

# ***Nppa Cas9-CKO Strategy***

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**Reviewer :**

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# Project Overview

**Project Name**

*Nppa*

**Project type**

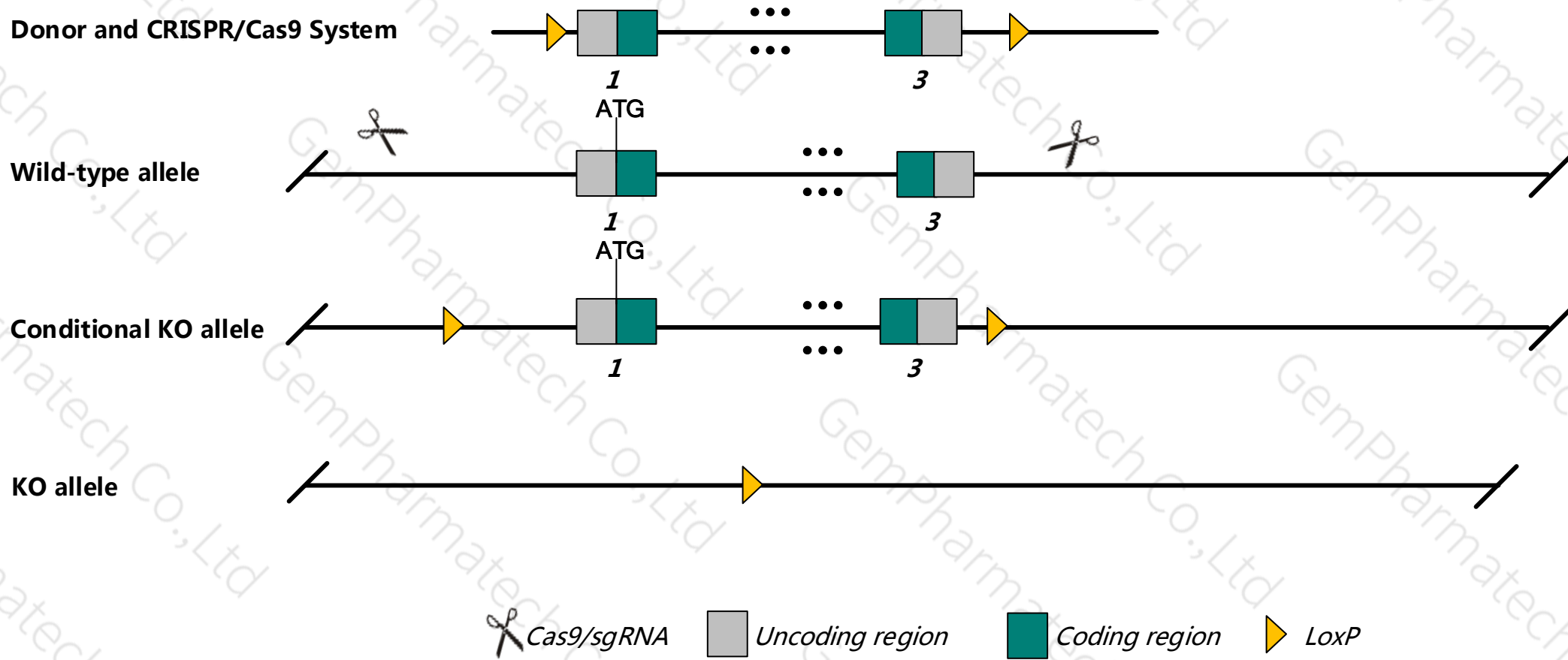
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

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



- The *Nppa* gene has 1 transcript. According to the structure of *Nppa* gene, exon1-exon3 of *Nppa*-201 (ENSMUST00000103230.4) transcript is recommended as the knockout region. The region contains all coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nppa* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA and Donor 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.
- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

- According to the existing MGI data , Homozygotes are chronically hypertensive partly due to changes in peripheral resistance and increased central AT1-receptor activation, and show salt-sensitive hypertension and abnormal pulmonary vascular remodeling with increased ventricular mass and muscularization of peripheral pulmonary vessels.
- The KO region contains functional region of the *Gm13054* gene. Knockout the region may affect the function of *Gm13054* gene.
- The *Nppa* gene is located on the Chr4. 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 )



