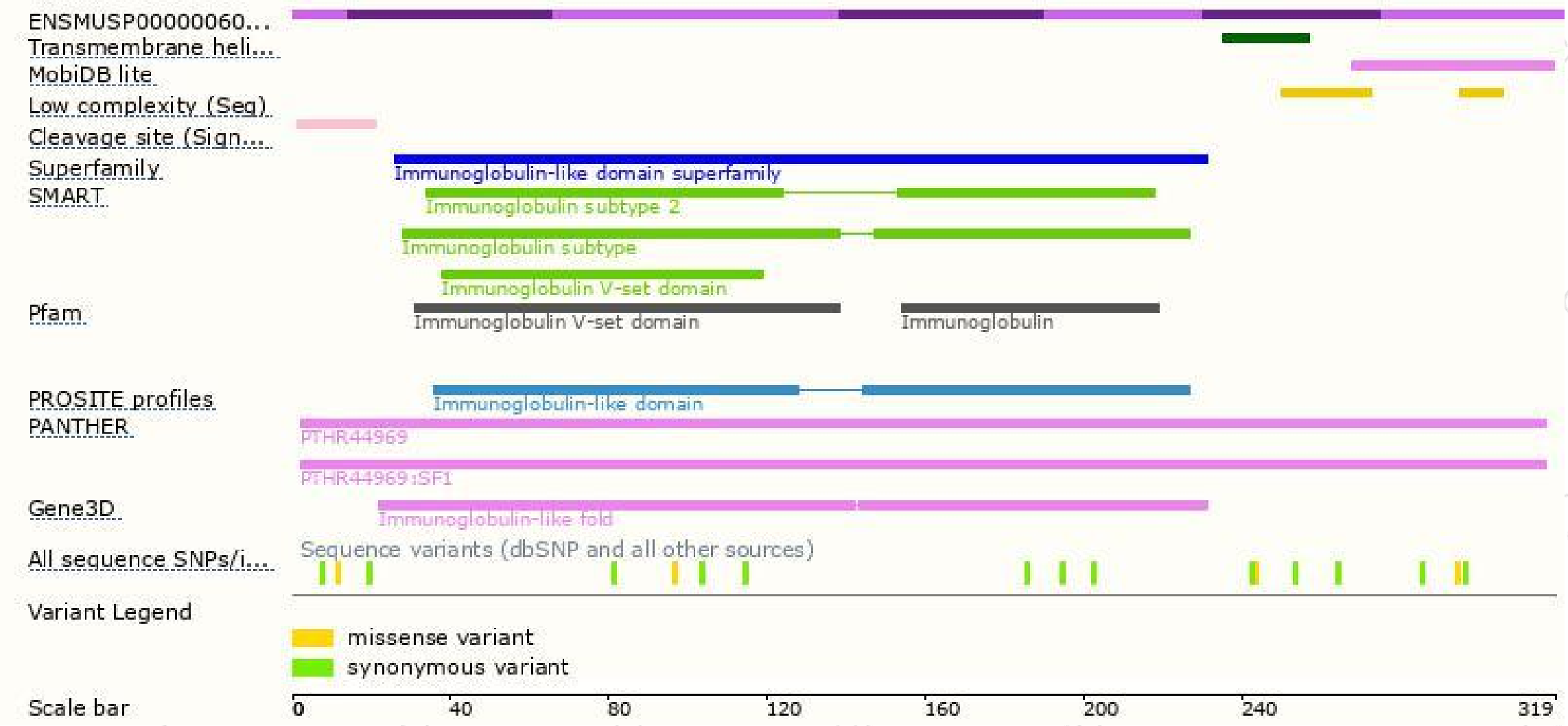
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gpa33-202	ENSMUST00000060833.13	2515	319aa	Protein coding	CCDS15447	A0A0R4J209	TSL:1 GENCODE basic APPRIS P1
Gpa33-204	ENSMUST00000166860.1	2227	319aa	Protein coding	CCDS15447	A0A0R4J209	TSL:1 GENCODE basic APPRIS P1
Gpa33-203	ENSMUST00000166159.1	499	36aa	Protein coding	-	E9PY15	CDS 3' incomplete TSL:5
Gpa33-201	ENSMUST00000027847.6	787	No protein	lncRNA	-	-	TSL:1

The strategy is based on the design of *Gpa33-202* transcript,The transcription is shown below

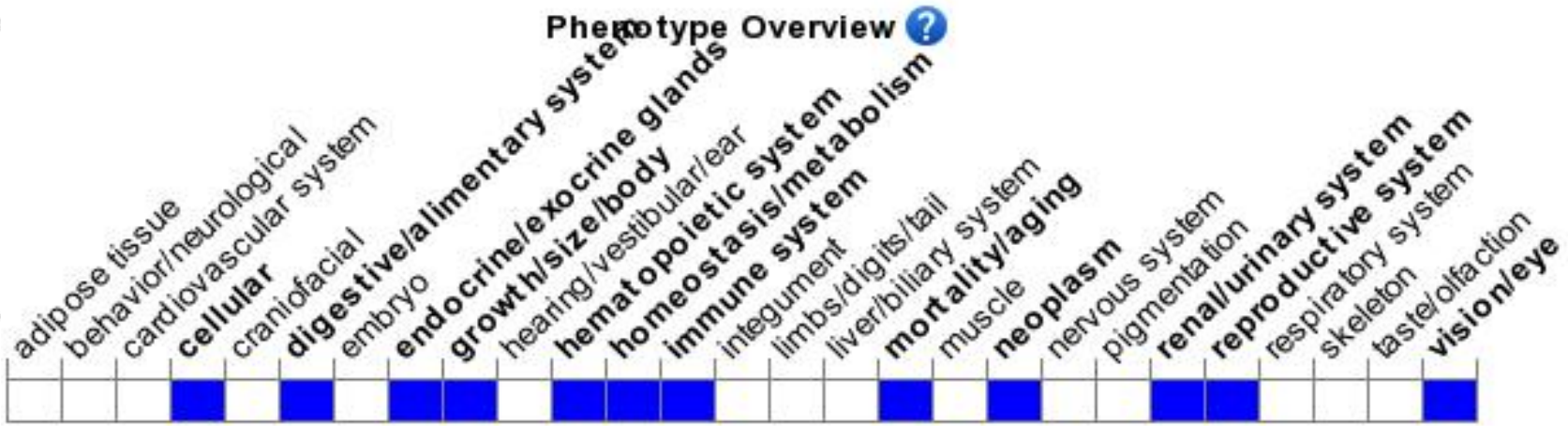
Genomic location distribution



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/).

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

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