集萃药康
GemPharmatech

Hepacam2 Cas9-KO Strategy

Designer: Zihe Cui

Reviewer: Ruirui Zhang

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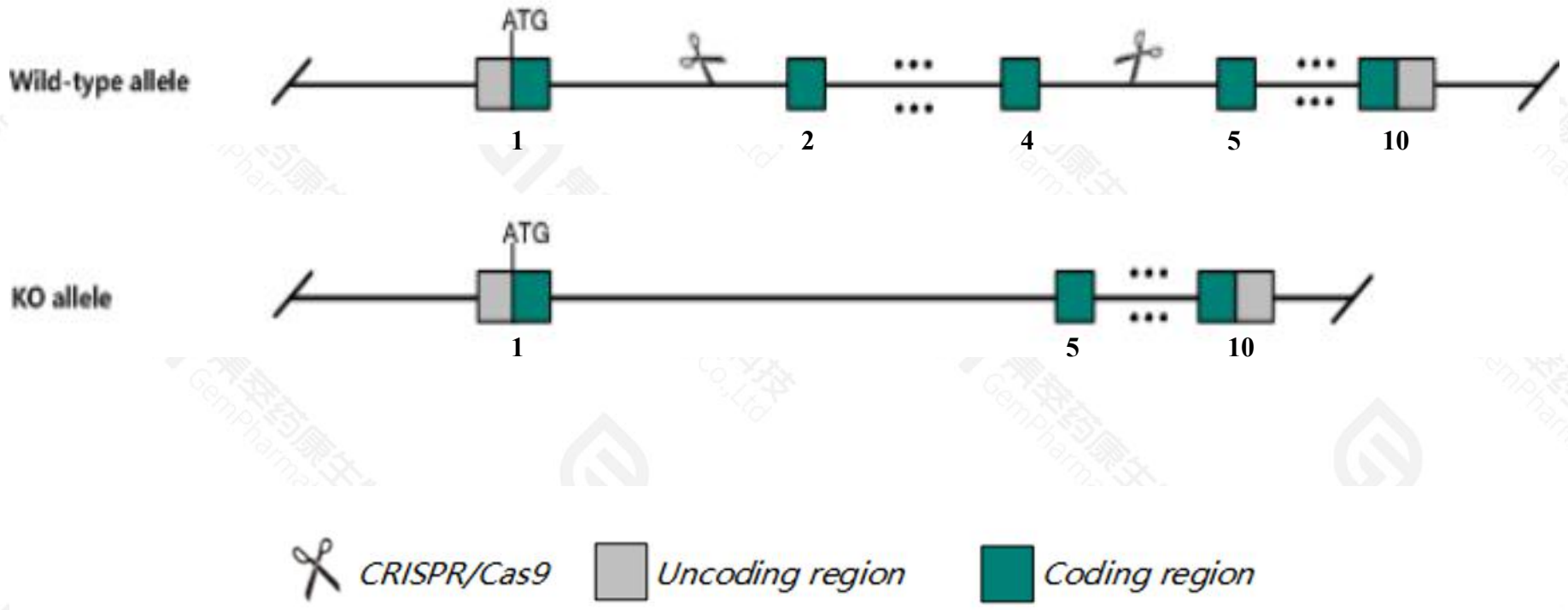
Project Overview

Project Name	***Hepacam2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hepacam2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Hepacam2* gene has 5 transcripts. According to the structure of *Hepacam2* gene, exon2-exon4 of *Hepacam2-201*(ENSMUST00000049985.14) transcript is recommended as the knockout region.The region contains most 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 *Hepacam2* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt 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/6JGpt mice.

Notice

➢ The KO region deletes most of the coding sequence, but does not result in frameshift.

➢ The *Hepacam2* gene is located on the Chr6. 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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Hepacam2 HEPACAM family member 2 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 101202, updated on 17-Feb-2021

Summary

Official Symbol	Hepacam2 provided by MGI
Official Full Name	HEPACAM family member 2 provided by MGI
Primary source	MGI:MGI:2141520
See related	Ensembl:ENSMUSG00000044156
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI987662
Expression	Biased expression in colon adult (RPKM 18.5), large intestine adult (RPKM 13.0) and 5 other tissues See more
Orthologs	human all

