

# Nr2f6 Cas9-KO Strategy

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**Reviewer:** 

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# **Project Overview**



**Project Name** 

Nr2f6

**Project type** 

Cas9-KO

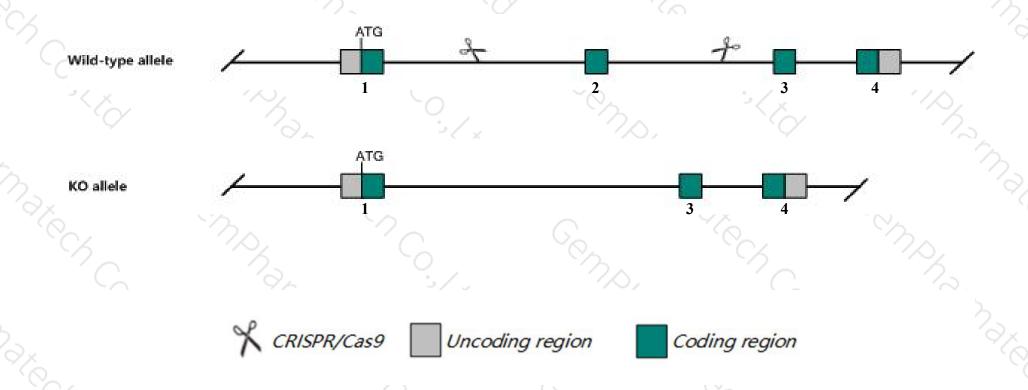
Strain background

C57BL/6JGpt

# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the Nr2f6 gene. The schematic diagram is as follows:



### **Technical routes**



- ➤ The Nr2f6 gene has 8 transcripts. According to the structure of Nr2f6 gene, exon2 of Nr2f6-201

  (ENSMUST0000002466.8) transcript is recommended as the knockout region. The region contains 95bp coding sequence.

  Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify Nr2f6 gene. The brief process is as follows: CRISPR/Cas9 system

### **Notice**



- ➤ According to the existing MGI data, Mice homozygous for a knock-out allele exhibit partial agenesis of the locus coeruleus, increased thermal nociception, and defective circadian behavior including a delayed entrainment to shifted light-dark cycles and reduced anticipatory locomotor activity in restricted feeding experiments.
- ➤ The effect on transcripts 202,204,205 is unknown.
- ➤ Transcripts 206,207,208 may not be affected.
- *➤Ocel1* gene may be destroyed.
- ➤ Some amino acids will remain at the N-terminus and some functions may be retained.
- The Nr2f6 gene is located on the Chr8. 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)



#### Nr2f6 nuclear receptor subfamily 2, group F, member 6 [ Mus musculus (house mouse) ]

Gene ID: 13864, updated on 27-Feb-2020

#### Summary

☆ ?

Official Symbol Nr2f6 provided by MGI

Official Full Name nuclear receptor subfamily 2, group F, member 6 provided by MGI

Primary source MGI:MGI:1352453

See related Ensembl: ENSMUSG00000002393

Gene type protein coding
RefSeq status VALIDATED
Organism <u>Mus musculus</u>

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as EAR2; Erbal2; AV090102; COUP-TF3

Expression Broad expression in duodenum adult (RPKM 104.5), colon adult (RPKM 86.8) and 26 other tissues See more

Orthologs human all

#### Genomic context



Location: 8 B3.3; 8 34.43 cM

See Nr2f6 in Genome Data Viewer

Exon count:

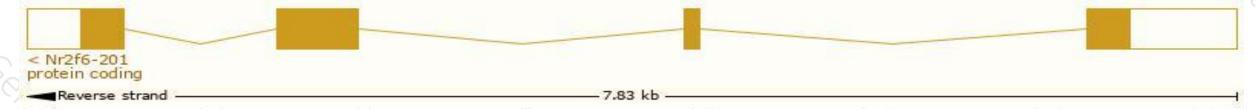
# Transcript information (Ensembl)



The gene has 8 transcripts, all transcripts are shown below:

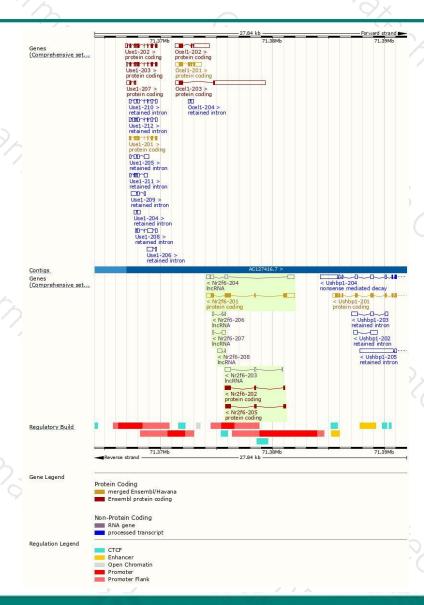
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nr2f6-201	ENSMUST00000002466.8	2218	390aa	Protein coding	CCDS22392	P43136	TSL:1 GENCODE basic APPRIS P1
Nr2f6-205	ENSMUST00000137058.1	810	<u>270aa</u>	Protein coding	+8	F6Q454	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Nr2f6-202	ENSMUST00000124732.1	761	<u>254aa</u>	Protein coding	40	F7DC78	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Nr2f6-204	ENSMUST00000132630.1	1372	No protein	Processed transcript	20	-	TSL:5
Nr2f6-203	ENSMUST00000127443.1	718	No protein	Processed transcript	1		TSL:5
Nr2f6-208	ENSMUST00000156270.1	427	No protein	Processed transcript	+8	÷	TSL:1
Nr2f6-207	ENSMUST00000155463.1	390	No protein	Processed transcript	40	- C	TSL:1
Nr2f6-206	ENSMUST00000137734.7	235	No protein	Processed transcript	20		TSL:1

The strategy is based on the design of Nr2f6-201 transcript, The transcription is shown below



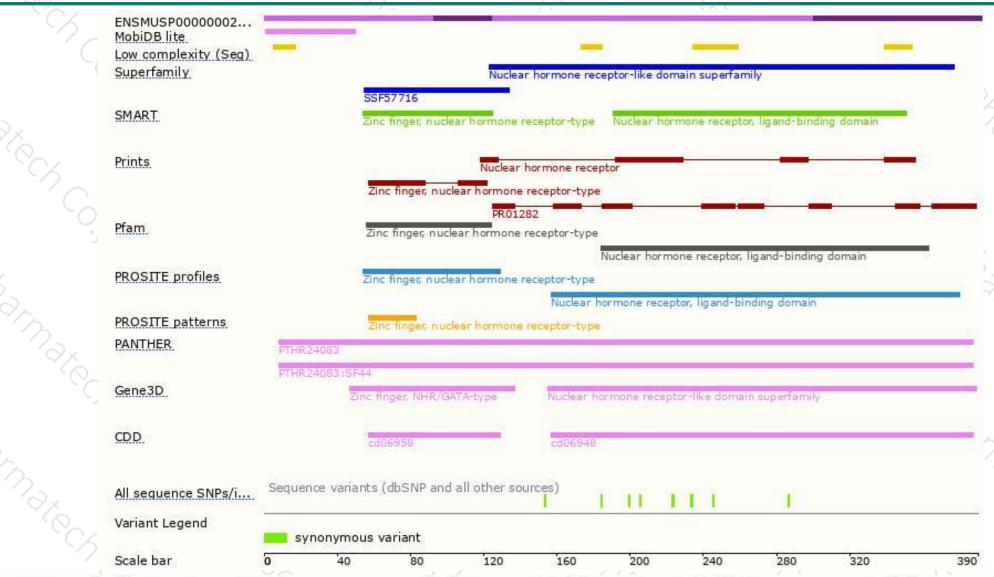
## Genomic location distribution





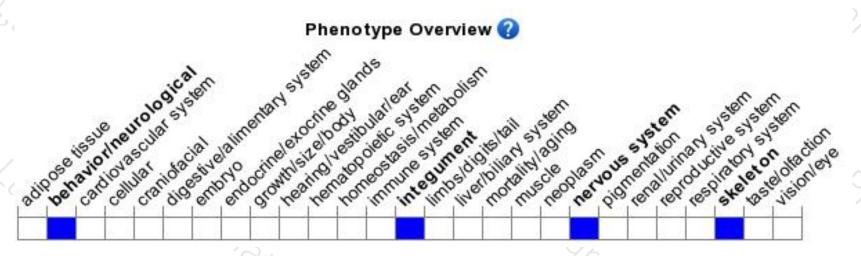
### Protein domain





# 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 partial agenesis of the locus coeruleus, increased thermal nociception, and defective circadian behavior including a delayed entrainment to shifted light-dark cycles and reduced anticipatory locomotor activity in restricted feeding experiments.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





