

# *Nkd2* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Nkd2*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nkd2* gene. The schematic diagram is as follows:



- The *Nkd2* gene has 5 transcripts. According to the structure of *Nkd2* gene, exon4-exon7 of *Nkd2-201* (ENSMUST00000022051.13) transcript is recommended as the knockout region. The region contains 430bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nkd2* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, mice homozygous for a reporter allele are viable and fertile but show a slight and background-sensitive reduction in average litter size relative to control mice.
- The *Nkd2* gene is located on the Chr13. 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)

## Nkd2 naked cuticle 2 [ *Mus musculus* (house mouse) ]

Gene ID: 72293, updated on 12-Aug-2019

### Summary

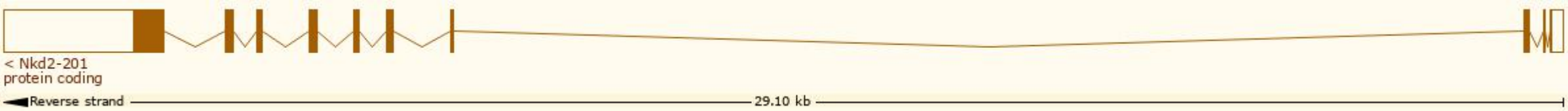
|                    |                                                                                                                                                                           |
|--------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Official Symbol    | Nkd2 provided by <a href="#">MGI</a>                                                                                                                                      |
| Official Full Name | naked cuticle 2 provided by <a href="#">MGI</a>                                                                                                                           |
| Primary source     | <a href="#">MGI:MGI:1919543</a>                                                                                                                                           |
| See related        | <a href="#">Ensembl:ENSMUSG000000021567</a>                                                                                                                               |
| Gene type          | protein coding                                                                                                                                                            |
| RefSeq status      | VALIDATED                                                                                                                                                                 |
| 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      | mNkd2; AW212591; 2210403L10Rik                                                                                                                                            |
| Expression         | Broad expression in bladder adult (RPKM 24.2), limb E14.5 (RPKM 15.3) and 16 other tissues <a href="#">See more</a>                                                       |
| Orthologs          | <a href="#">human</a> <a href="#">all</a>                                                                                                                                 |