NEW **Try the new Gene table**

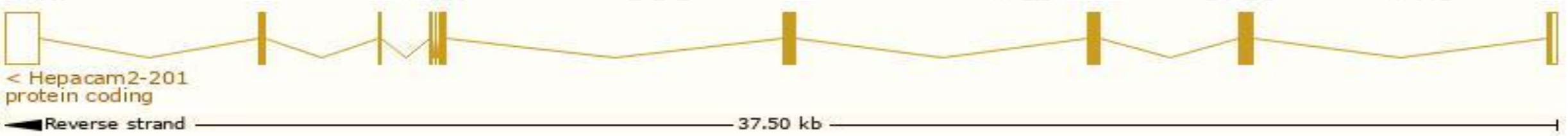
Try the new Transcript table

Transcript information Ensembl

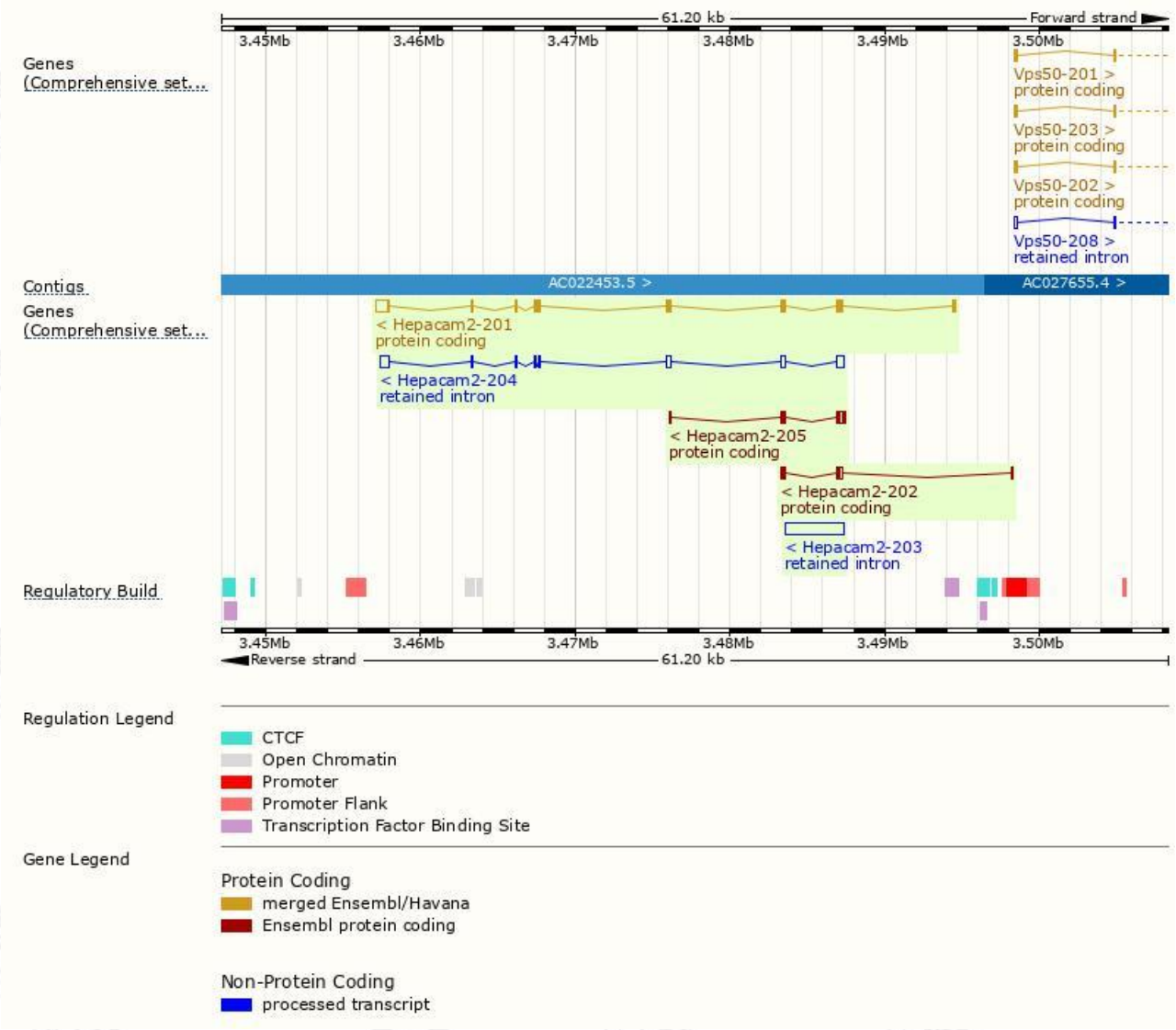
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hepacam2-201	ENSMUST00000049985.14	2328	463aa	Protein coding	CCDS39414	Q4VAH7	TSL:1 GENCODE basic APPRIS P1
Hepacam2-205	ENSMUST00000201607.3	796	206aa	Protein coding	-	A0A0J9YTS9	CDS 3' incomplete TSL:5
Hepacam2-202	ENSMUST00000200854.1	690	153aa	Protein coding	-	V9GX19	CDS 3' incomplete TSL:3
Hepacam2-203	ENSMUST00000200972.1	3786	No protein	Retained intron	-	-	TSL:NA
Hepacam2-204	ENSMUST00000201276.1	1945	No protein	Retained intron	-	-	TSL:5

