Ramp1 Cas9-KO *Strategy*

Designer: Daohua Xu

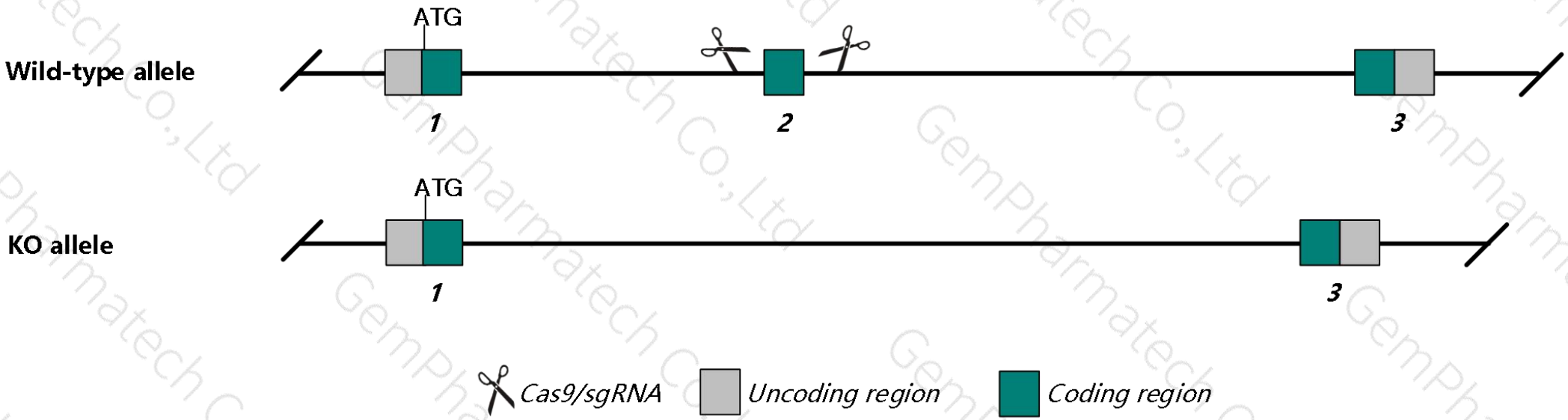
Design Date: 2019-8-6

Project Overview

Project Name	***Ramp1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Ramp1* gene. The schematic diagram is as follows:



Technical routes

- The *Ramp1* gene has 3 transcripts.According to the structure of *Ramp1* gene, exon2 of *Ramp1*-201 (ENSMUST00000097648.5) transcript is recommended as the knockout region.The region contains 139bp coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR-Cas9 technology to modify *Ramp1* 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

- According to the existing MGI data，Mice homozygous for a knock-out allele exhibit high systolic blood pressure due to a disruption in vasodilatory regulation as well as significantly increased serum levels of proinflammatory cytokines following LPS administration.
- The *Ramp1* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI)

Ramp1 receptor (calcitonin) activity modifying protein 1 [*Mus musculus* (house mouse)]

Gene ID: 51801, updated on 18-Sep-2018

Summary

Official Symbol	Ramp1 provided by MGI
Official Full Name	receptor (calcitonin) activity modifying protein 1 provided by MGI
Primary source	MGI:MGI:1858418
See related	Ensembl:ENSMUSG00000034353 Vega:OTTMUSG00000048487
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	9130218E19Rik
Expression	Broad expression in thymus adult (RPKM 23.9), colon adult (RPKM 15.0) and 16 other tissues See more
Orthologs	human all

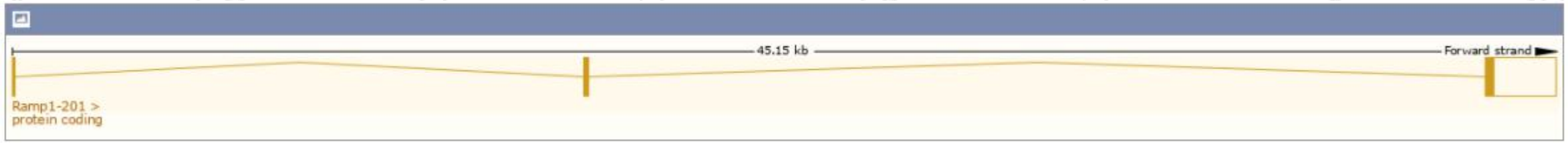
Transcript information （Ensembl）

The gene has 3 transcripts, and all transcripts are shown below:

