

Npr1 Cas9-KO Strategy

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Project Overview

Project Name

Npr1

Project type

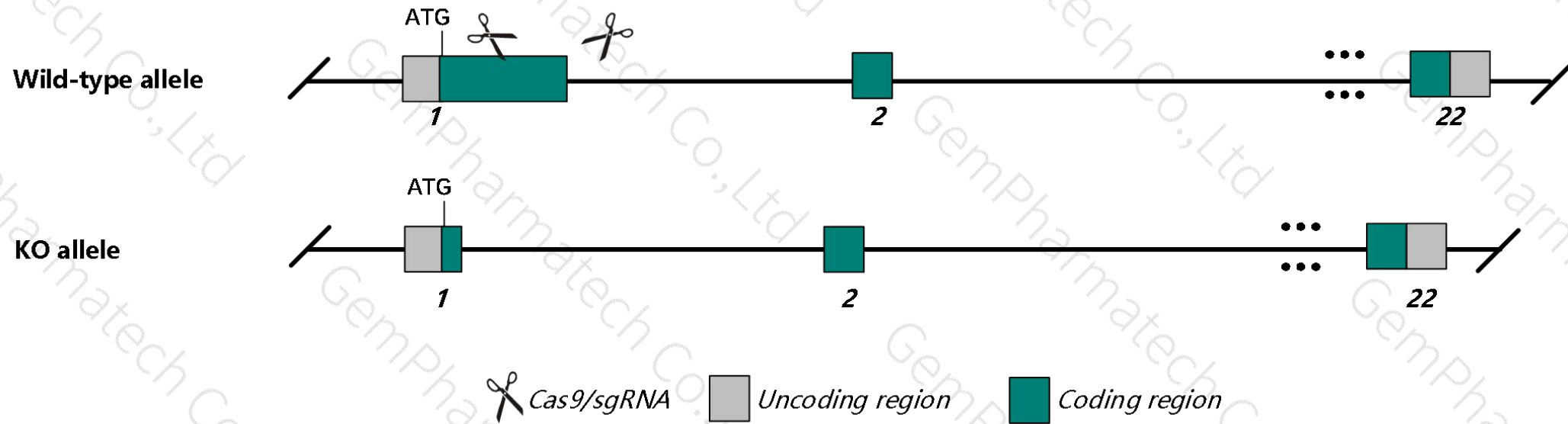
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Npr1* gene. The schematic diagram is as follows:



- The *Npr1* gene has 5 transcripts. According to the structure of *Npr1* gene, exon1 of *Npr1-201* (ENSMUST00000029540.12) transcript is recommended as the knockout region. Part of exon1 and intron1 was deleted, which will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Npr1* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, Homozygous inactivation of this gene can lead to hypertension, cardiac hypertrophy, lethal vascular events, congestive heart failure in response to volume overload, reduced serum testosterone levels, altered steroidogenesis, and reduced myocardial PMN infiltration and infarct size after I/R injury.
- The *Npr1* gene is located on the Chr3. 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)

Npr1 natriuretic peptide receptor 1 [Mus musculus (house mouse)]

Gene ID: 18160, updated on 3-Feb-2019

Summary



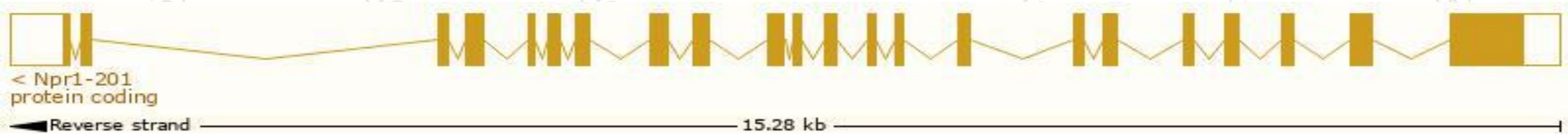
Official Symbol	Npr1 provided by MGI
Official Full Name	natriuretic peptide receptor 1 provided by MGI
Primary source	MGI:MGI:97371
See related	Ensembl:ENSMUSG000000027931
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI893888, GC-A, NPR-A, NPRA, Pndr
Expression	Biased expression in adrenal adult (RPKM 198.6), ovary adult (RPKM 80.4) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