## Nppa natriuretic peptide type A [ *Mus musculus* (house mouse) ]

Gene ID: 230899, updated on 23-Dec-2018

Summary

Official Symbol	Nppa provided by <a href="#">MGI</a>
Official Full Name	natriuretic peptide type A provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:97367</a>
See related	<a href="#">Ensembl:ENSMUSG00000041616</a>
Gene type	protein coding
RefSeq status	REVIEWED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ANP; Anf, Pnd
Summary	This gene encodes members of the natriuretic family of peptides that play an important role in the control of extracellular fluid volume and electrolyte homeostasis. The encoded protein precursor undergoes proteolytic processing to generate multiple functional peptides. Mice lacking the encoded peptides exhibit salt-sensitive hypertension. The transgenic overexpression of the encoded peptides in mice decreases arterial blood pressure without inducing diuresis and natriuresis. This gene is located adjacent to another member of the natriuretic family of peptides on chromosome 4. [provided by RefSeq, Oct 2015]
Expression	Restricted expression toward heart adult (RPKM 1334.2) <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

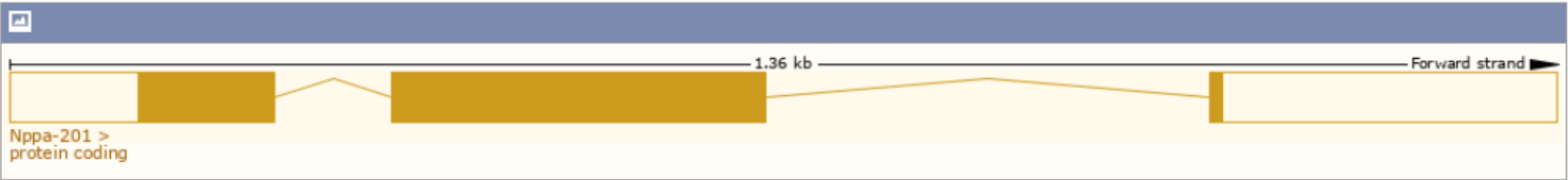


# Transcript information ( Ensembl )

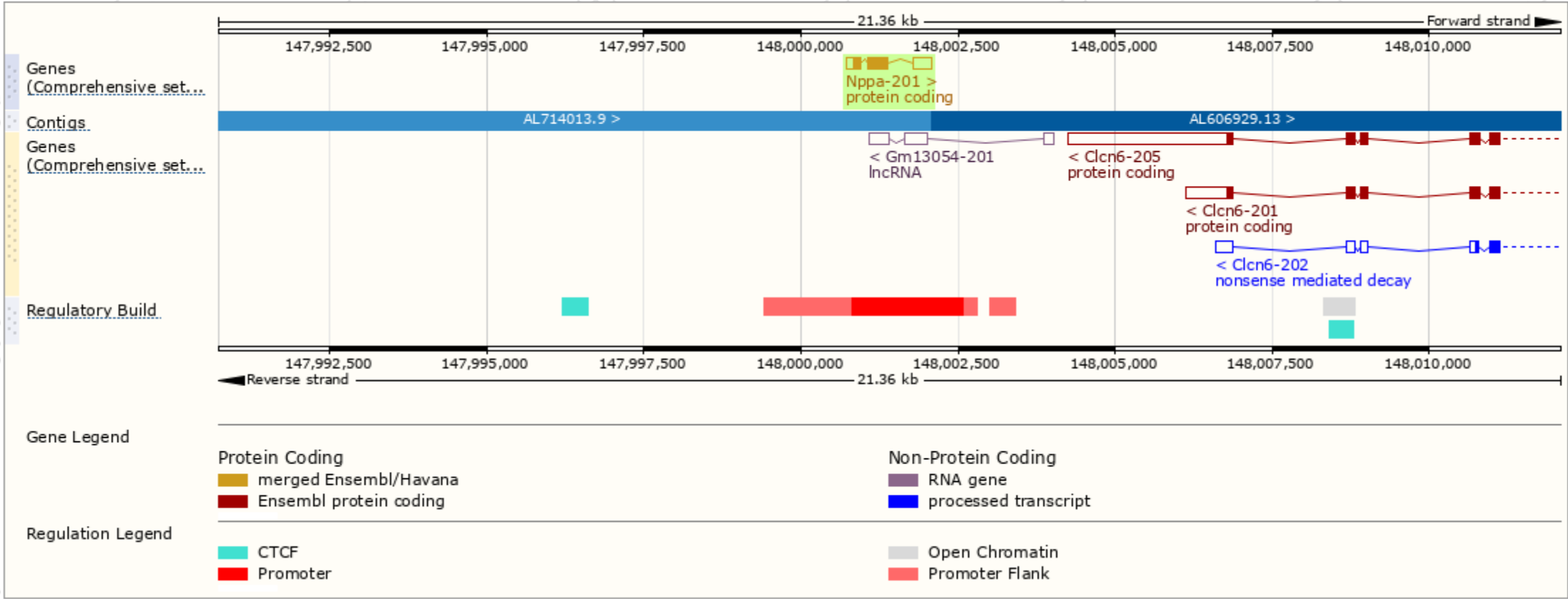
The gene has 1 transcript, and the transcript is shown below:

