

Gpr174 Cas9-KO Strategy

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Project Overview



Project Name

Gpr174

Project type

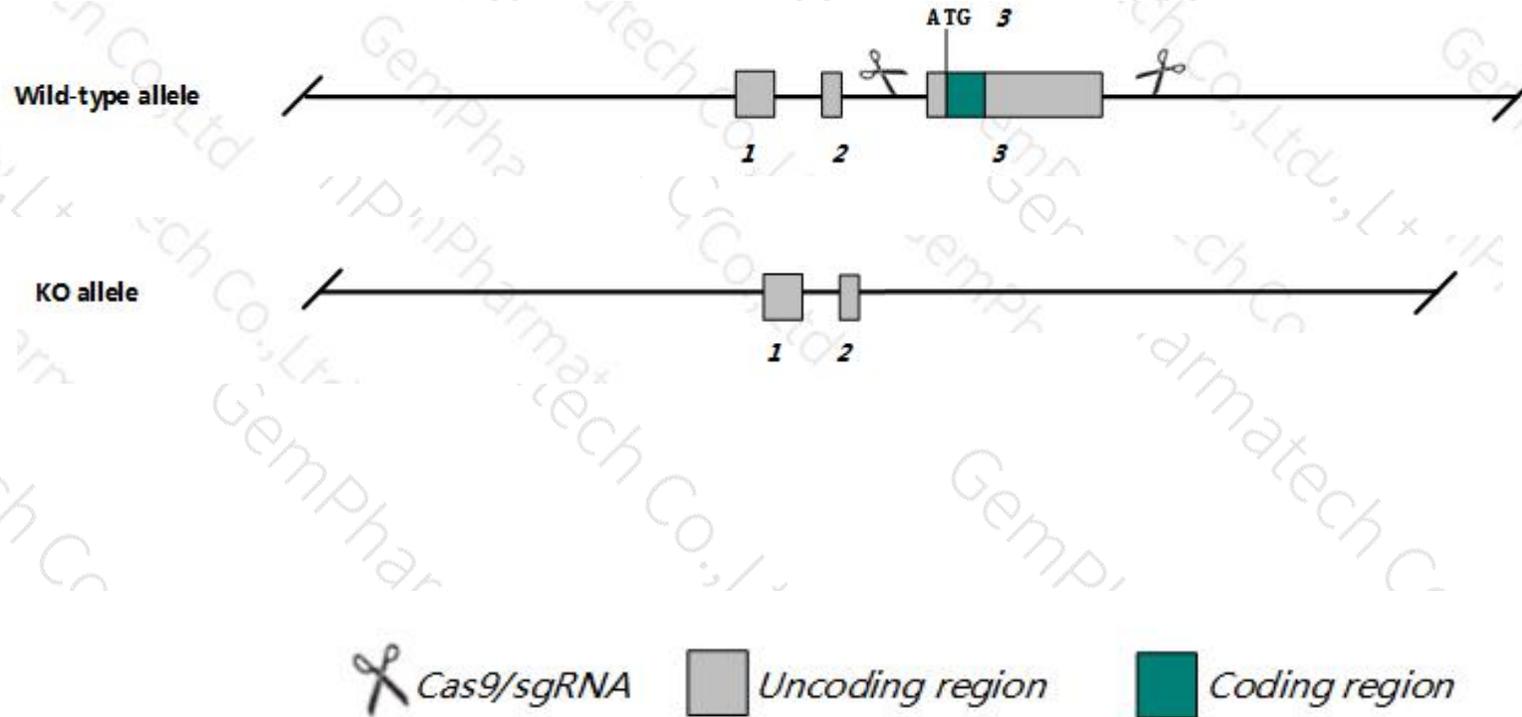
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gpr174* gene. The schematic diagram is as follows:



- The *Gpr174* gene has 7 transcripts. According to the structure of *Gpr174* gene, exon3 of *Gpr174-207* (ENSMUST00000178838.1) 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 *Gpr174* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Male mice hemizygous for a knock-out allele exhibit abnormal T cell proliferation, abnormal regulatory T cell physiology and decreased susceptibility to EAE.
- The *Gpr174* 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)