# Transcript information (Ensembl)

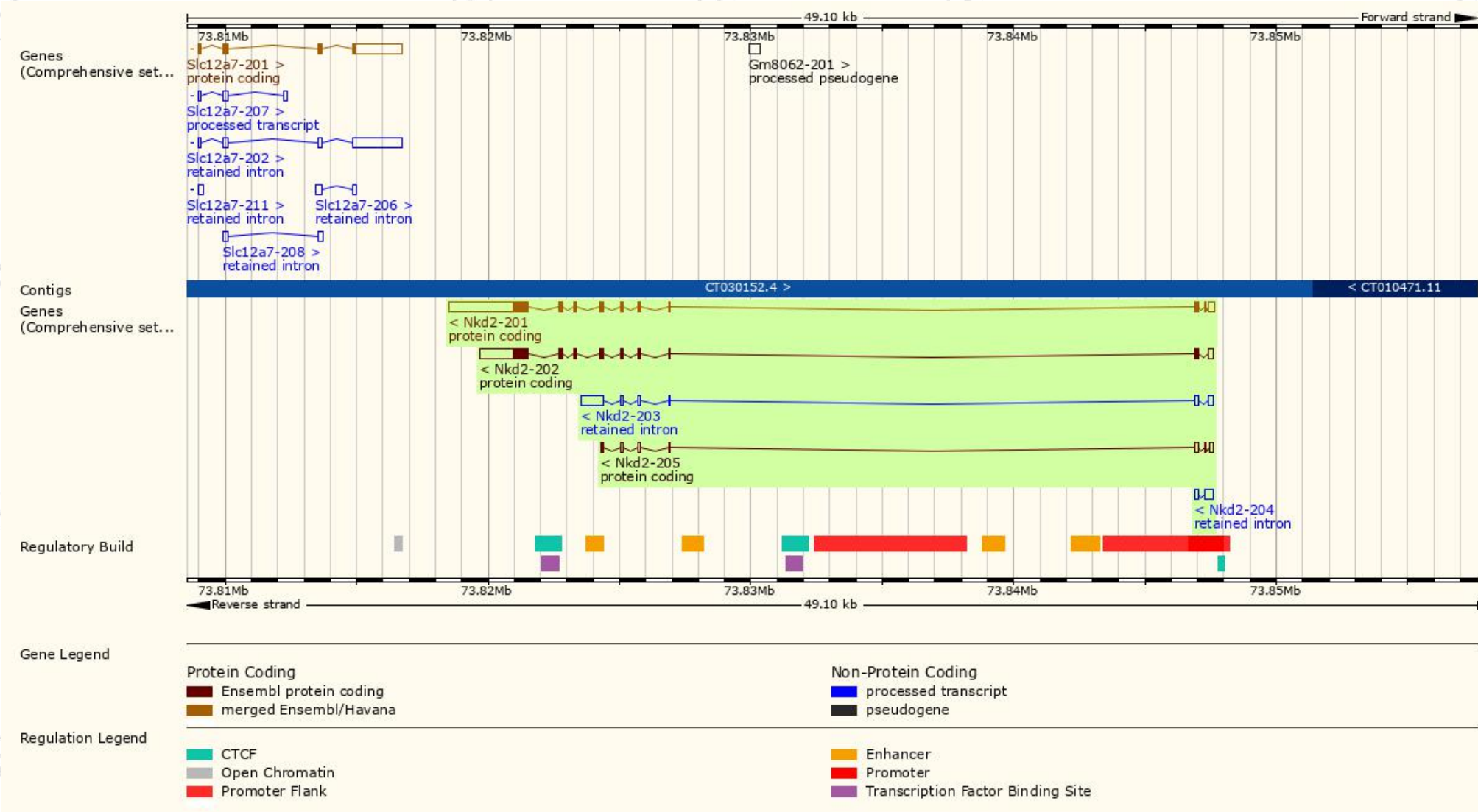
The gene has 5 transcripts,all transcripts are shown below:

| Name     | Transcript ID                         | bp   | Protein               | Biotype         | CCDS                      | UniProt                    | Flags                           |
|----------|---------------------------------------|------|-----------------------|-----------------|---------------------------|----------------------------|---------------------------------|
| Nkd2-201 | <a href="#">ENSMUST00000022051.13</a> | 4016 | <a href="#">461aa</a> | Protein coding  | <a href="#">CCDS26636</a> | <a href="#">Q8VE28</a>     | TSL:1 GENCODE basic APPRIS P3   |
| Nkd2-202 | <a href="#">ENSMUST00000118096.1</a>  | 2801 | <a href="#">449aa</a> | Protein coding  | <a href="#">CCDS84036</a> | <a href="#">Q8VE28</a>     | TSL:1 GENCODE basic APPRIS ALT2 |
| Nkd2-205 | <a href="#">ENSMUST00000222004.1</a>  | 705  | <a href="#">38aa</a>  | Protein coding  | -                         | <a href="#">A0A1Y7VJ02</a> | CDS 3' incomplete TSL:3         |
| Nkd2-203 | <a href="#">ENSMUST00000138899.1</a>  | 1456 | No protein            | Retained intron | -                         | -                          | TSL:1                           |
| Nkd2-204 | <a href="#">ENSMUST00000221679.1</a>  | 447  | No protein            | Retained intron | -                         | -                          | TSL:3                           |

