

Npr3 Cas9-KO Strategy

Designer:

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Project Overview

Project Name

Npr3

Project type

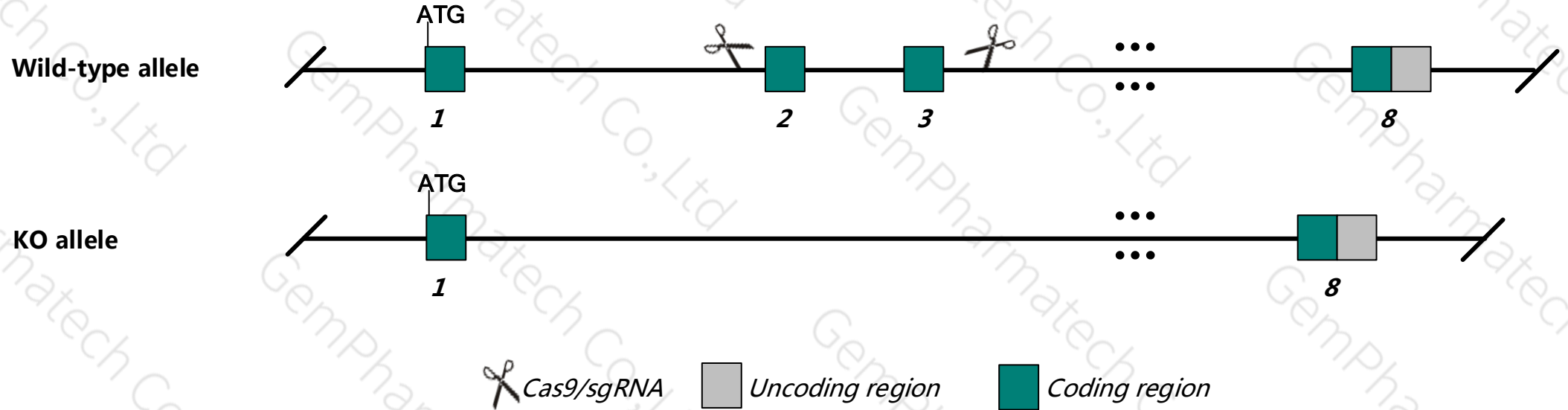
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Npr3* gene. The schematic diagram is as follows:



Technical routes

- The *Npr3* gene has 5 transcripts. According to the structure of *Npr3* gene, exon2-exon3 of *Npr3*-201 (ENSMUST00000066529.4) transcript is recommended as the knockout region. The region contains 290bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Npr3* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data , Homozygous inactivation of this gene leads to partial postnatal lethality, altered blood homeostasis, polyuria, hypovolemia, hypotension, increased bone turnover, skeletal deformities and altered adipose morphology. Spontaneous and ENU-induced mutations cause a skeletal-overgrowth phenotype.
- The *Npr3* gene is located on the Chr15. 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, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Npr3 natriuretic peptide receptor 3 [*Mus musculus* (house mouse)]

Gene ID: 18162, updated on 30-Apr-2019

Summary

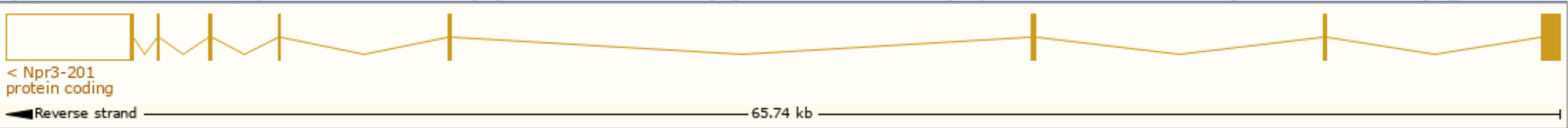
Official Symbol	Npr3 provided by MGI
Official Full Name	natriuretic peptide receptor 3 provided by MGI
Primary source	MGI:MGI:97373
See related	Ensembl:ENSMUSG00000022206
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Igj; EF-2; stri; ANP-C; NPR-C; ANPR-C
Expression	Biased expression in genital fat pad adult (RPKM 24.7), subcutaneous fat pad adult (RPKM 23.3) and 8 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