Gpr174 G protein-coupled receptor 174 [Mus musculus (house mouse)]

Gene ID: 213439, updated on 19-Mar-2019

Summary



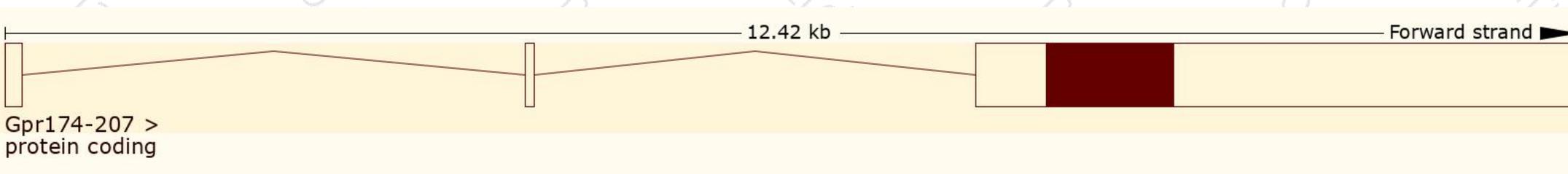
Official Symbol	Gpr174 provided by MGI
Official Full Name	G protein-coupled receptor 174 provided by MGI
Primary source	MGI:MGI:2685222
See related	Ensembl:ENSMUSG00000073008
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Gm376, Lypsr3
Expression	Low expression observed in reference dataset See more
Orthologs	human all

Transcript information (Ensembl)