Show/hide columns (1 hidden)								Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags	
Nppa-201	<a href="#">ENSMUST00000103230.4</a>	865	<a href="#">152aa</a>	Protein coding	<a href="#">CCDS18927</a>	<a href="#">P05125</a>	<a href="#">NM_008725</a> <a href="#">NP_032751</a>	TSL:1	GENCODE basic APPRIS P1

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



# Genomic location distribution

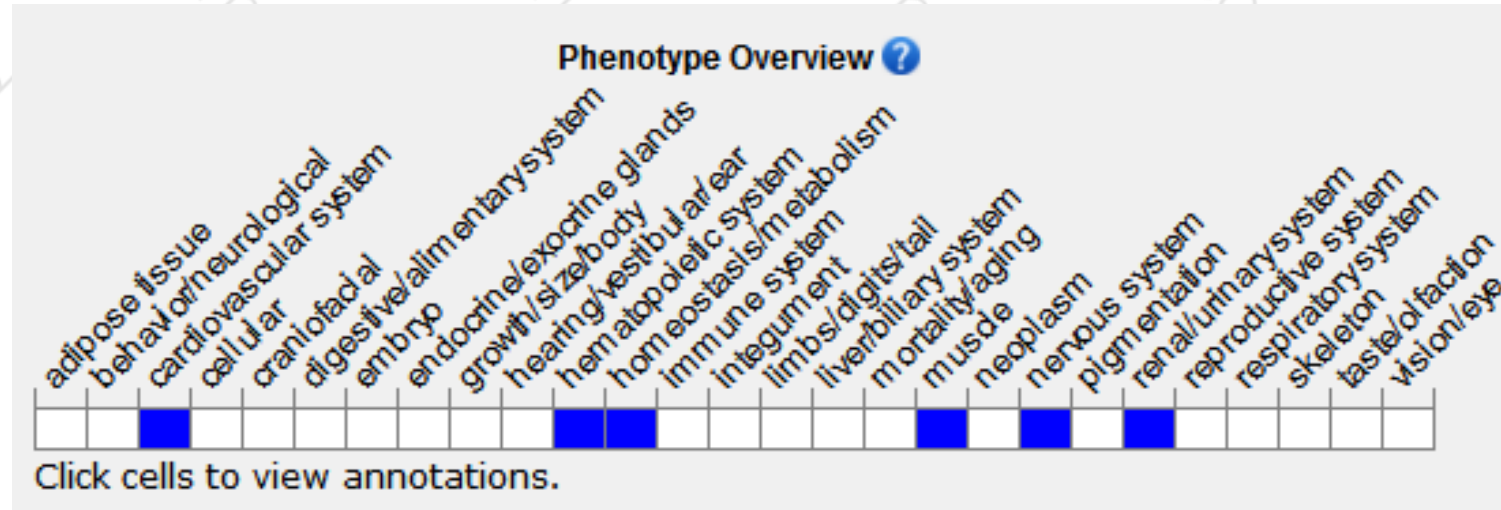




# Protein domain



# 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, Homozygotes are chronically hypertensive partly due to changes in peripheral resistance and increased central AT1-receptor activation, and show salt-sensitive hypertension and abnormal pulmonary vascular remodeling with increased ventricular mass and muscularization of peripheral pulmonary vessels.

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