

# *Npr2* Cas9-KO Strategy

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Design Date: 2019-7-22

# Project Overview

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**Project Name**

*Npr2*

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**Project type**

**Cas9-KO**

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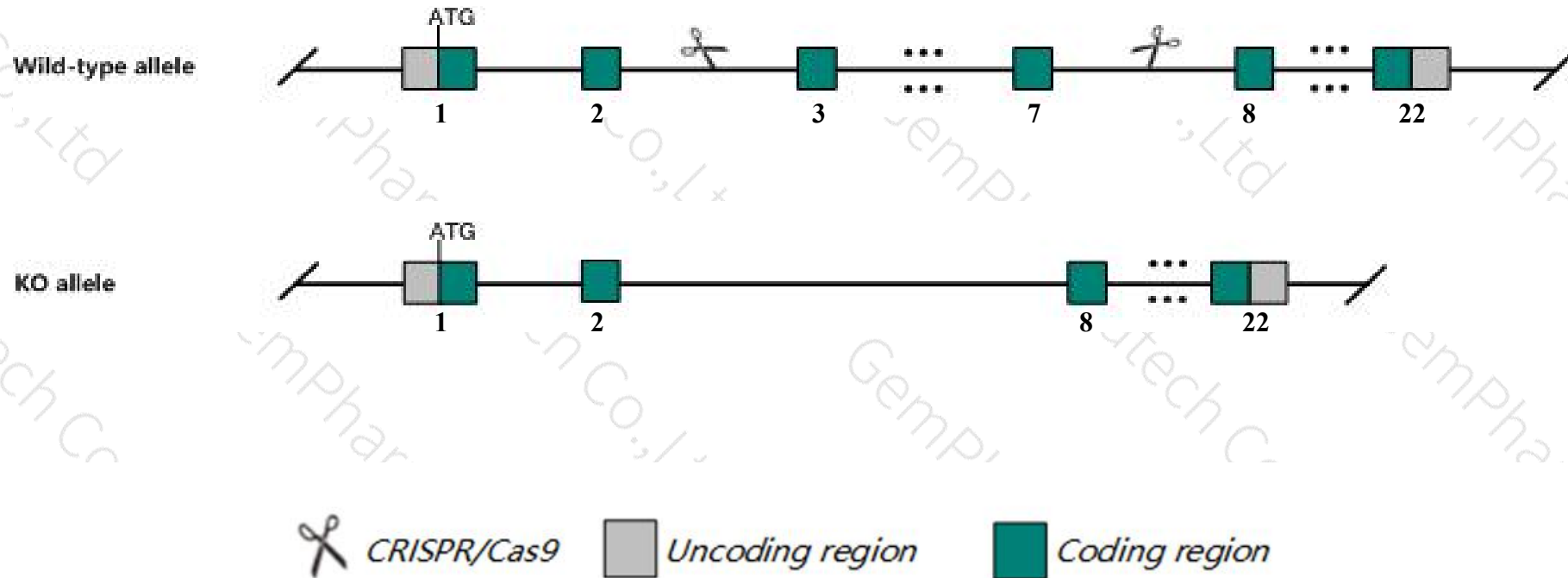
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Npr2* gene. The schematic diagram is as follows:



- The *Npr2* gene has 10 transcripts. According to the structure of *Npr2* gene, exon3-exon7 of *Npr2-201* (ENSMUST00000030191.14) transcript is recommended as the knockout region. The region contains 563bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Npr2* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mutations in this gene result in skeletal abnormalities, malocclusion, and reduced viability.
- The N-terminal of *Npr2* gene will remain 291aa, it may remain the partial function of *Npr2* gene.
- Transcript *Npr2*-206&207&209&210 may not be affected. And the effect on transcript *Npr2*-203&205 is unknown.
- *Gm12473* gene will be deleted together in the strategy.
- The *Npr2* 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 gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

