Gpr132 Cas9-KO *Strategy*

Designer: **Huan Fan**

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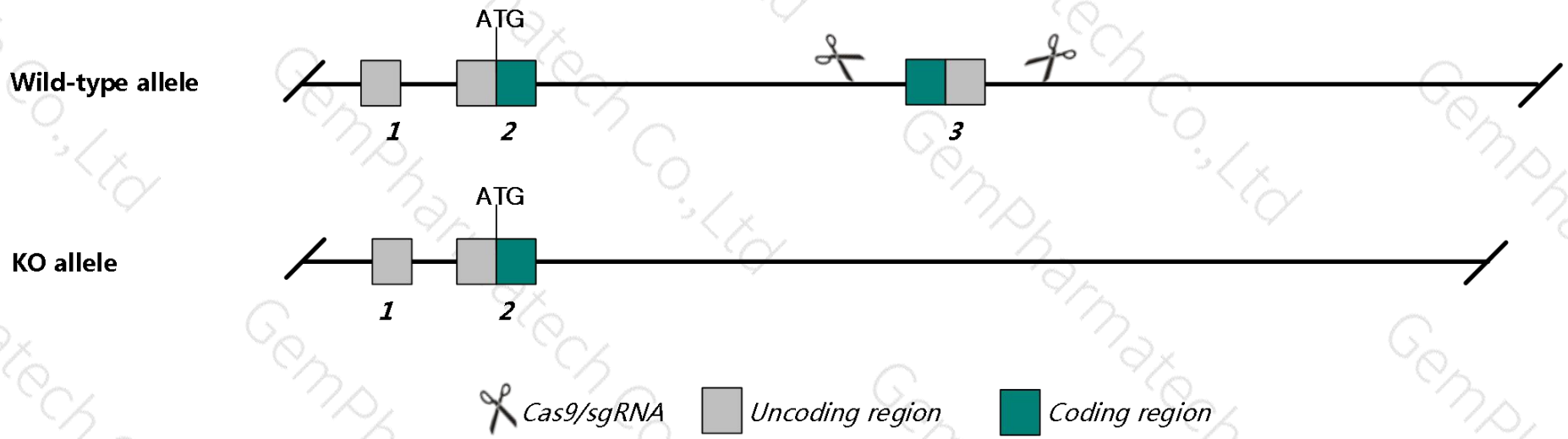
Project Overview

Project Name	***Gpr132***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gpr132* gene. The schematic diagram is as follows:



Technical routes

- The *Gpr132* gene has 2 transcripts.According to the structure of *Gpr132* gene, exon3 of *Gpr132*-201 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 *Gpr132* gene. The brief process is as follows: gRNA was transcribed in vitro.Cas9 and gRNA 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

- According to the existing MGI data，Mice homozygous for disruptions in this gene display a generally normal phenotype but eventually develop a “late onset lymphoproliferative autoimmune syndrome”.
- The *Gpr132* gene is located on the Chr12. 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）

集萃药康 GemPharmatech

Gpr132 G protein-coupled receptor 132 [*Mus musculus* (house mouse)]

Gene ID: 56696, updated on 12-Aug-2019

Summary

Official Symbol	Gpr132 provided by MGI
Official Full Name	G protein-coupled receptor 132 provided by MGI
Primary source	MGI:MGI:1890220
See related	Ensembl:ENSMUSG00000021298
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	G2a
Expression	Biased expression in thymus adult (RPKM 78.1), spleen adult (RPKM 34.3) and 2 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 2 transcripts, and all transcripts are shown below:

