

Nrg2 Cas9-KO Strategy

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Project Overview

Project Name

Nrg2

Project type

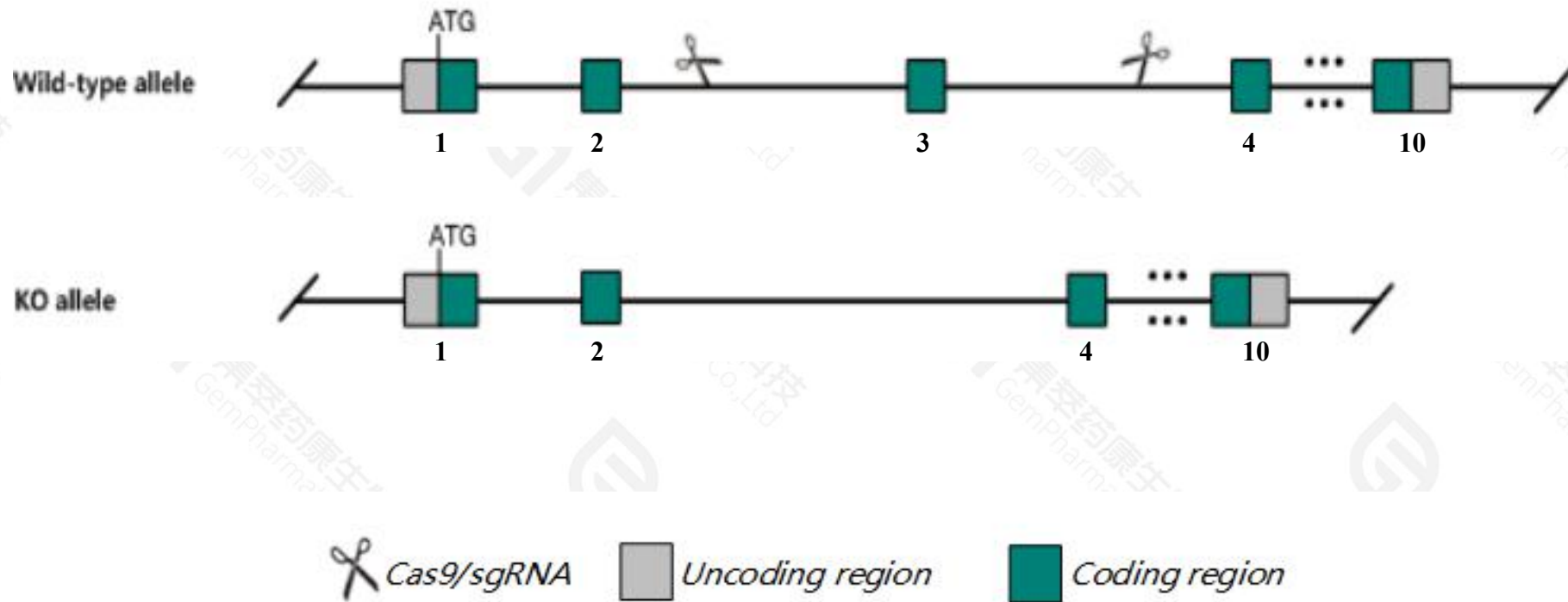
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nrg2* gene. The schematic diagram is as follows:



- The *Nrg2* gene has 6 transcripts. According to the structure of *Nrg2* gene, exon3 of *Nrg2*-203(ENSMUST00000115713.9) transcript is recommended as the knockout region. The region contains 119bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nrg2* 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, about one third of mice homozygous for a knock-out allele die prior to weaning in the absence of cardiac defects or other morphological abnormalities. Homozygotes display an early but transient postnatal growth deficit and reduced reproductive capacity.
- The *Nrg2* gene is located on the Chr18. 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)

Nrg2 neuregulin 2 [Mus musculus (house mouse)]

Gene ID: 100042150, updated on 9-Mar-2021

Summary



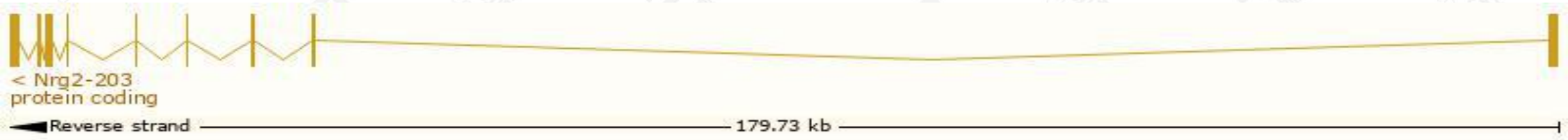
Official Symbol	Nrg2 provided by MGI
Official Full Name	neuregulin 2 provided by MGI
Primary source	MGI:MGI:1098246
See related	Ensembl:ENSMUSG00000060275
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Do, Don1, NT, NTAK
Expression	Broad expression in cerebellum adult (RPKM 3.5), ovary adult (RPKM 2.6) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

