

# *Nxn* Cas9-KO Strategy

**Designer: QiongZhou**

# Project Overview

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**Project Name**

***Nxn***

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**Project type**

**Cas9-KO**

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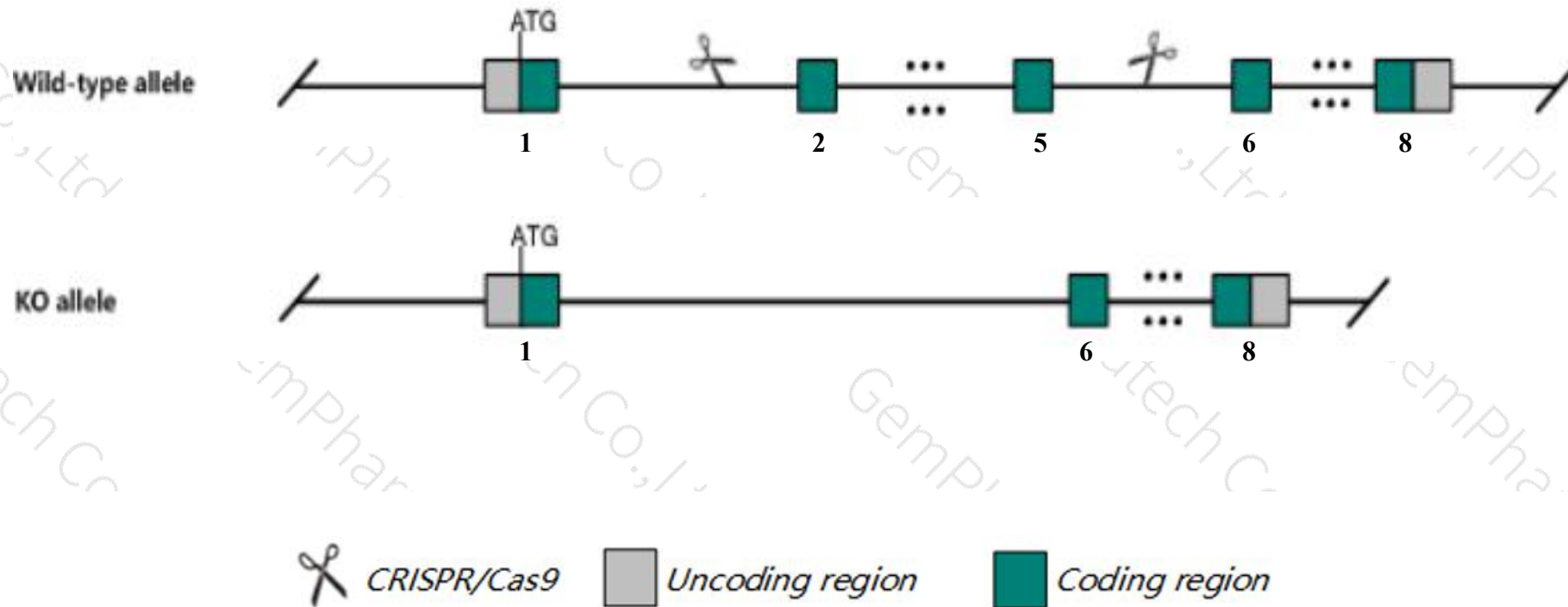
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

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



- The *Nxn* gene has 2 transcripts. According to the structure of *Nxn* gene, exon2-exon5 of *Nxn-201* (ENSMUST00000021204.3) transcript is recommended as the knockout region. The region contains 460bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nxn* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, homozygous null mice die by p1 and exhibit craniofacial bone defects and cleft palate.
- The *Nxn* gene is located on the Chr11. 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)

## Nxn nucleoredoxin [Mus musculus (house mouse)]

Gene ID: 18230, updated on 13-Mar-2020

### Summary



**Official Symbol** Nxn provided by [MGI](#)

**Official Full Name** nucleoredoxin provided by [MGI](#)

**Primary source** [MGI:MGI:109331](#)

**See related** [Ensembl:ENSMUSG00000020844](#)

**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** l11Jus13

**Expression** Broad expression in testis adult (RPKM 33.3), limb E14.5 (RPKM 23.7) and 24 other tissues [See more](#)

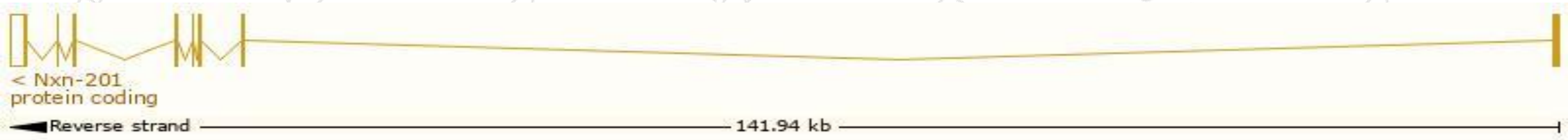
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