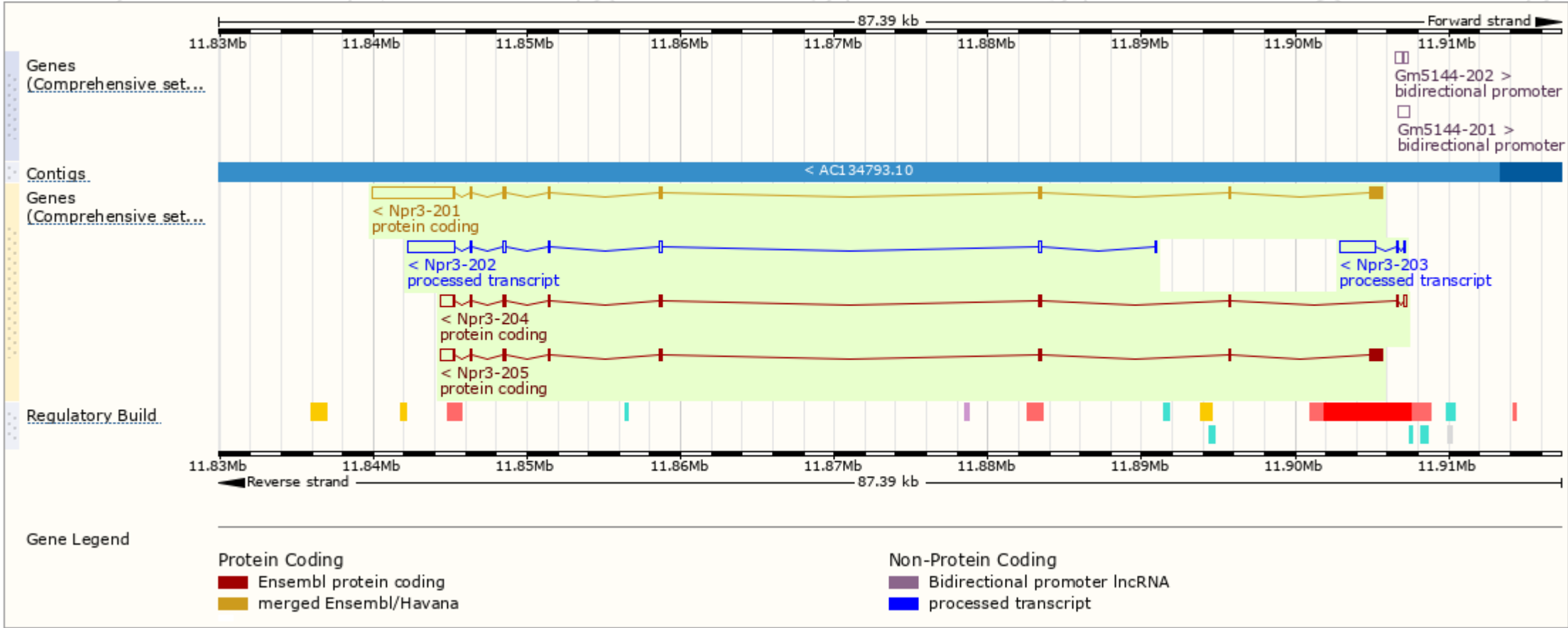
The gene has 5 transcripts, and all transcripts are shown below:

Show/hide columns (1 hidden)							Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
Npr3-201	ENSMUST00000066529.4	6892	536aa	Protein coding	CCDS27386	P70180	TSL:1	GENCODE basic APPRIS P2
Npr3-205	ENSMUST00000228603.1	2437	535aa	Protein coding	-	Q7TMG7	GENCODE basic	APPRIS ALT2
Npr3-204	ENSMUST00000228489.1	1969	281aa	Protein coding	-	A0A2I3BPR9	GENCODE basic	
Npr3-202	ENSMUST00000226139.1	3788	No protein	Processed transcript	-	-	-	
Npr3-203	ENSMUST00000226878.1	2533	No protein	Processed transcript	-	-	-	