Show/hide columns (1 hidden) Filter

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags
Ramp1-201	ENSMUST00000097648.5	2325	148aa	Protein coding	CCDS15158	Q3TNJ3 Q9WTJ5	NM_016894 NP_058590	TSL:1 GENCODE basic APPRIS P1
Ramp1-202	ENSMUST00000165855.7	852	103aa	Protein coding	CCDS78648	E9Q915	NM_178401 NP_848488	TSL:2 GENCODE basic
Ramp1-203	ENSMUST00000188475.6	711	105aa	Protein coding	CCDS48321	A0A087WPC6	NM_001168392 NP_001161864	TSL:3 GENCODE basic

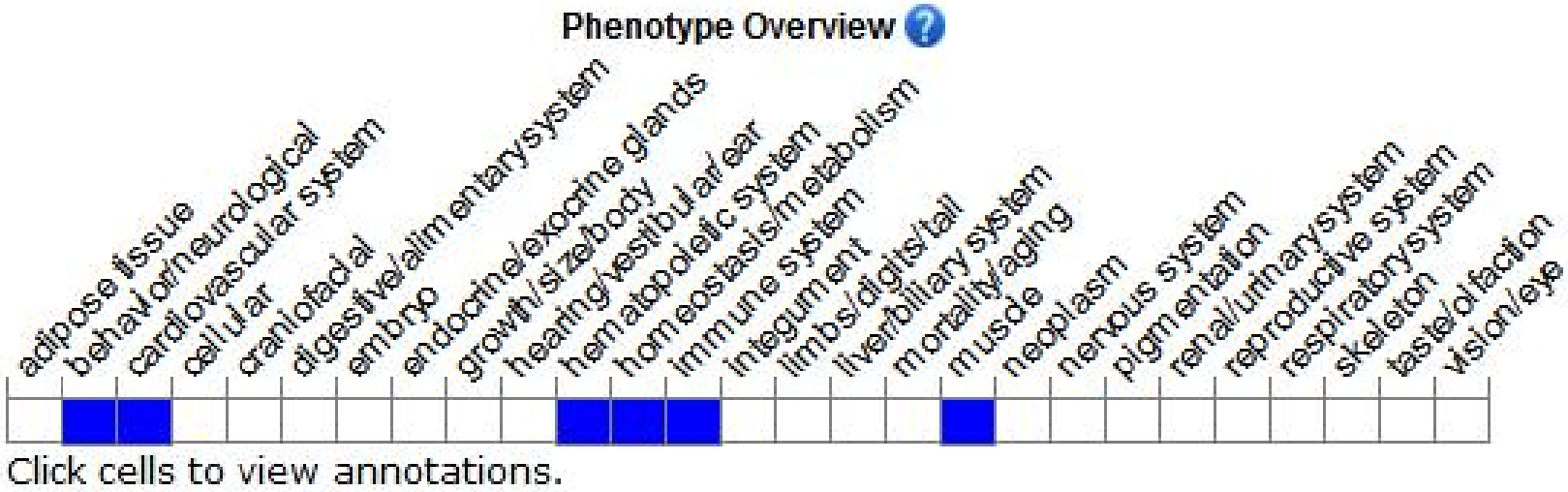
The strategy is based on the design of *Ramp1*-201 transcript,The transcription is shown below



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,Mice homozygous for a knock-out allele exhibit high systolic blood pressure due to a disruption in vasodilatory regulation as well as significantly increased serum levels of proinflammatory cytokines following LPS administration.

If you have any questions, you are welcome to inquire.
Tel: 400-966 0890

集萃药康生物科技
GemPharmatech Co.,Ltd