

# Nup37 Cas9-KO Strategy

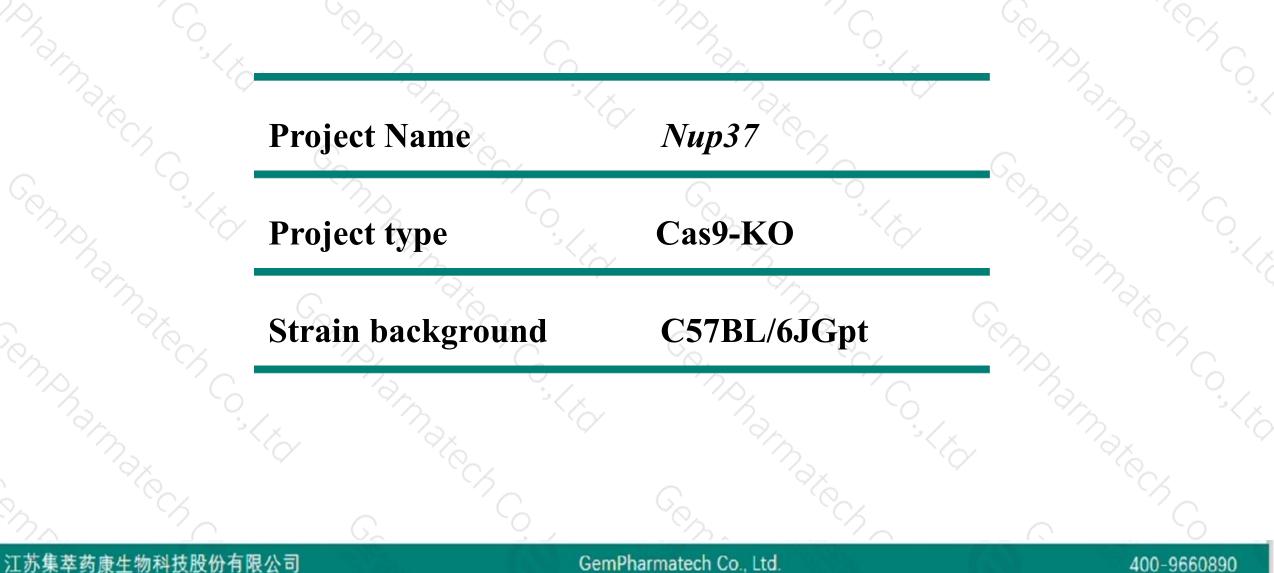
**Designer: Ruirui Zhang** 

**Reviewer: Huimin Su** 

Design Date: 2020-6-16

# **Project Overview**

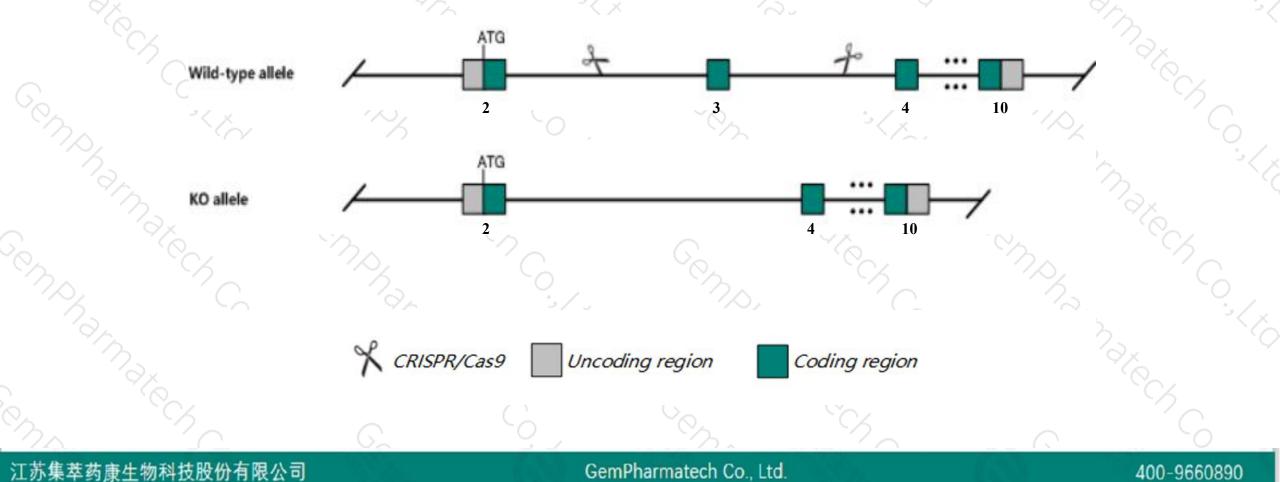




# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the Nup37 gene. The schematic diagram is as follows:





- The Nup37 gene has 6 transcripts. According to the structure of Nup37 gene, exon3 of Nup37-202 (ENSMUST00000169309.2) transcript is recommended as the knockout region. The region contains 125bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Nup37 gene. The brief process is as follows: CRISPR/Cas9 system

- > The *Nup37* gene is located on the Chr10. 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.