# Gene information (NCBI)

## Npr2 natriuretic peptide receptor 2 [Mus musculus (house mouse)]

Gene ID: 230103, updated on 19-Feb-2019

### Summary



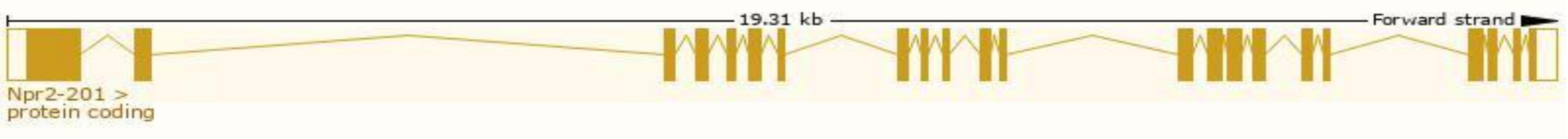
|                           |                                                                                                                                                                           |
|---------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Official Symbol</b>    | Npr2 provided by <a href="#">MGI</a>                                                                                                                                      |
| <b>Official Full Name</b> | natriuretic peptide receptor 2 provided by <a href="#">MGI</a>                                                                                                            |
| <b>Primary source</b>     | <a href="#">MGI:MGI:97372</a>                                                                                                                                             |
| <b>See related</b>        | <a href="#">Ensembl:ENSMUSG00000028469</a>                                                                                                                                |
| <b>Gene type</b>          | protein coding                                                                                                                                                            |
| <b>RefSeq status</b>      | VALIDATED                                                                                                                                                                 |
| <b>Organism</b>           | <a href="#">Mus musculus</a>                                                                                                                                              |
| <b>Lineage</b>            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| <b>Also known as</b>      | GC-B, GC-B2, GC-B3, cn, mNPR-B, pwe                                                                                                                                       |
| <b>Expression</b>         | Broad expression in ovary adult (RPKM 38.6), lung adult (RPKM 29.1) and 22 other tissues <a href="#">See more</a>                                                         |
| <b>Orthologs</b>          | <a href="#">human</a> <a href="#">all</a>                                                                                                                                 |

# Transcript information (Ensembl)

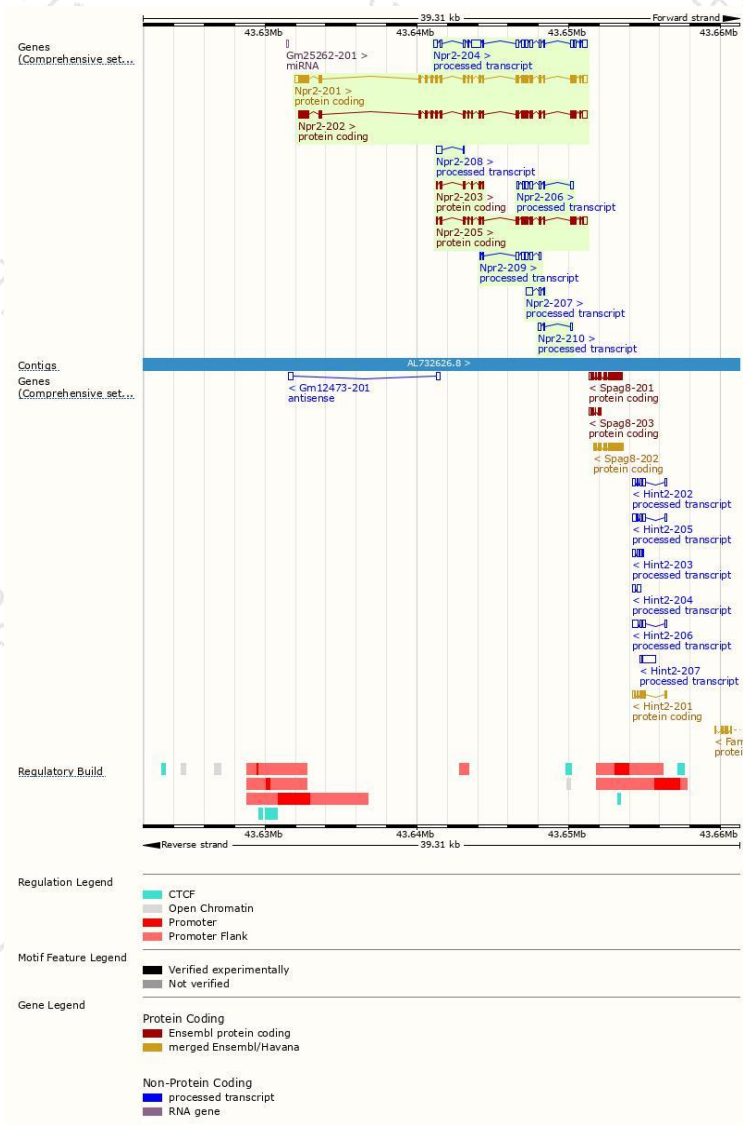
The gene has 10 transcripts,all transcripts are shown below:

| Name     | Transcript ID                         | bp   | Protein                | Biotype              | CCDS                      | UniProt                 | Flags                                                                                                                               |
|----------|---------------------------------------|------|------------------------|----------------------|---------------------------|-------------------------|-------------------------------------------------------------------------------------------------------------------------------------|
| Npr2-201 | <a href="#">ENSMUST00000030191.14</a> | 3660 | <a href="#">1047aa</a> | Protein coding       | <a href="#">CCDS18105</a> | <a href="#">Q6V VW5</a> | TSL:1 GENCODE basic APPRIS P1                                                                                                       |
| Npr2-202 | <a href="#">ENSMUST00000107874.8</a>  | 3480 | <a href="#">1033aa</a> | Protein coding       | -                         | <a href="#">B1A W17</a> | TSL:5 GENCODE basic                                                                                                                 |
| Npr2-205 | <a href="#">ENSMUST00000128549.2</a>  | 2106 | <a href="#">613aa</a>  | Protein coding       | -                         | <a href="#">F6Y T88</a> | CDS 5' incomplete TSL:1                                                                                                             |
| Npr2-203 | <a href="#">ENSMUST00000123351.7</a>  | 526  | <a href="#">176aa</a>  | Protein coding       | -                         | <a href="#">F6Y N80</a> | 5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5 |
| Npr2-204 | <a href="#">ENSMUST00000123883.7</a>  | 2669 | No protein             | Processed transcript | -                         | -                       | TSL:5                                                                                                                               |
| Npr2-206 | <a href="#">ENSMUST00000130093.7</a>  | 913  | No protein             | Processed transcript | -                         | -                       | TSL:5                                                                                                                               |
| Npr2-209 | <a href="#">ENSMUST00000145817.7</a>  | 871  | No protein             | Processed transcript | -                         | -                       | TSL:3                                                                                                                               |
| Npr2-207 | <a href="#">ENSMUST00000143160.1</a>  | 599  | No protein             | Processed transcript | -                         | -                       | TSL:3                                                                                                                               |
| Npr2-208 | <a href="#">ENSMUST00000144418.1</a>  | 424  | No protein             | Processed transcript | -                         | -                       | TSL:5                                                                                                                               |
| Npr2-210 | <a href="#">ENSMUST00000151603.1</a>  | 347  | No protein             | Processed transcript | -                         | -                       | TSL:5                                                                                                                               |

The strategy is based on the design of *Npr2-201* transcript,The transcription is shown below