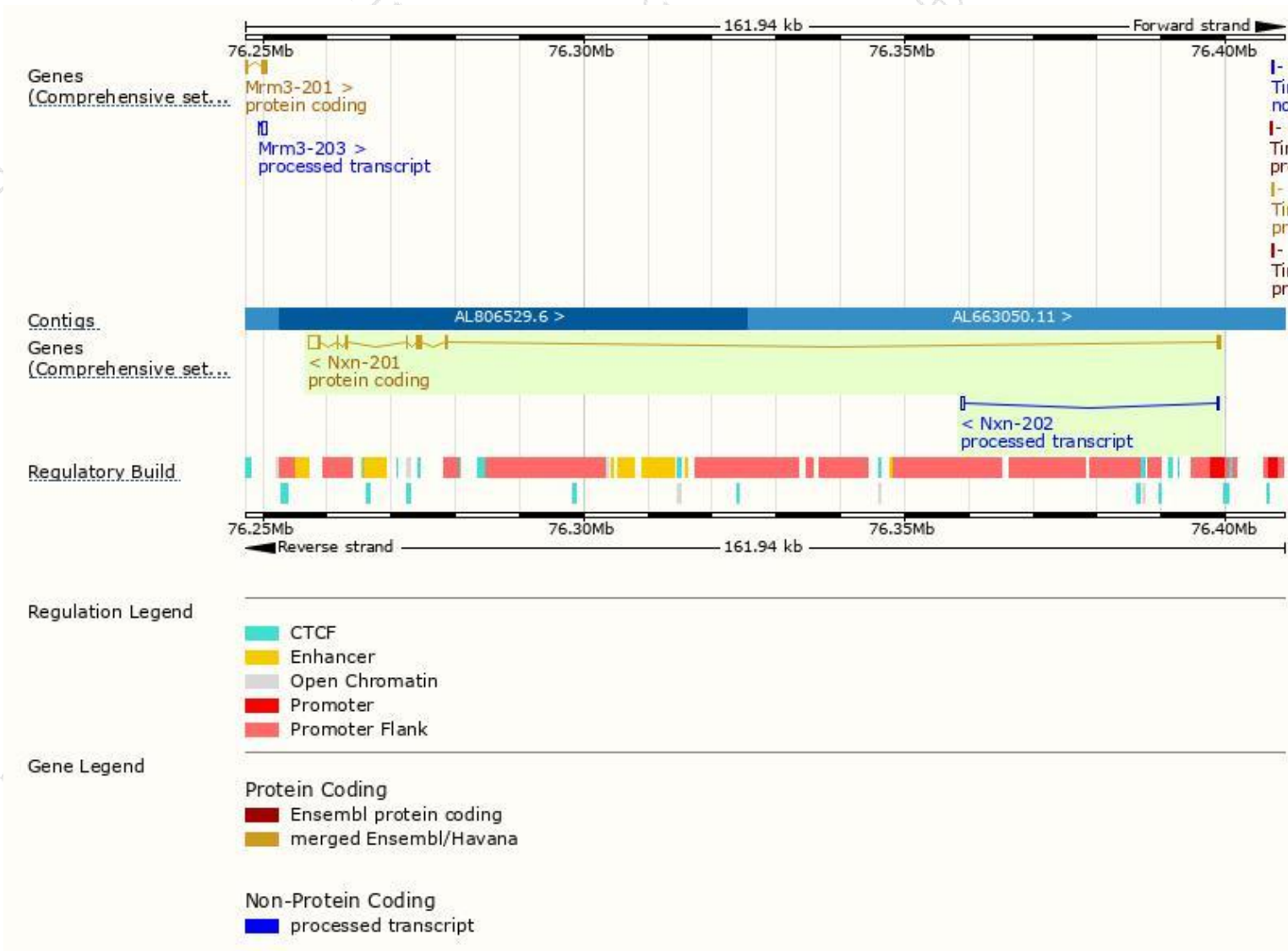
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nxn-201	<a href="#">ENSMUST00000021204.3</a>	2755	<a href="#">435aa</a>	Protein coding	<a href="#">CCDS25064</a>	<a href="#">P97346</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Nxn-202	<a href="#">ENSMUST00000131472.1</a>	852	No protein	Processed transcript	-	-	TSL:1

