Npr2 Cas9-CKO Strategy

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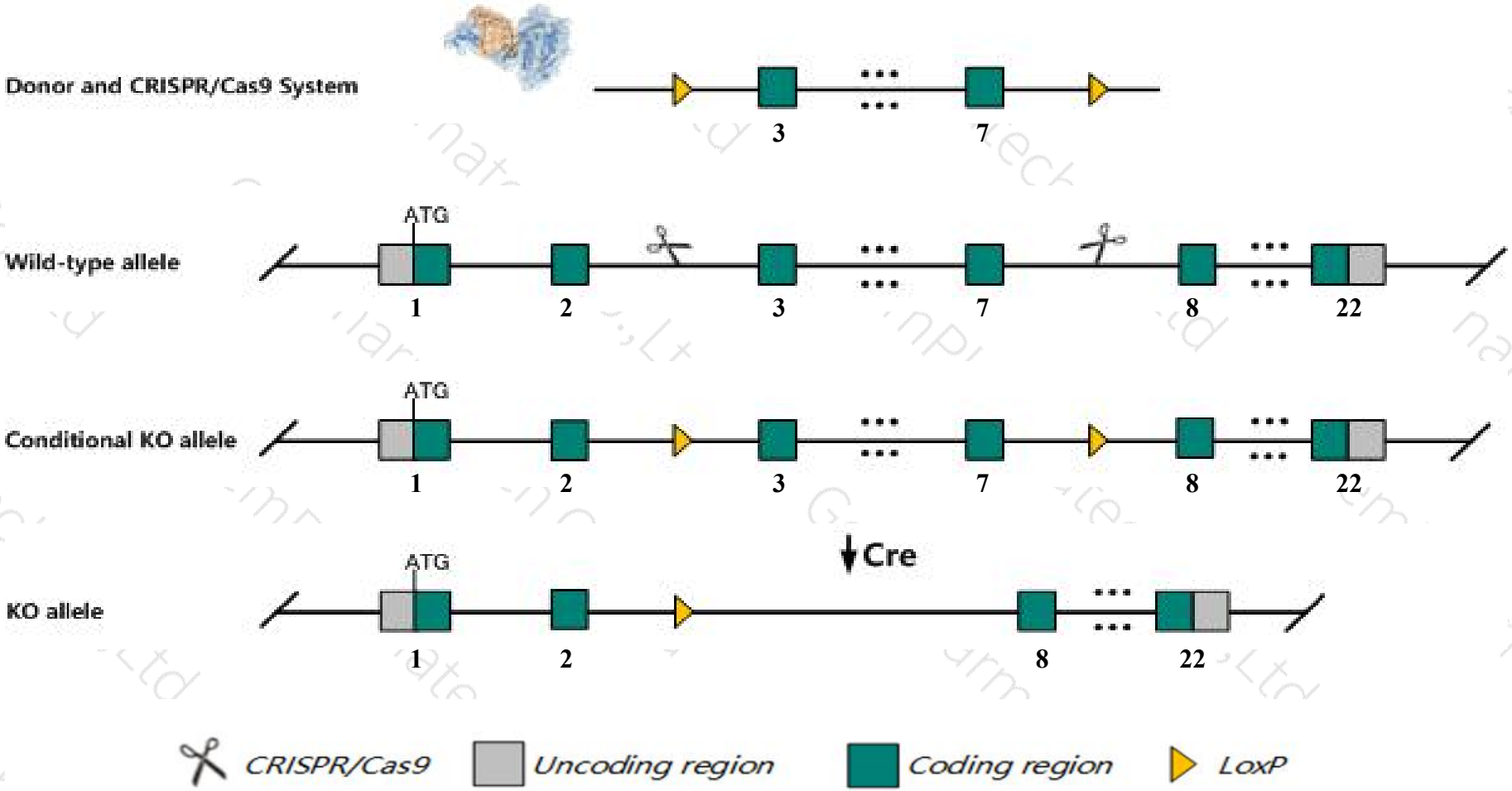
Project Overview