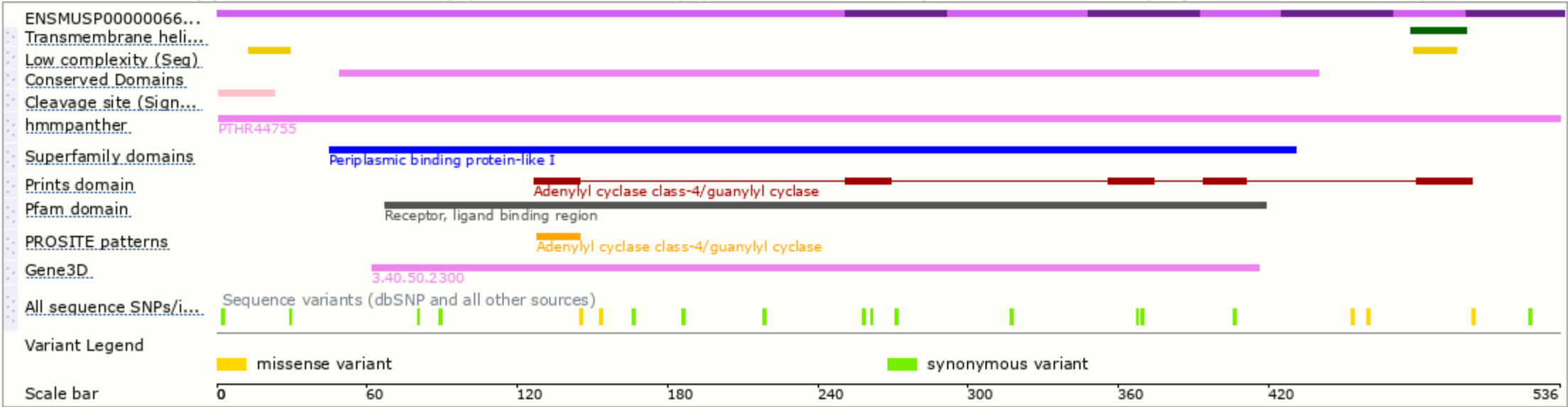
The strategy is based on the design of *Npr3-201* transcript,The transcription is shown below



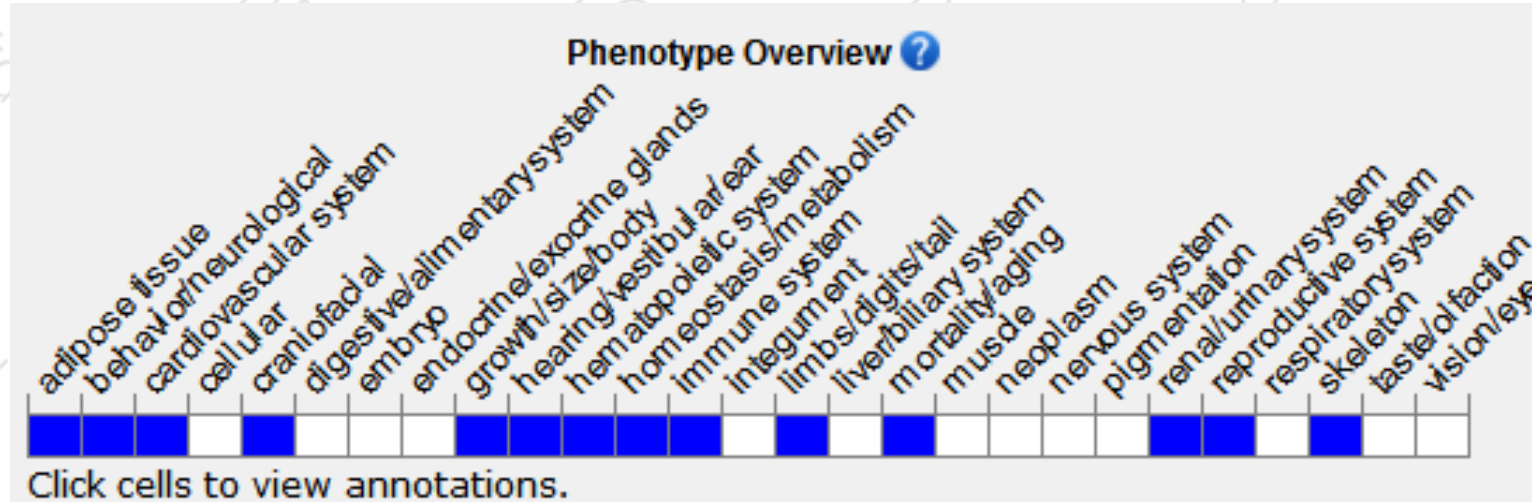
Genomic location distribution



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 inactivation of this gene leads to partial postnatal lethality, altered blood homeostasis, polyuria, hypovolemia, hypotension, increased bone turnover, skeletal deformities and altered adipose morphology. Spontaneous and ENU-induced mutations cause a skeletal-overgrowth phenotype.

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