Aplnr Cas9-KO Strategy

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Project Overview

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

Knockout strategy

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

Technical routes

➢ The *Aplnr* gene has 2 transcripts. According to the structure of *Aplnr* gene, exon1 of *Aplnr-201* (ENSMUST00000057019.8) 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 *Aplnr* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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 early lethality, decreased cardiac contractility, and decreased exercise endurance. Mice for another knock-out allele develop pulmonary venoocclusive disease with heart right ventricle hypertrophy and elevated pulmonary pressures.

➢ The *Aplnr* gene is located on the Chr2. 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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Aplnr apelin receptor [*Mus musculus* (house mouse)]

Gene ID: 23796, updated on 24-Feb-2019

Summary

Official Symbol	Aplnr provided by MGI
Official Full Name	apelin receptor provided by MGI
Primary source	MGI:MGI:1346086
See related	Ensembl:ENSMUSG00000044338
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	APJ; Agtrl1; msr/apj
Orthologs	human all

Genomic context

Location: 2; 2 D

See Aplnr in Genome Data Viewer

Exon count: 1

Annotation release	Status	Assembly	Chr	Location
106	current	GRCm38.p4 (GCF_000001635.24)	2	NC_000068.7 (85136360..85139923)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (84976517..84980080)

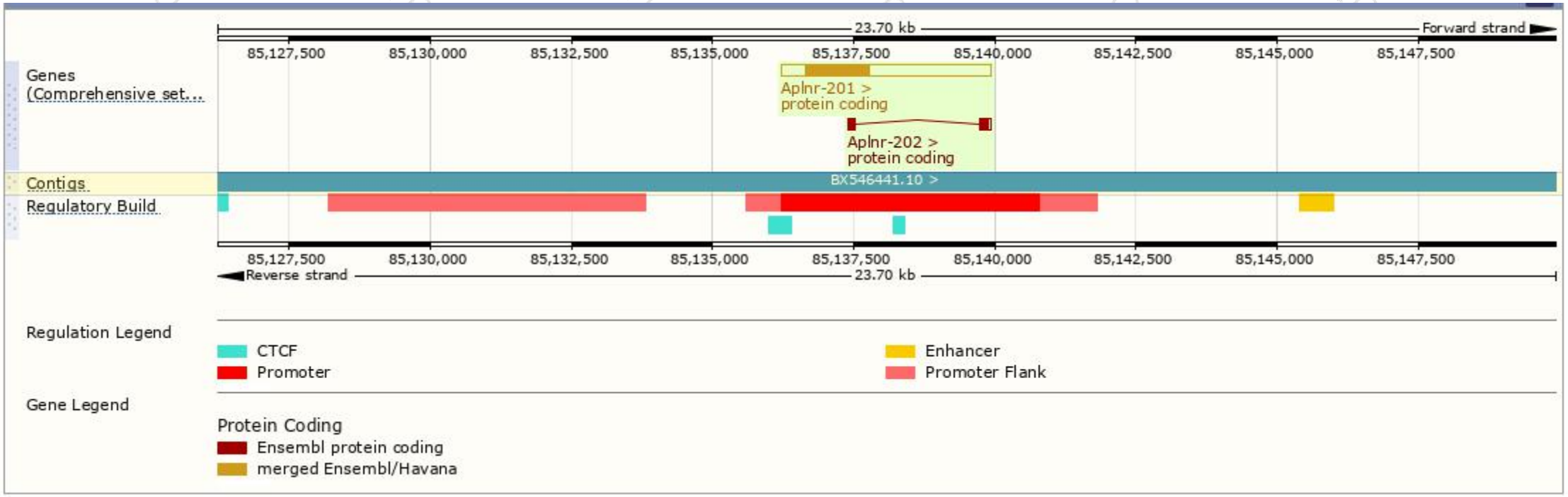
Transcript information（Ensembl）

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

Name	Transcript ID ▲	bp	Protein	Biotype	CCDS	UniProt	Flags
Aplnr-201	ENSMUST00000057019.8	3699	377aa	Protein coding	CCDS16201	Q9WV08	TSL:NA GENCODE basic APPRIS P1
Aplnr-202	ENSMUST00000184728.1	313	88aa	Protein coding	-	V9GXG8	CDS 5' incomplete TSL:5

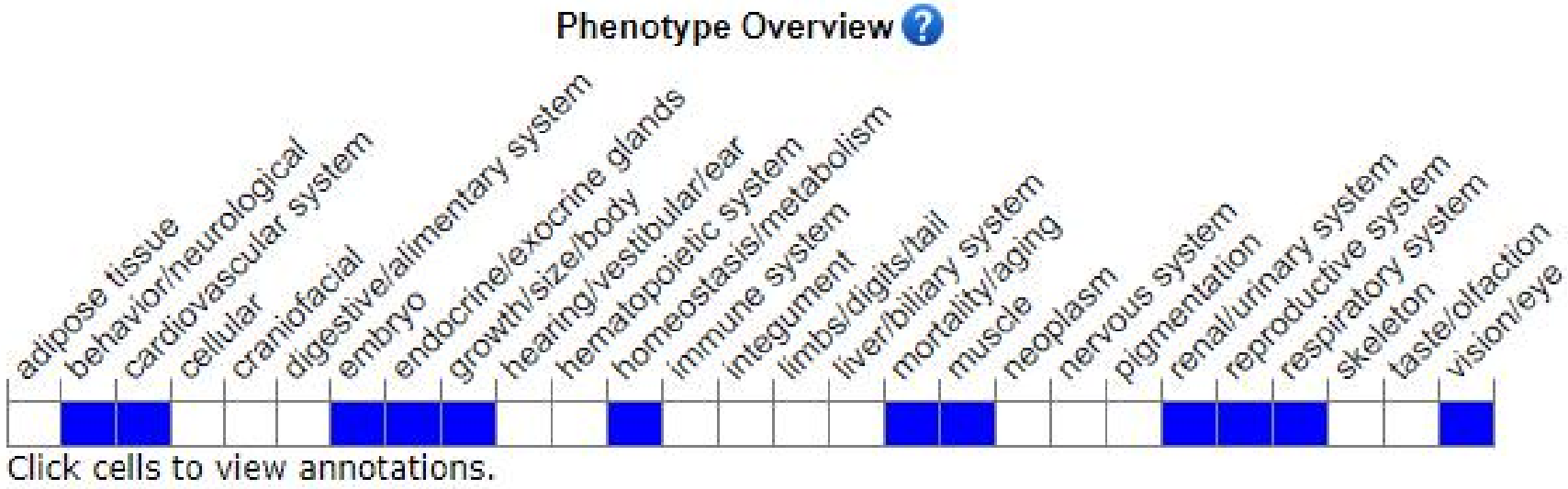
The strategy is based on the design of *Aplnr-201* transcript,The transcription is shown below

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/).

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

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