Project Name	***Npr2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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



Technical routes

- 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 and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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

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

Summary

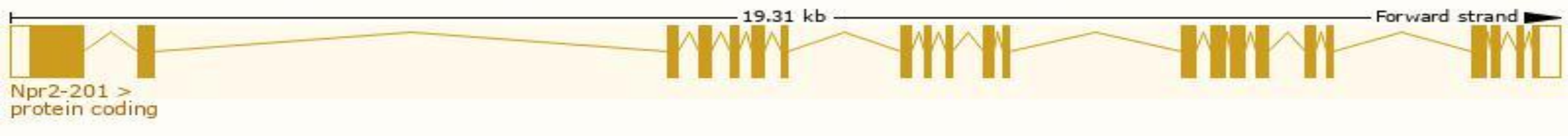
Official Symbol	Npr2 provided by MGI
Official Full Name	natriuretic peptide receptor 2 provided by MGI
Primary source	MGI:MGI:97372
See related	Ensembl:ENSMUSG00000028469
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;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

Transcript information（Ensembl）

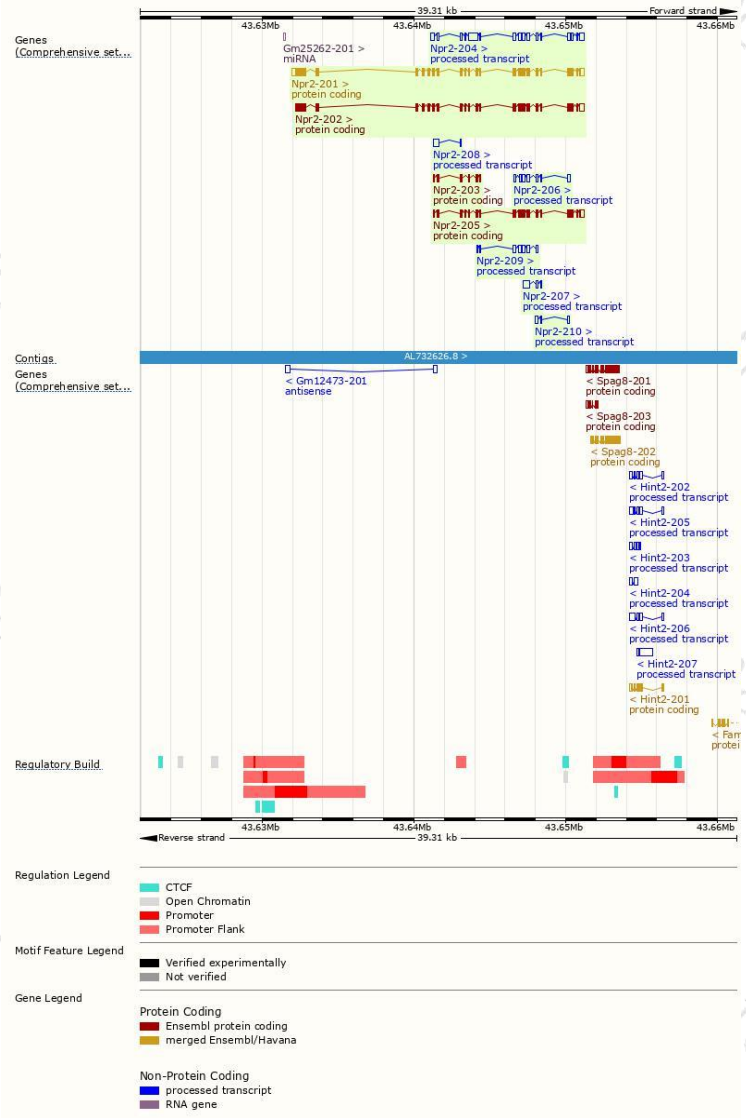
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Npr2-201	ENSMUST00000030191.14	3660	1047aa	Protein coding	CCDS18105	Q6VVW5	TSL:1 GENCODE basic APPRIS P1
Npr2-202	ENSMUST00000107874.8	3480	1033aa	Protein coding	-	B1AWI7	TSL:5 GENCODE basic
Npr2-205	ENSMUST00000128549.2	2106	613aa	Protein coding	-	F6YT88	CDS 5' incomplete TSL:1
Npr2-203	ENSMUST00000123351.7	526	176aa	Protein coding	-	F6YN80	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	ENSMUST00000123883.7	2669	No protein	Processed transcript	-	-	TSL:5
Npr2-206	ENSMUST00000130093.7	913	No protein	Processed transcript	-	-	TSL:5
Npr2-209	ENSMUST00000145817.7	871	No protein	Processed transcript	-	-	TSL:3
Npr2-207	ENSMUST00000143160.1	599	No protein	Processed transcript	-	-	TSL:3
Npr2-208	ENSMUST00000144418.1	424	No protein	Processed transcript	-	-	TSL:5
Npr2-210	ENSMUST00000151603.1	347	No protein	Processed transcript	-	-	TSL:5