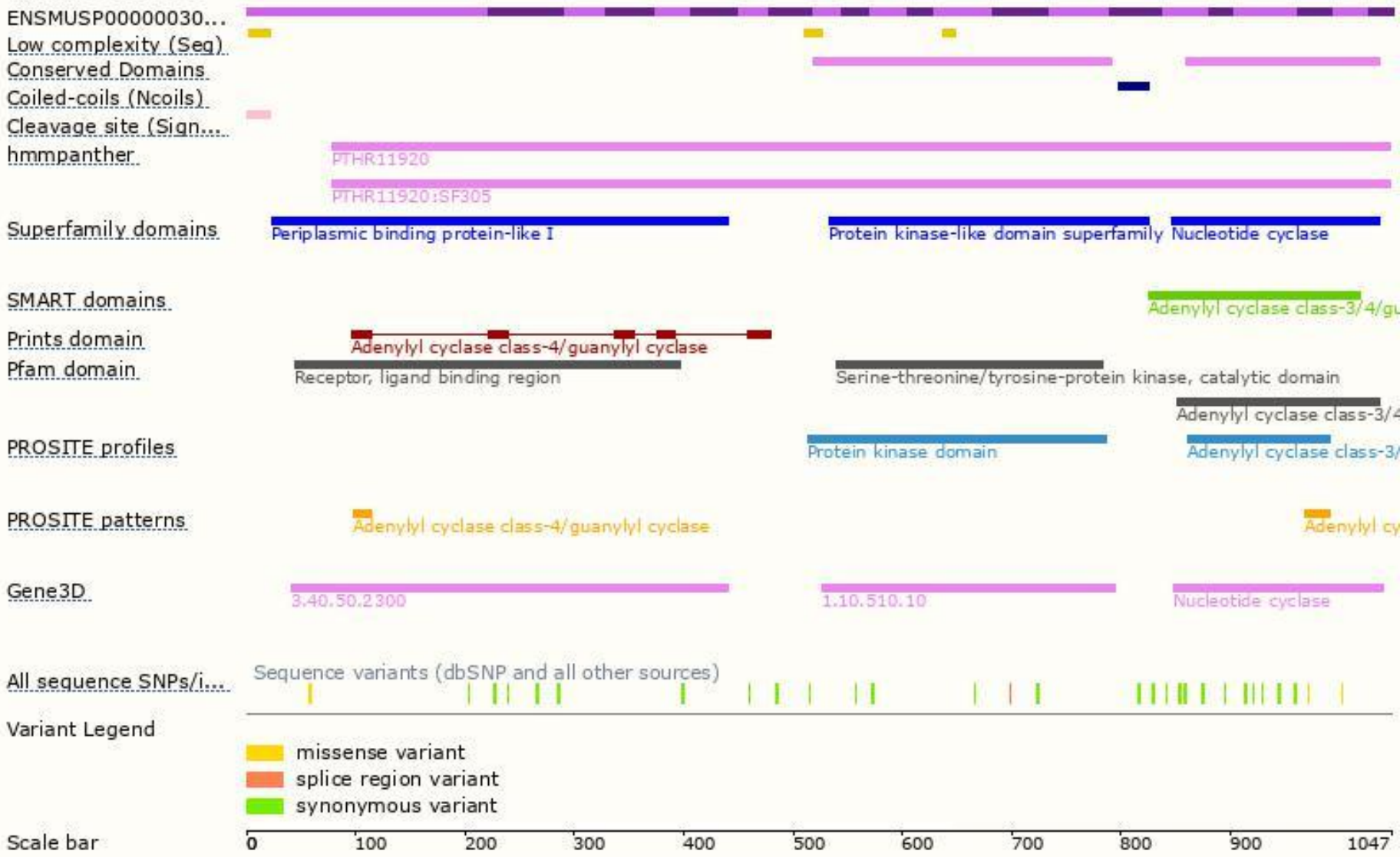
# Genomic location distribution



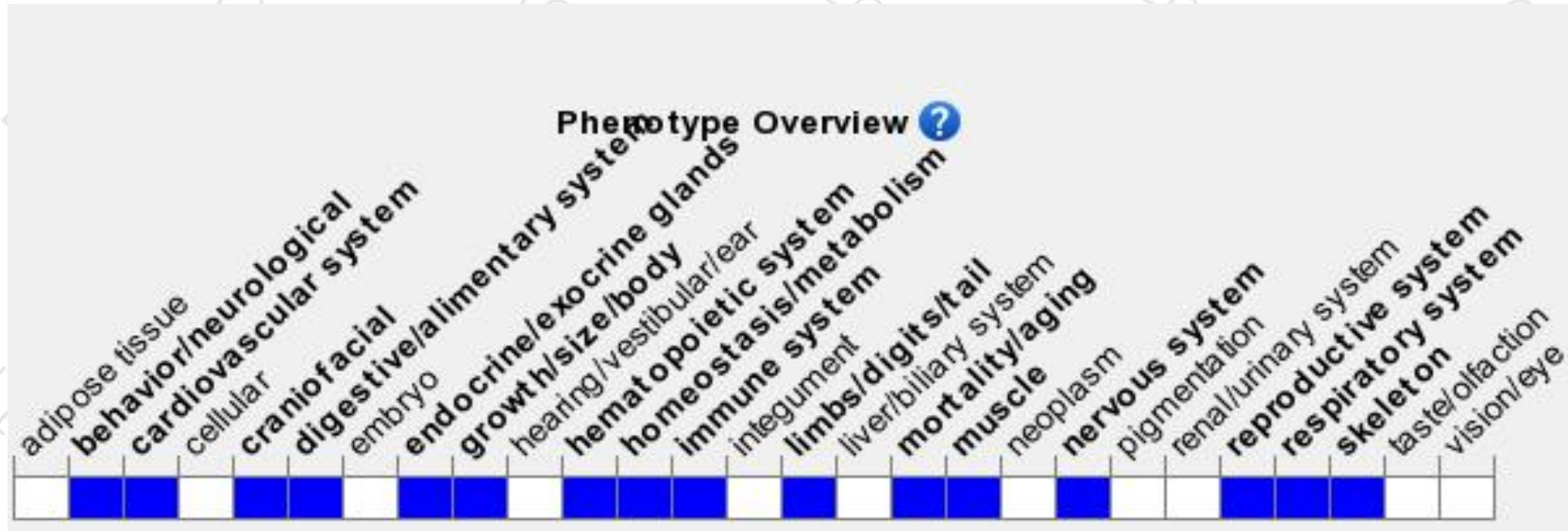
# Protein domain



集萃药康  
GemPharmatech



# 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, Mutations in this gene result in skeletal abnormalities, malocclusion, and reduced viability.

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

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