

Gpr34 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Gpr34

Project type

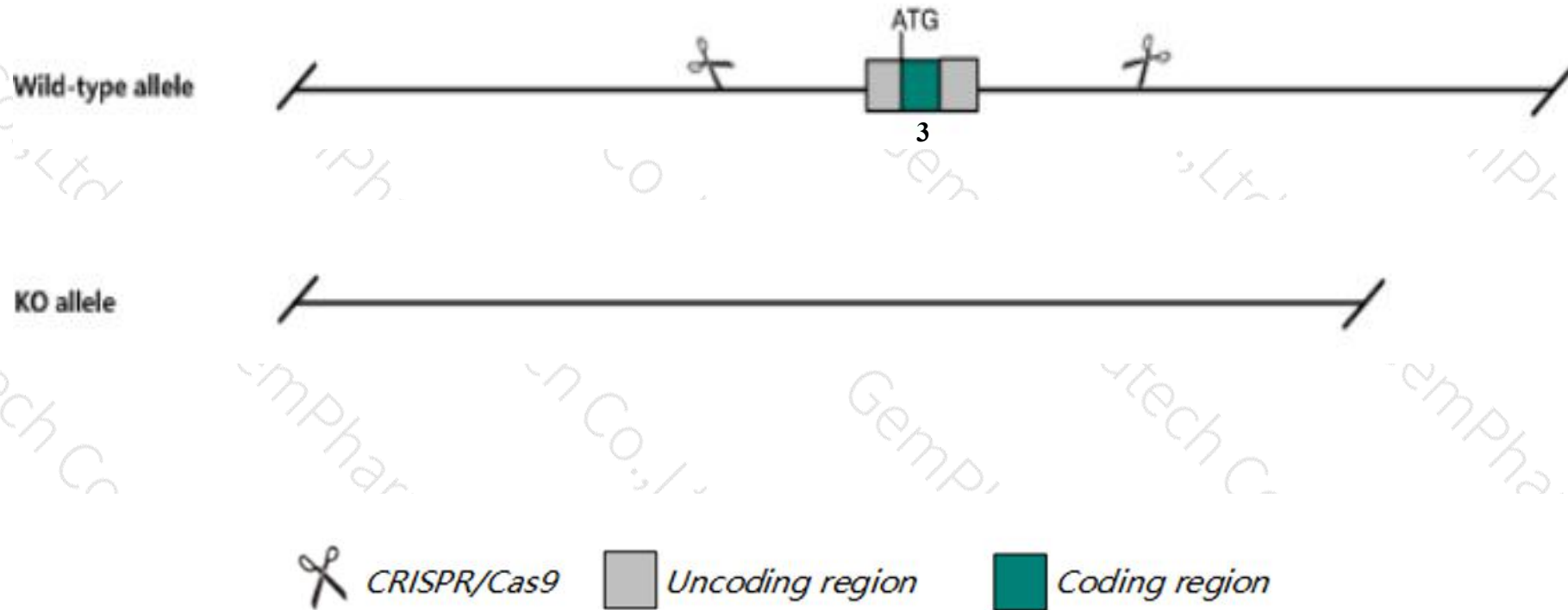
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gpr34* gene. The schematic diagram is as follows:



- The *Gpr34* gene has 2 transcripts. According to the structure of *Gpr34* gene, exon3 of *Gpr34-202* (ENSMUST00000096492.3) transcript is recommended as the knockout region. The region contains all 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 *Gpr34* 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit increased monocyte migration and susceptibility to type iv hypersensitivity and fungal infection.
- The KO region contains functional region of the *Cask* gene. Knockout the region may affect the function of *Cask* gene .
- The *Gpr34* gene is located on the ChrX. 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)

Gpr34 G protein-coupled receptor 34 [Mus musculus (house mouse)]

Gene ID: 23890, updated on 13-Mar-2020

Summary



Official Symbol	Gpr34 provided by MGI
Official Full Name	G protein-coupled receptor 34 provided by MGI
Primary source	MGI:MGI:1346334
See related	Ensembl:ENSMUSG00000040229
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	Lypsr1
Expression	Biased expression in frontal lobe adult (RPKM 2.0), cortex adult (RPKM 2.0) and 14 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