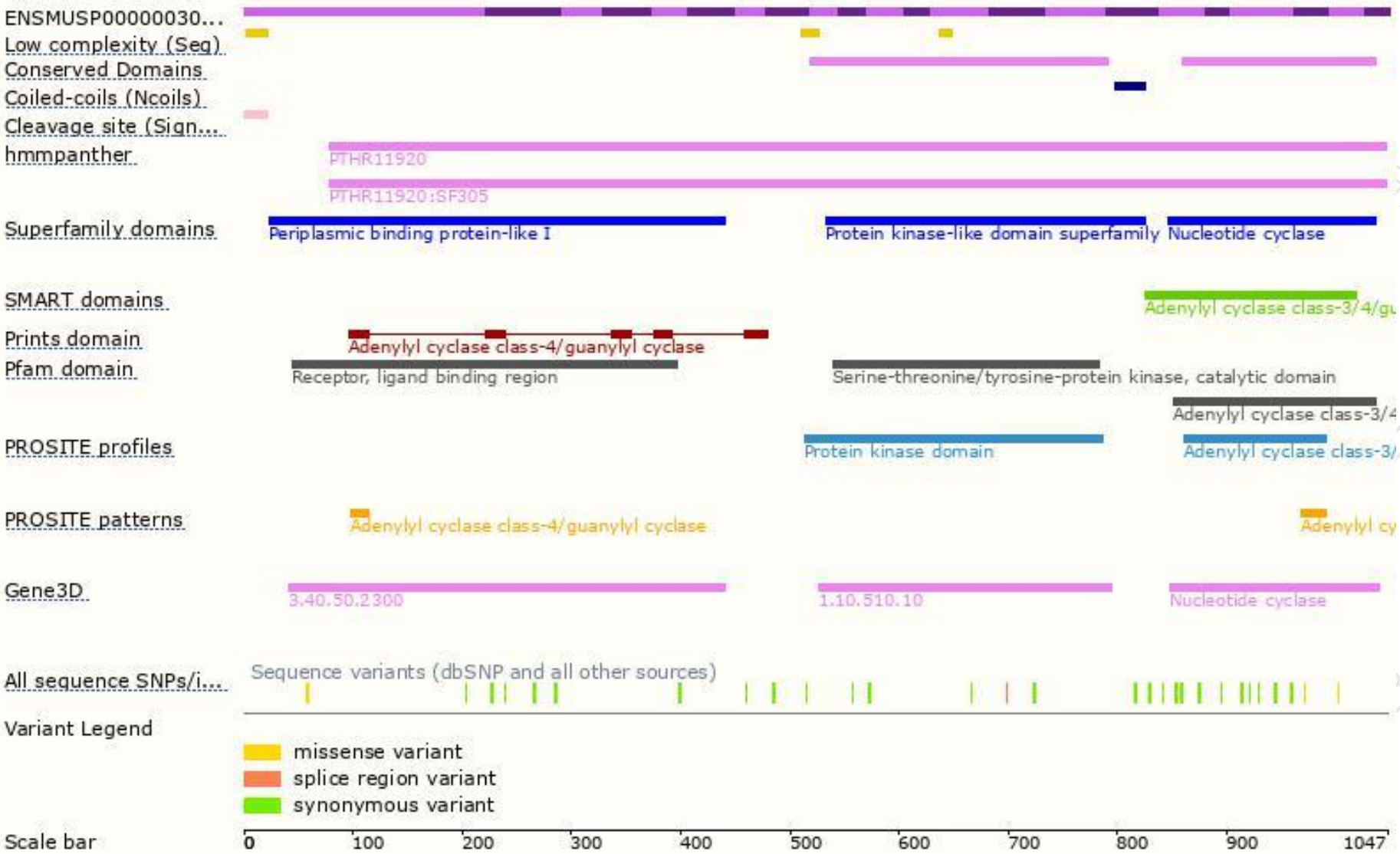
The strategy is based on the design of *Npr2-201* transcript,The transcription is shown below