Notice

# **Gene information (NCBI)**



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#### Nup37 nucleoporin 37 [Mus musculus (house mouse)]

Gene ID: 69736, updated on 13-Mar-2020

#### Summary

| Official Symbol       | Nup37 provided by MGI  |
|-----------------------|--|
| Official Full Name    | nucleoporin 37 provided byMGI  |
| <b>Primary source</b> | MGI:MGI:1919964  |
| See related           | Ensembl:ENSMUSG00000035351   |
| Gene type             | protein coding   |
| <b>RefSeq status</b>  | 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         | 2410003L22Rik, 2810039M17Rik   |
| Expression            | Broad expression in CNS E11.5 (RPKM 13.9), placenta adult (RPKM 12.5) and 24 other tissues See more                                  |
| Orthologs             | human all  |

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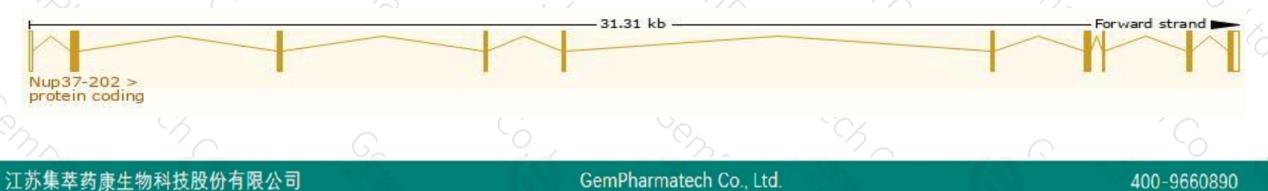
# **Transcript information (Ensembl)**



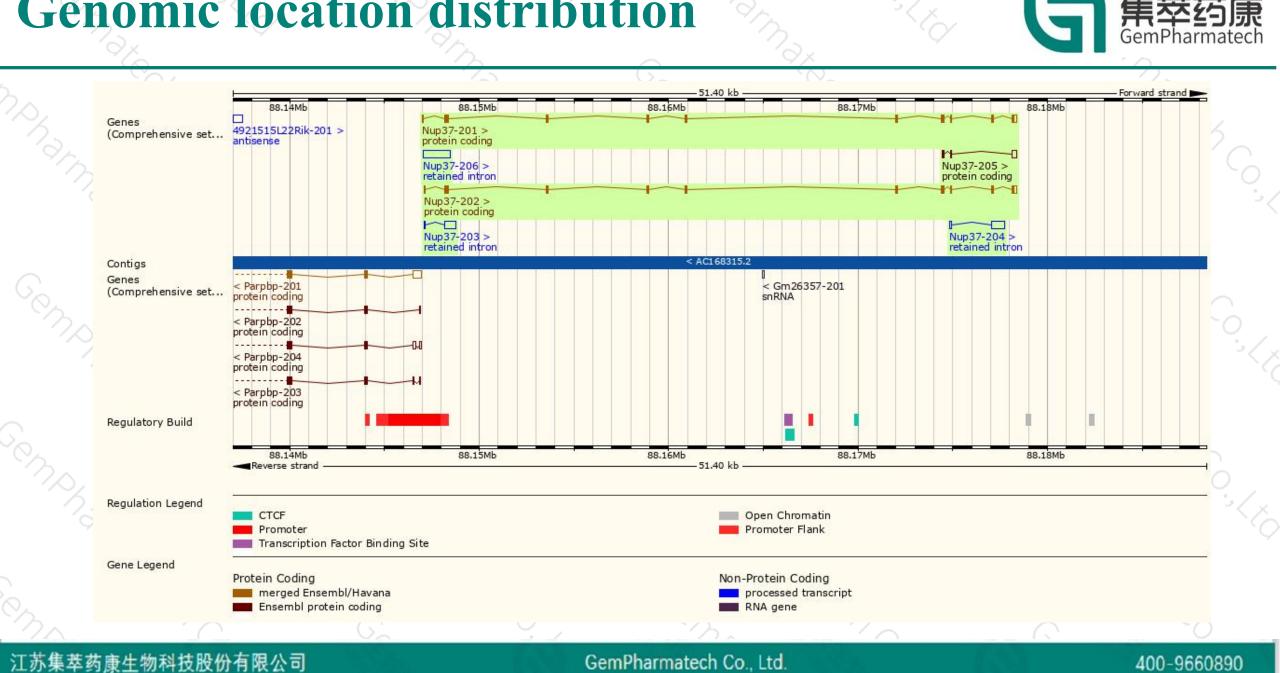
#### The gene has 6 transcripts, all transcripts are shown below:

| Name      | Transcript ID        | bp          | Protein                     | Biotype                          | CCDS      | UniProt    | Flags                         |
|-----------|----------------------|-------------|-----------------------------|----------------------------------|-----------|------------|-------------------------------|
| Nup37-202 | ENSMUST00000169309.2 | 1277        | <u>326aa</u>                | Protein coding                   | CCDS24107 | Q9CWU9     | TSL:1 GENCODE basic APPRIS P1 |
| Nup37-201 |                      | 1267<br>430 | <u>326aa</u><br><u>67aa</u> | Protein coding<br>Protein coding | CCDS24107 |            | TSL:1 GENCODE basic APPRIS P1 |
| Nup37-205 |                      |             |                             |                                  | 10        | A0A1W2P6V2 | CDS 5' incomplete TSL:3       |
| Nup37-206 | ENSMUST00000219859.1 | 1448        | No protein                  | Retained intron                  | 20        | -          | TSL:NA                        |
| Nup37-204 | ENSMUST00000219059.1 | 721         | No protein                  | Retained intron                  | 54        | 7          | TSL:2                         |
| Nup37-203 | ENSMUST00000218935.1 | 679         | No protein                  | Retained intron                  | -8        | -          | TSL:2                         |

The strategy is based on the design of *Nup37-202* transcript, the transcription is shown below:



### **Genomic location distribution**



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## **Protein domain**



| uperfamily         | WD40-repea        | t-containing domain   | superfamily       |                |              |     |     |     |
|--------------------|-------------------|-----------------------|-------------------|----------------|--------------|-----|-----|-----|
| MART               |                   | WD40 repeat           |                   |                |              |     |     |     |
| fam                |                   |                       | WD40 rep          | eat            |              |     |     |     |
| ROSITE profiles    |                   |                       | WD40-rep          | eat-containing | domain       |     |     |     |
|                    |                   |                       | WD40 rep          | eat            |              |     |     |     |
| ROSITE patterns    |                   |                       |                   | D40 repeat, co | nserved site |     |     |     |
| ANTHER             | Nucleoporin Nup37 | 7                     |                   |                |              |     |     |     |
| ene3D              | WD40/YVTN rep     | eat-like-containing d | omain superfamily |                |              |     |     |     |
| ll sequence SNPs/i | Sequence variar   | nts (dbSNP and all o  | other sources)    | 11             | 11           | i i |     |     |
| ariant Legend      | missense v        |                       |                   | **             | <i>241</i> , | 10  |     |     |
| cale bar           | 0 40              | 80                    | 120               | 160            | 200          | 240 | 280 | 326 |
|                    |                   |                       |                   |                |              |     |     |     |

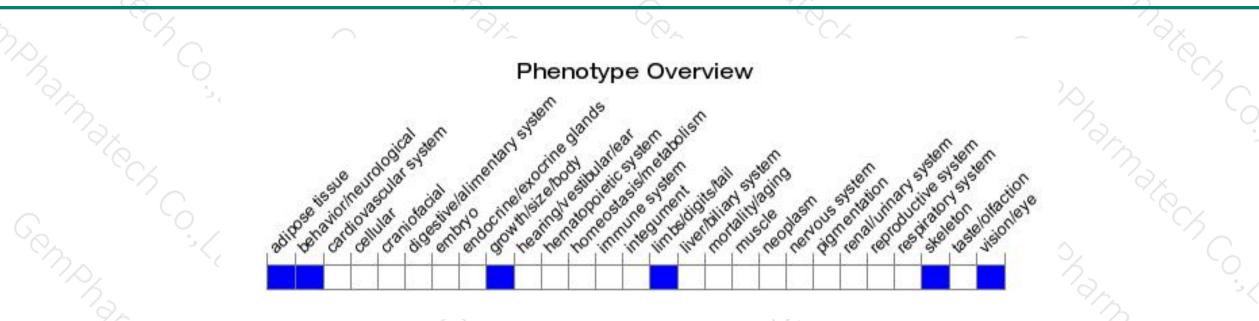
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# Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).



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