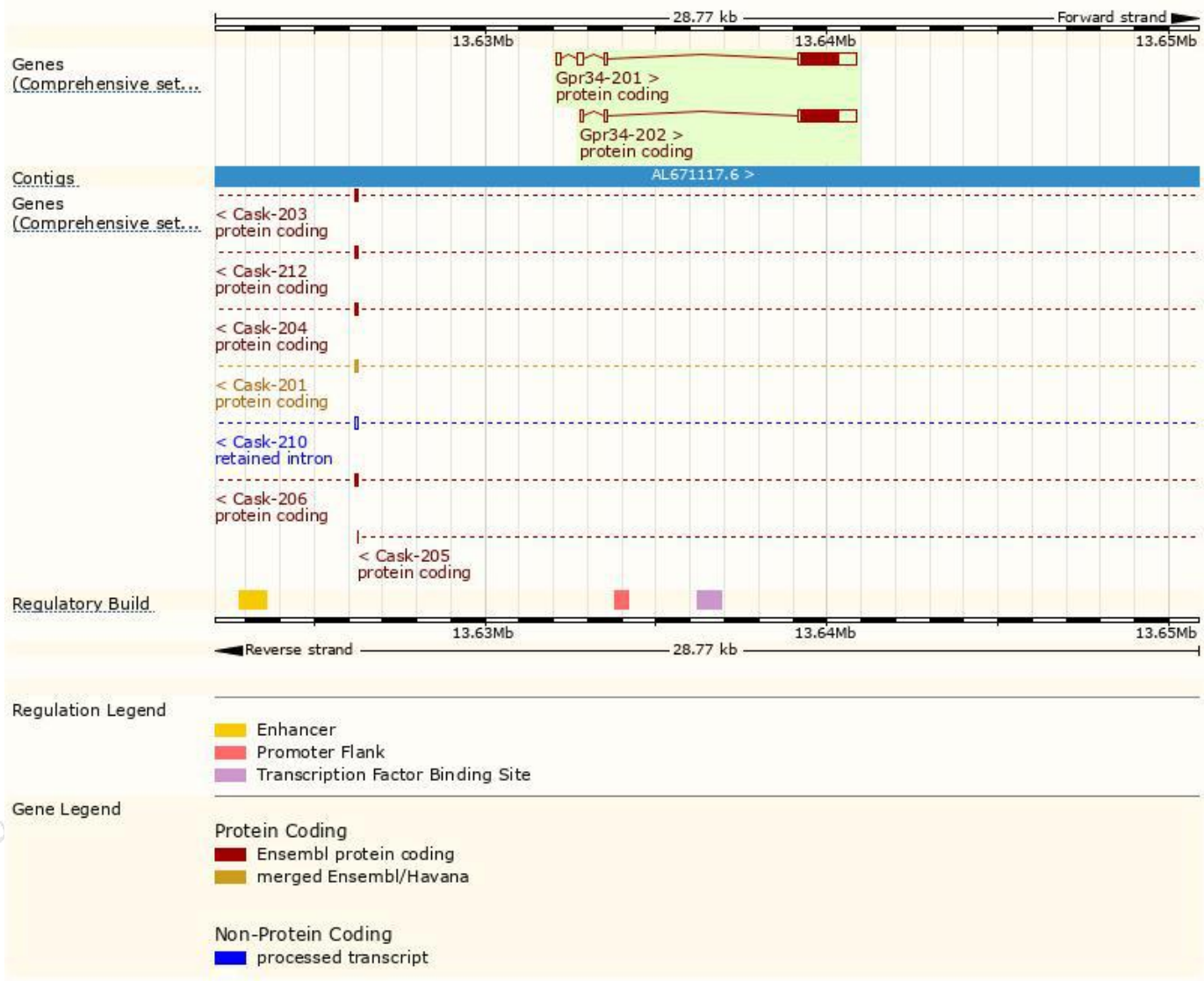
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gpr34-201	ENSMUST00000041708.9	2088	375aa	Protein coding	CCDS30028	Q3YL73 Q9R1K6	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Gpr34-202	ENSMUST00000096492.3	1898	375aa	Protein coding	CCDS30028	Q3YL73 Q9R1K6	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

The strategy is based on the design of *Gpr34-202* transcript,the transcription is shown below



Genomic location distribution

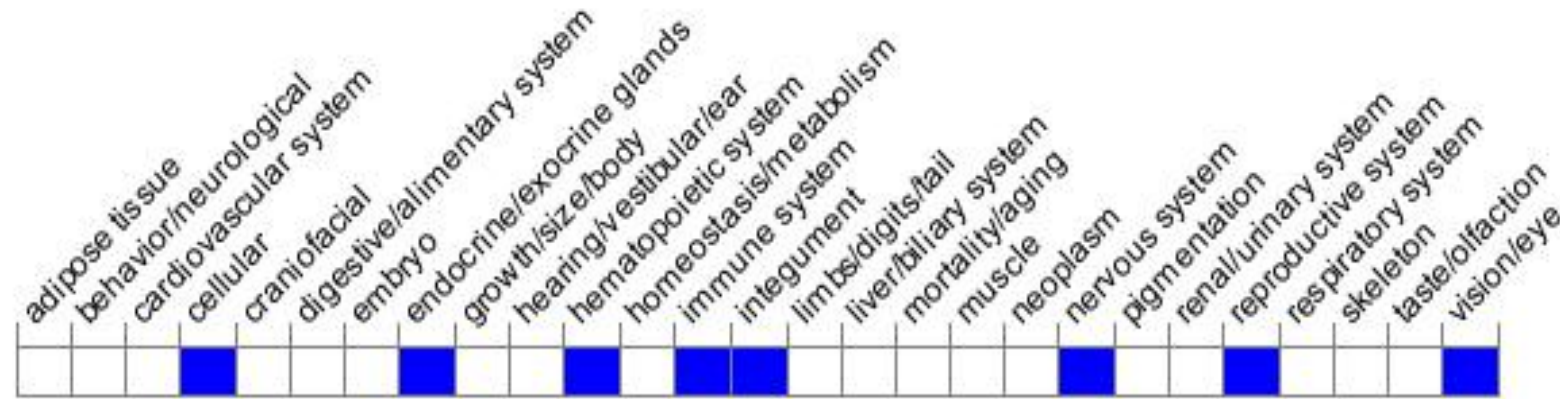


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



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, mice homozygous for a knock-out allele exhibit increased monocyte migration and susceptibility to type IV hypersensitivity and fungal infection.

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

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