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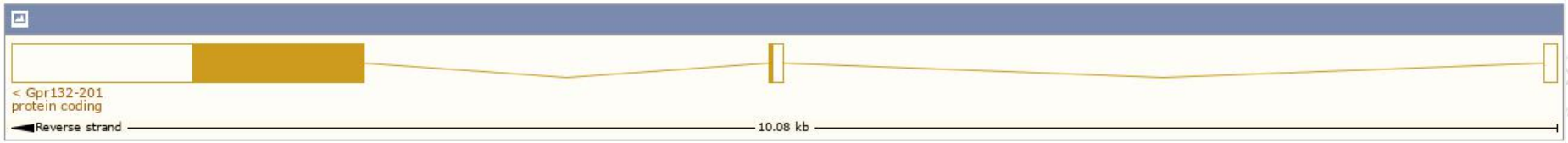
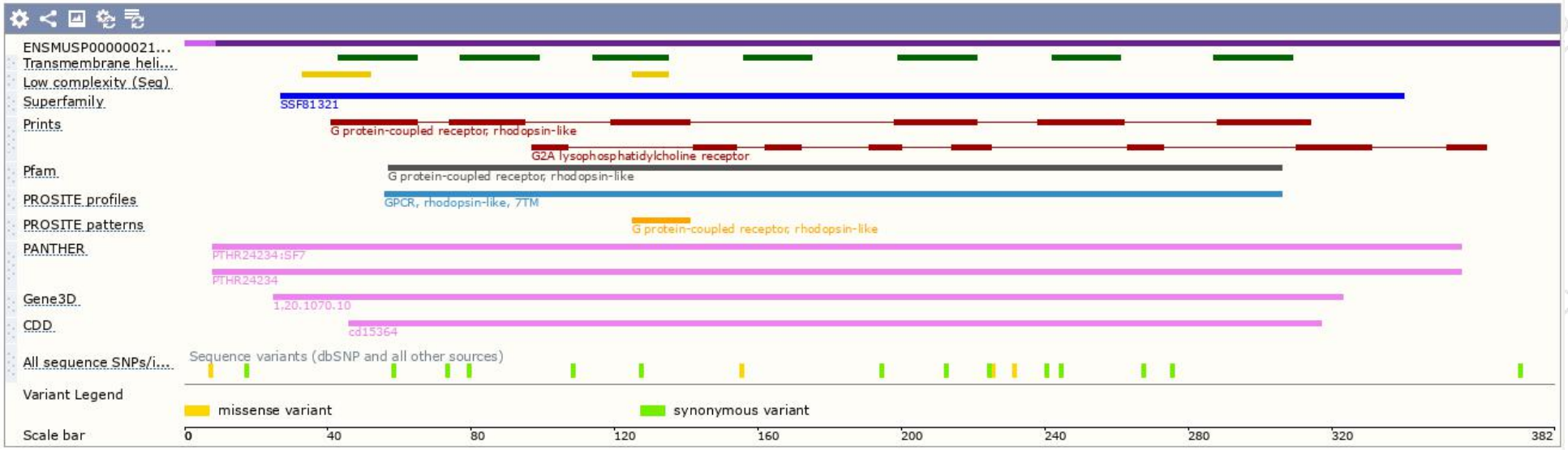
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gpr132-201	ENSMUST00000021729.8	2478	382aa	Protein coding	CCDS26199	Q9Z282	TSL:1 GENCODE basic APPRIS P1
Gpr132-202	ENSMUST00000222776.1	358	19aa	Protein coding	-	A0A1Y7VNN0	CDS 3' incomplete TSL:5

The strategy is based on the design of *Gpr132*-201 transcript,The transcription is shown below

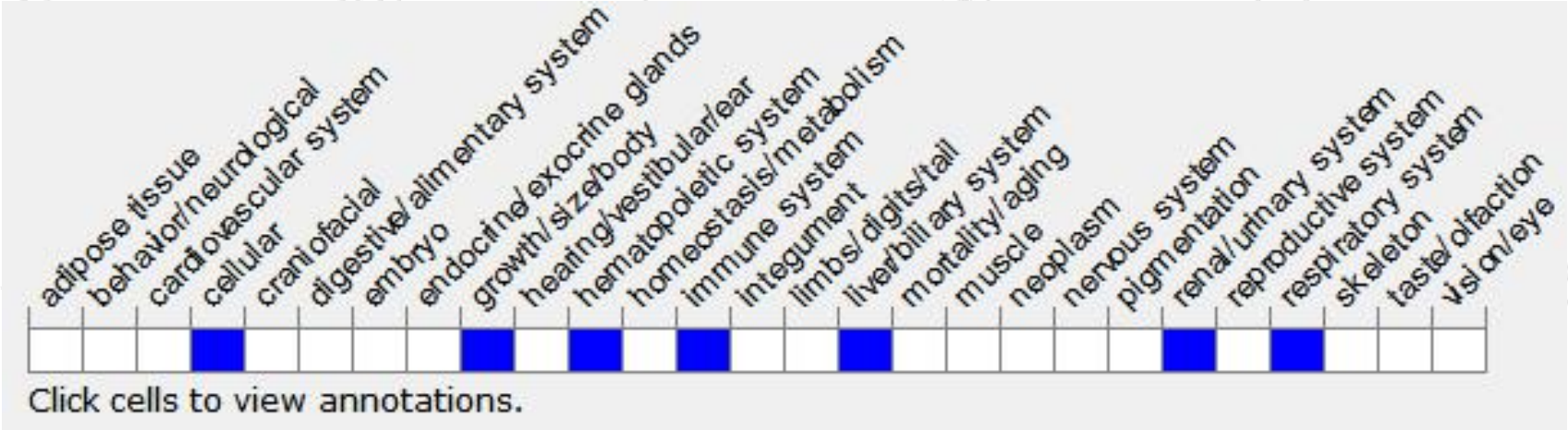


Genomic location distribution

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,Mutations in this locus affect cell-cycle regulation and apoptos is. Null homozygotes show high, early-onset tumor incidence; some have persistent hyaloid vasculature and cataracts. Truncated or temperature-sensitive alleles cause early aging phenotypes.

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

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