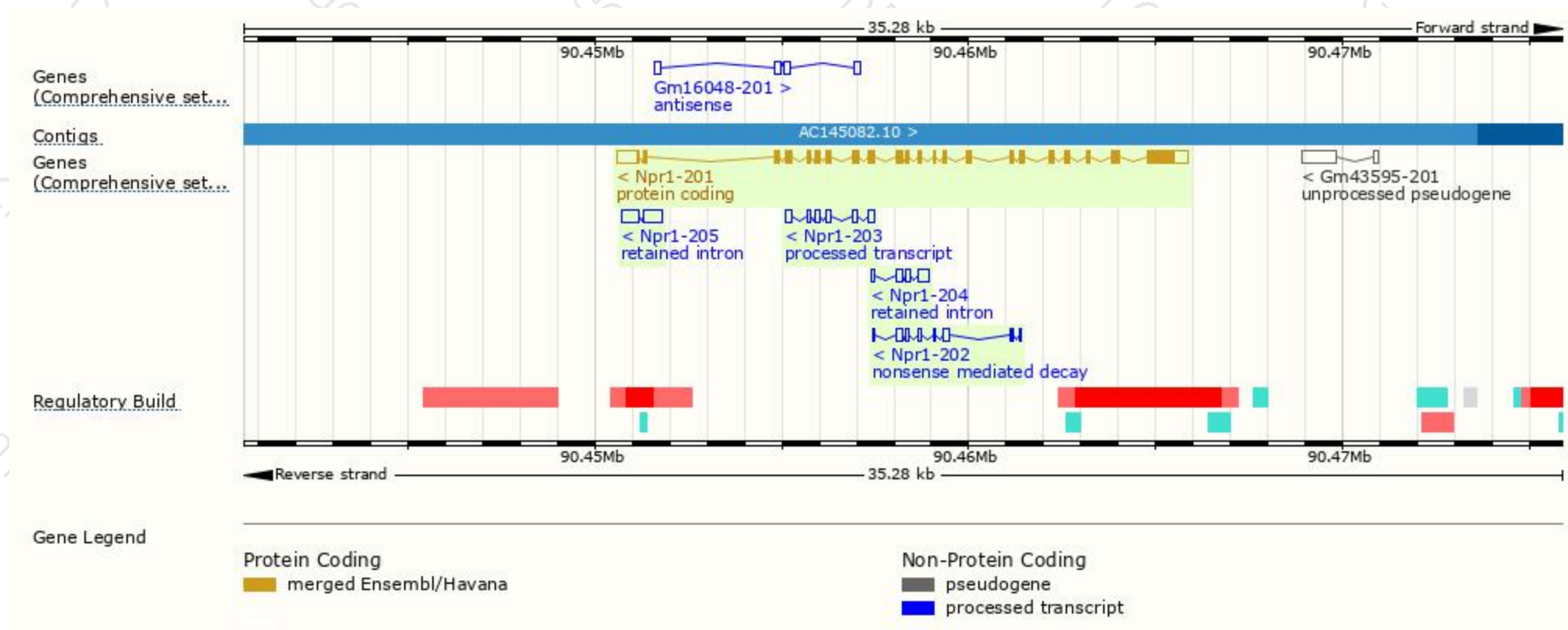
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Npr1-201	ENSMUST00000029540.12	4066	1057aa	Protein coding	CCDS17529	P18293 Q2TAY4	TSL:1 GENCODE basic APPRIS P1
Npr1-202	ENSMUST00000124760.1	790	51aa	Nonsense mediated decay	-	F6W125	CDS 5' incomplete TSL:5
Npr1-203	ENSMUST00000142243.1	767	No protein	Processed transcript	-	-	TSL:5
Npr1-205	ENSMUST00000152510.1	949	No protein	Retained intron	-	-	TSL:2
Npr1-204	ENSMUST00000146991.1	643	No protein	Retained intron	-	-	TSL:3