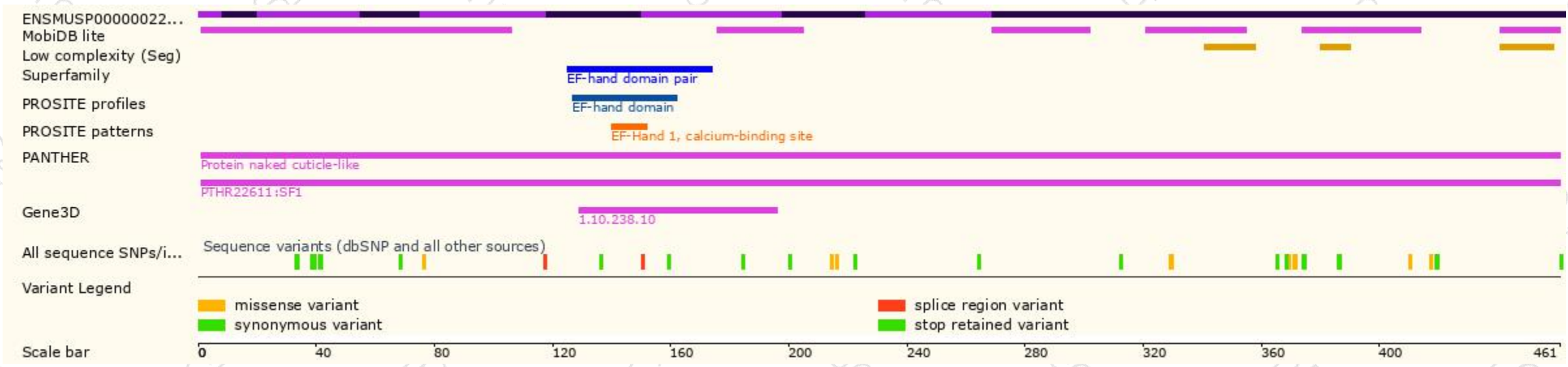
The strategy is based on the design of *Nkd2-201* transcript, the transcription is shown below:



# Genomic location distribution

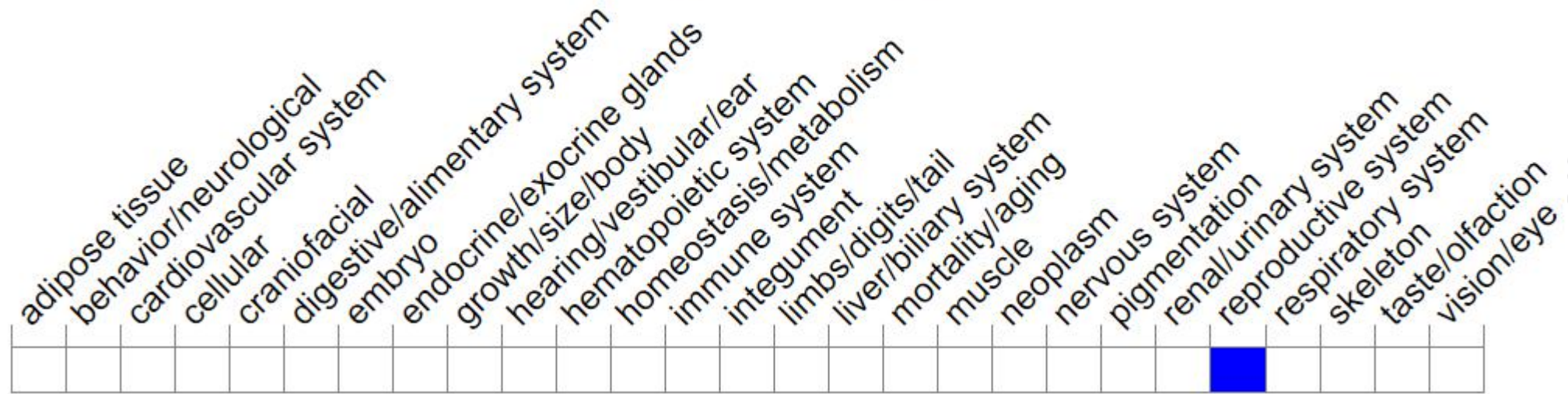


# Protein domain



# Mouse phenotype description(MGI )

## Phenotype Overview ?



*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 reporter allele are viable and fertile but show a slight and background-sensitive reduction in average litter size relative to control mice.

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

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