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

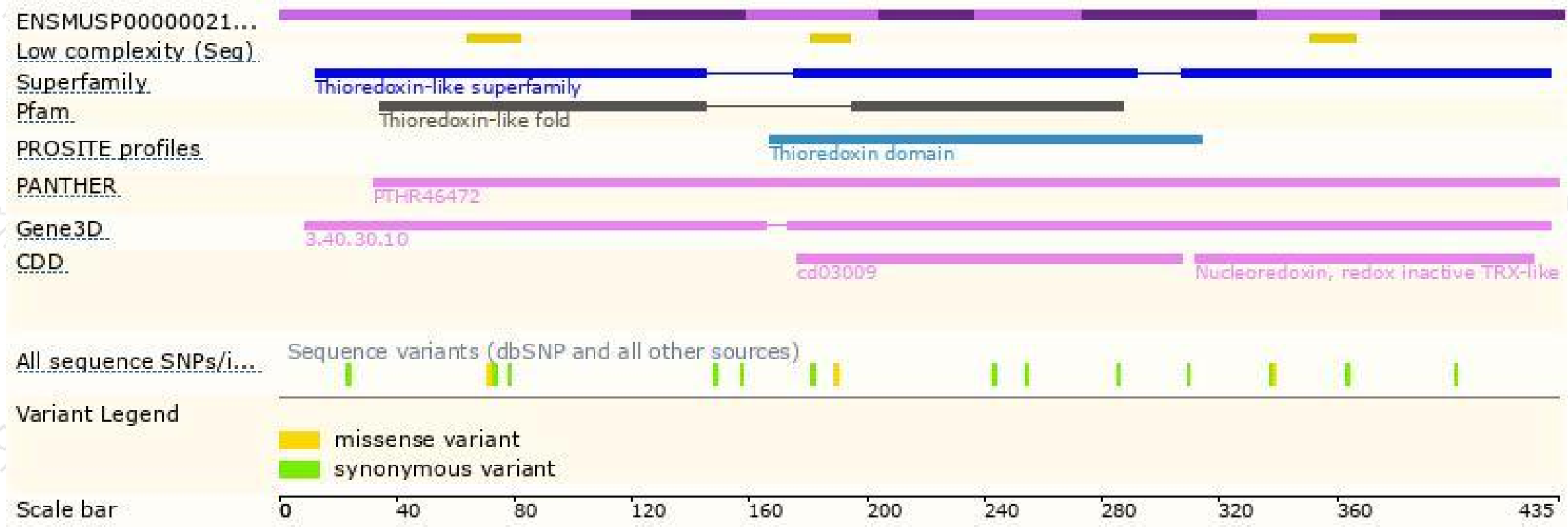


# Genomic location distribution

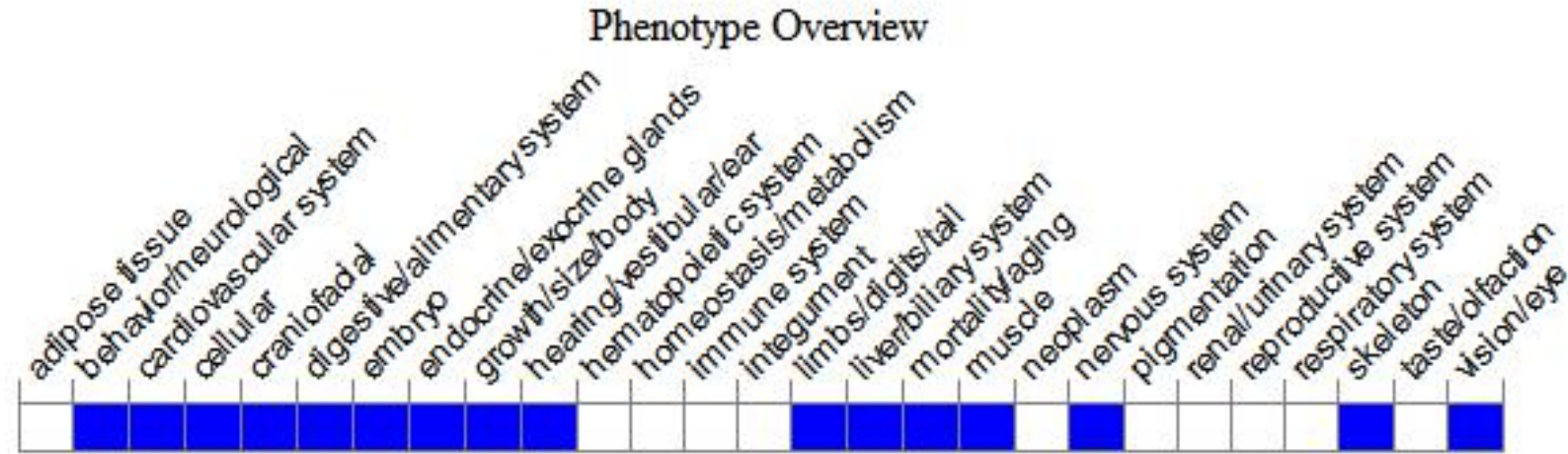




# Protein domain



# 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 null mice die by P1 and exhibit craniofacial bone defects and cleft palate.

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

Tel: 400-9660890