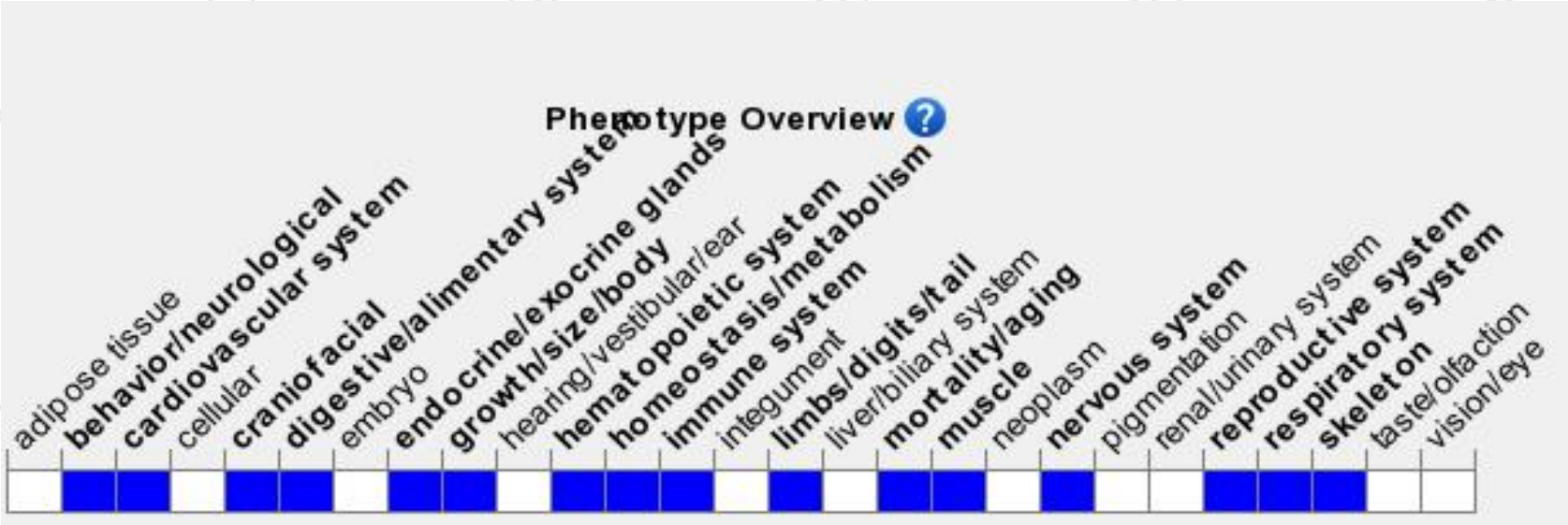
Genomic location distribution



Protein domain



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.

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

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