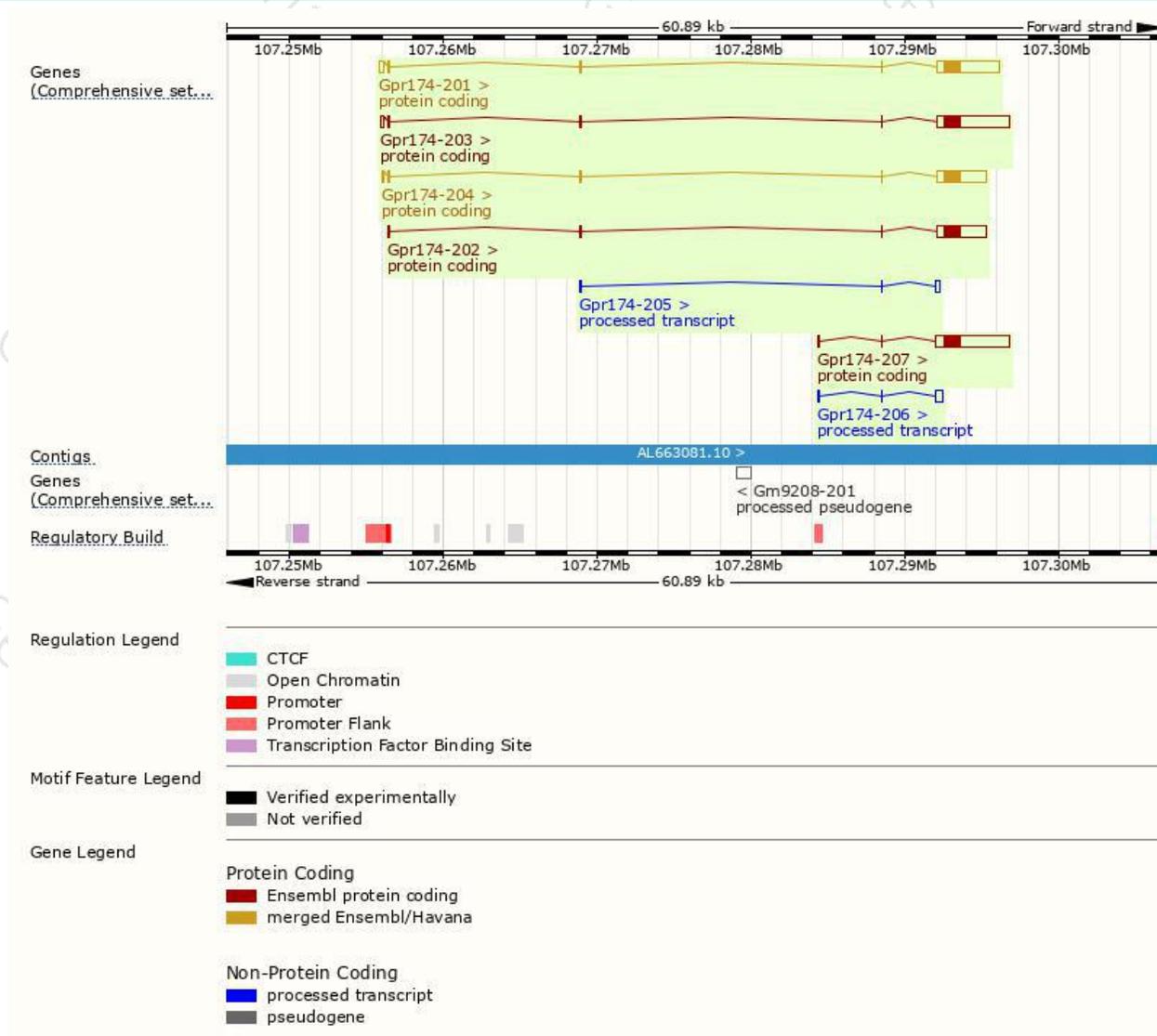
The gene has 7 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gpr174-203	ENSMUST00000118820.7	5112	335aa	Protein coding	CCDS30348	Q3U507	TSL:1 GENCODE basic APPRIS P1
Gpr174-207	ENSMUST00000178838.1	4955	335aa	Protein coding	CCDS30348	Q3U507	TSL:2 GENCODE basic APPRIS P1
Gpr174-201	ENSMUST00000101294.8	4614	335aa	Protein coding	CCDS30348	Q3U507	TSL:1 GENCODE basic APPRIS P1
Gpr174-204	ENSMUST00000120971.7	3588	335aa	Protein coding	CCDS30348	Q3U507	TSL:1 GENCODE basic APPRIS P1
Gpr174-202	ENSMUST00000117310.7	3536	335aa	Protein coding	CCDS30348	Q3U507	TSL:1 GENCODE basic APPRIS P1
Gpr174-206	ENSMUST00000156709.7	639	No protein	Processed transcript	-	-	TSL:2
Gpr174-205	ENSMUST00000138031.7	455	No protein	Processed transcript	-	-	TSL:3