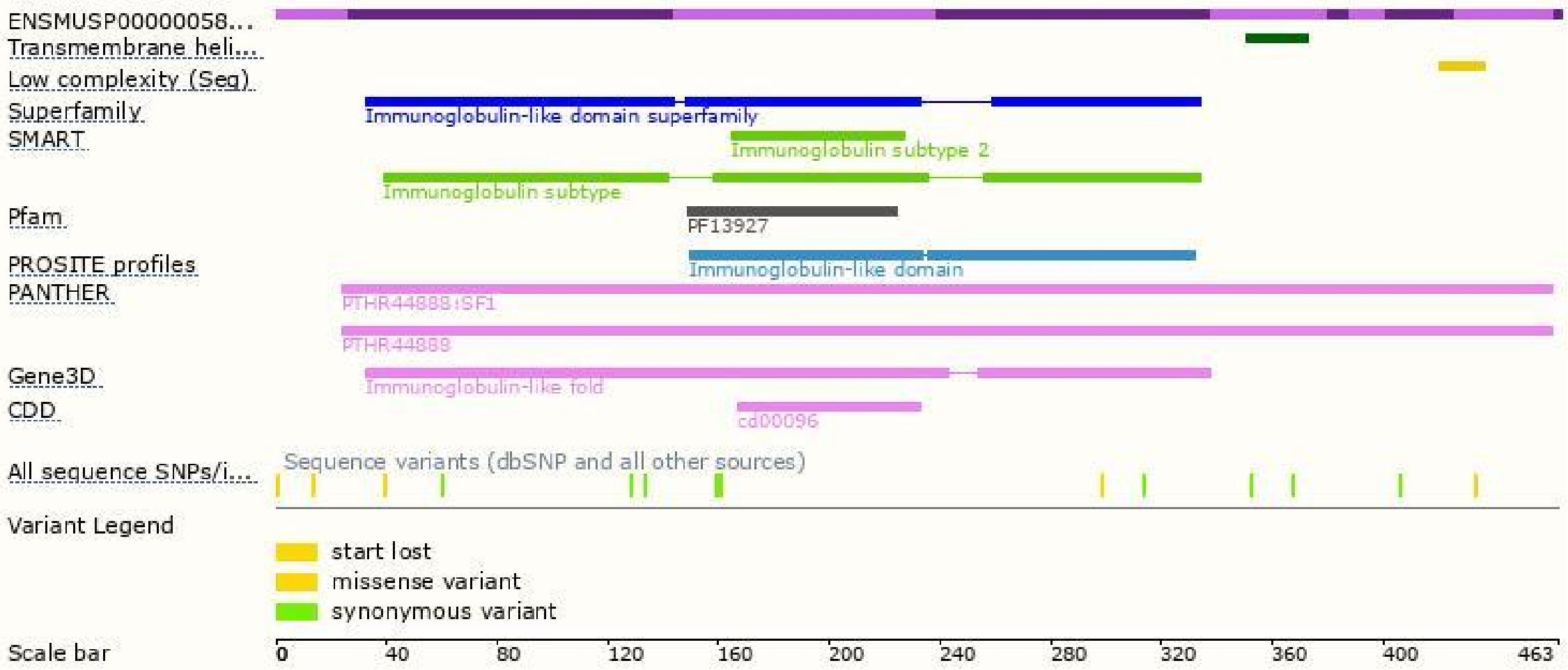
The strategy is based on the design of *Hepacam2-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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If you have any questions, you are welcome to inquire.
Tel: 400-9660890

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GemPharmatech Co.,Ltd