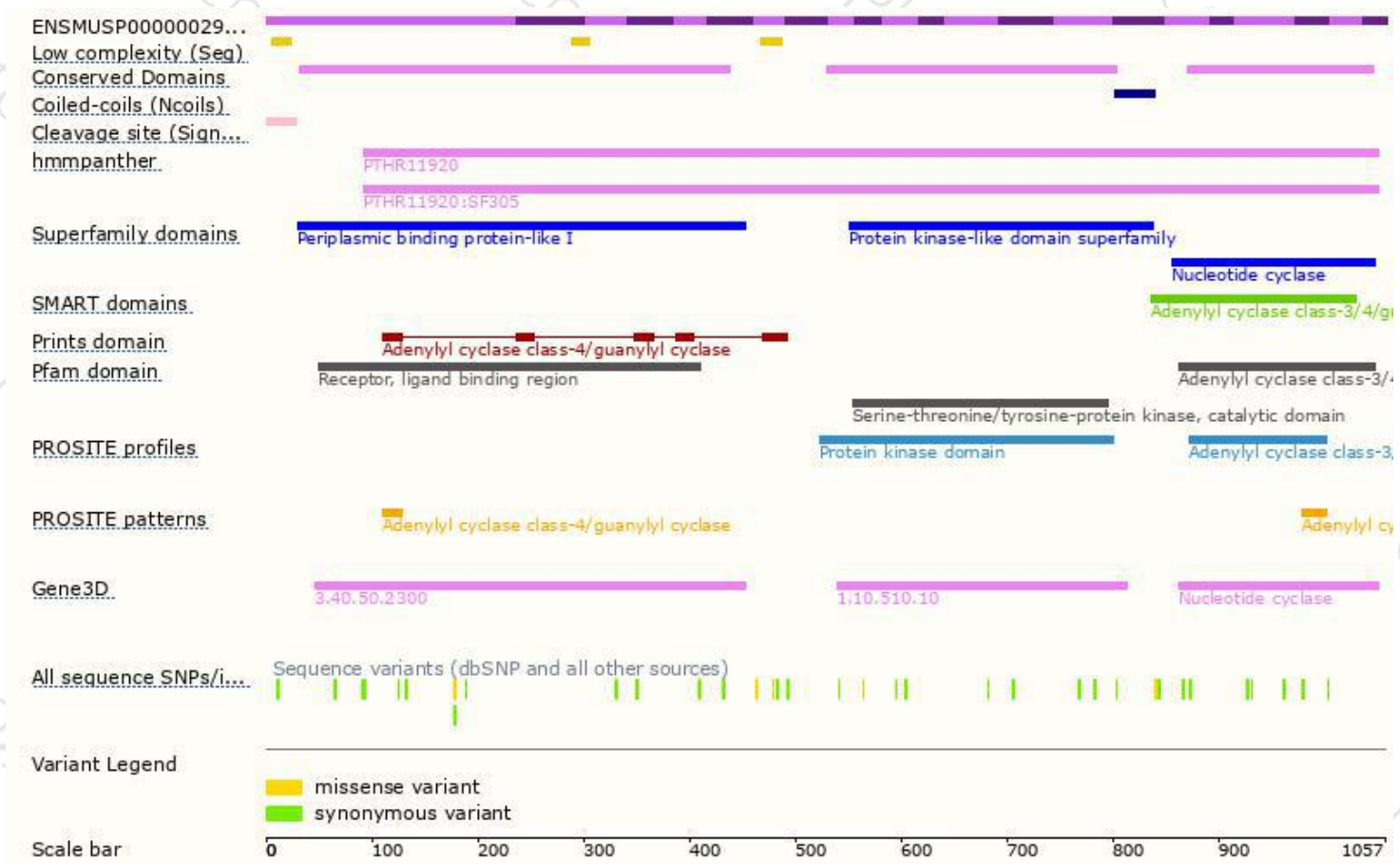
The strategy is based on the design of *Npr1-201* transcript,The transcription is shown below



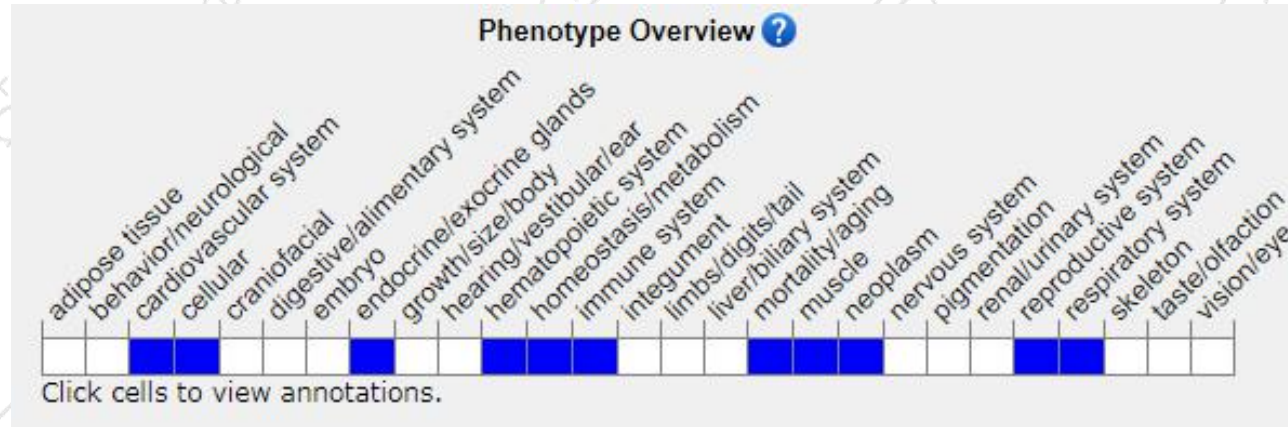
Genomic location distribution



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, Homozygous inactivation of this gene can lead to hypertension, cardiac hypertrophy, lethal vascular events, congestive heart failure in response to volume overload, reduced serum testosterone level, altered steroidogenesis, and reduced myocardial PMN infiltration and infarct size after I/R injury.

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

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