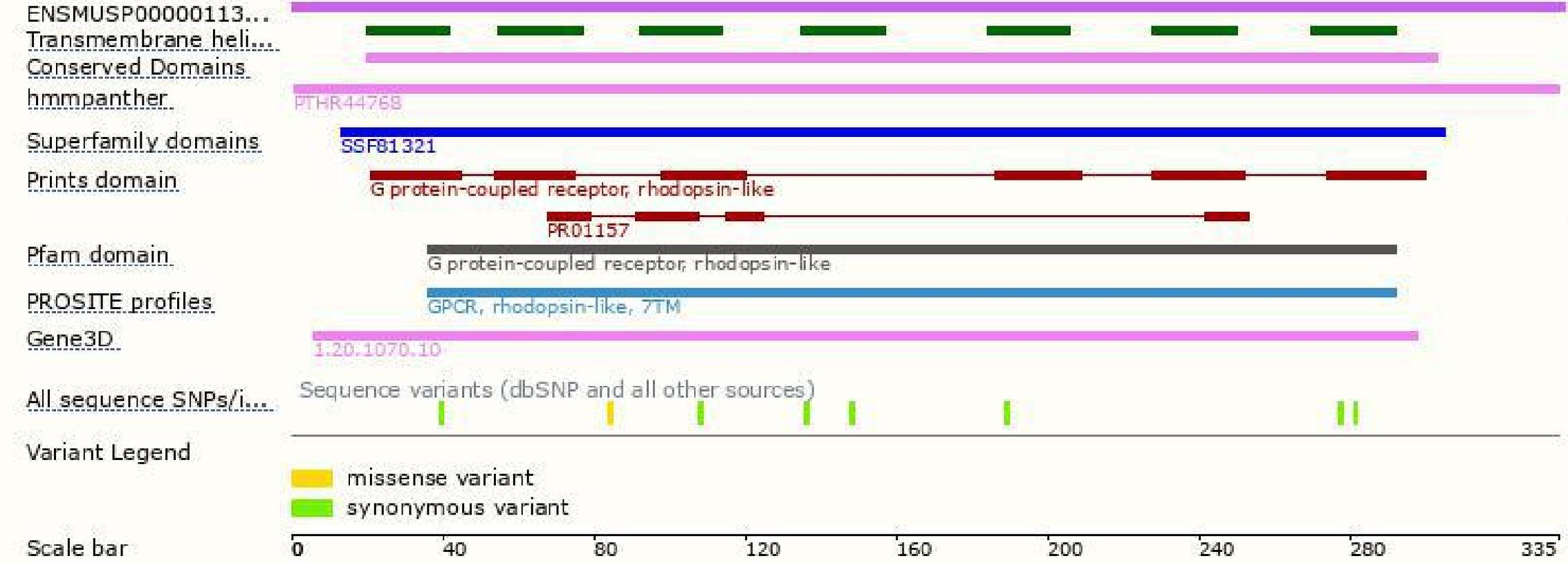
The strategy is based on the design of *Gpr174-207* transcript, The transcription is shown below



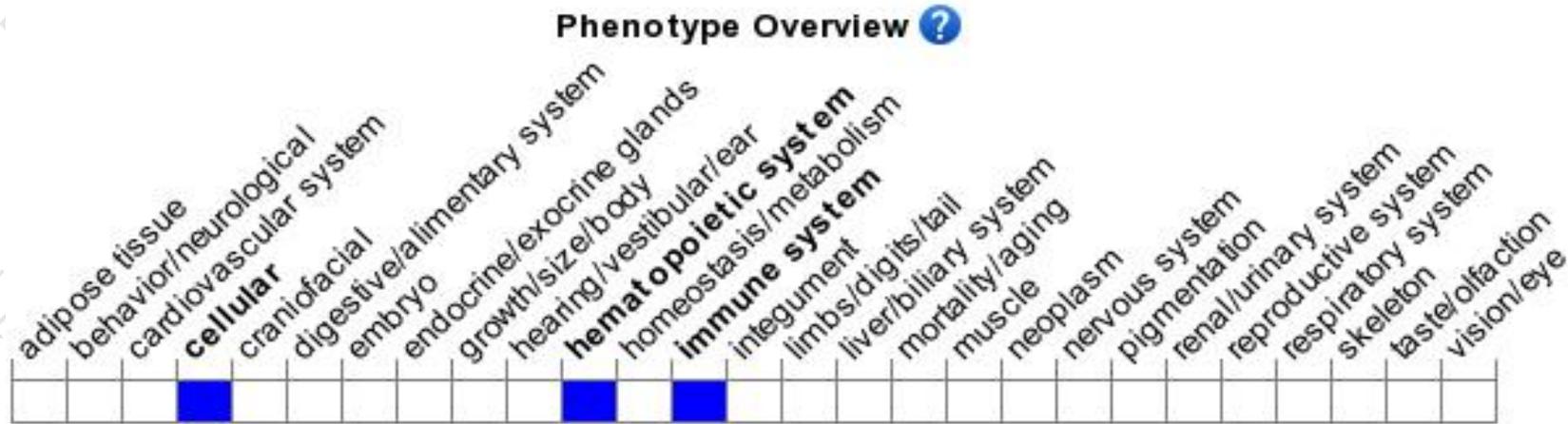
Genomic location distribution



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, Male mice hemizygous for a knock-out allele exhibit abnormal T cell proliferation, abnormal regulatory T cell physiology and decreased susceptibility to EAE.

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

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