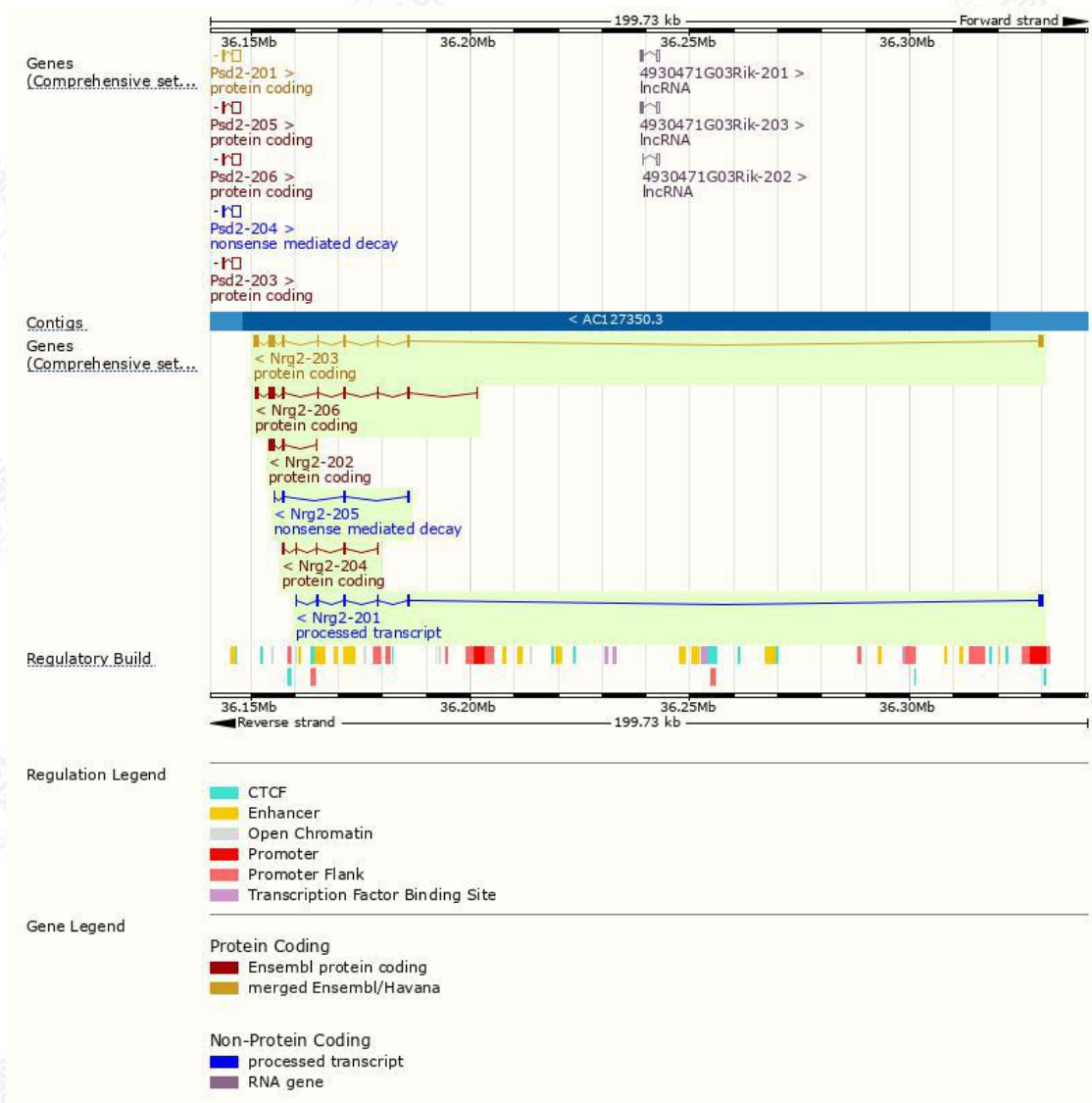
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nrg2-203	ENSMUST00000115713.9	3056	857aa	Protein coding	CCDS50255		TSL:5 , GENCODE basic , APPRIS P2 ,
Nrg2-206	ENSMUST00000239409.2	2017	643aa	Protein coding	-		GENCODE basic , APPRIS ALT2 ,
Nrg2-202	ENSMUST00000115712.10	630	210aa	Protein coding	-		CDS 5' and 3' incomplete , TSL:5 ,
Nrg2-204	ENSMUST00000225173.3	328	109aa	Protein coding	-		CDS 5' and 3' incomplete ,
Nrg2-205	ENSMUST00000237681.2	453	51aa	Nonsense mediated decay	-		CDS 5' incomplete ,
Nrg2-201	ENSMUST00000115705.2	899	No protein	Processed transcript	-		TSL:5 ,

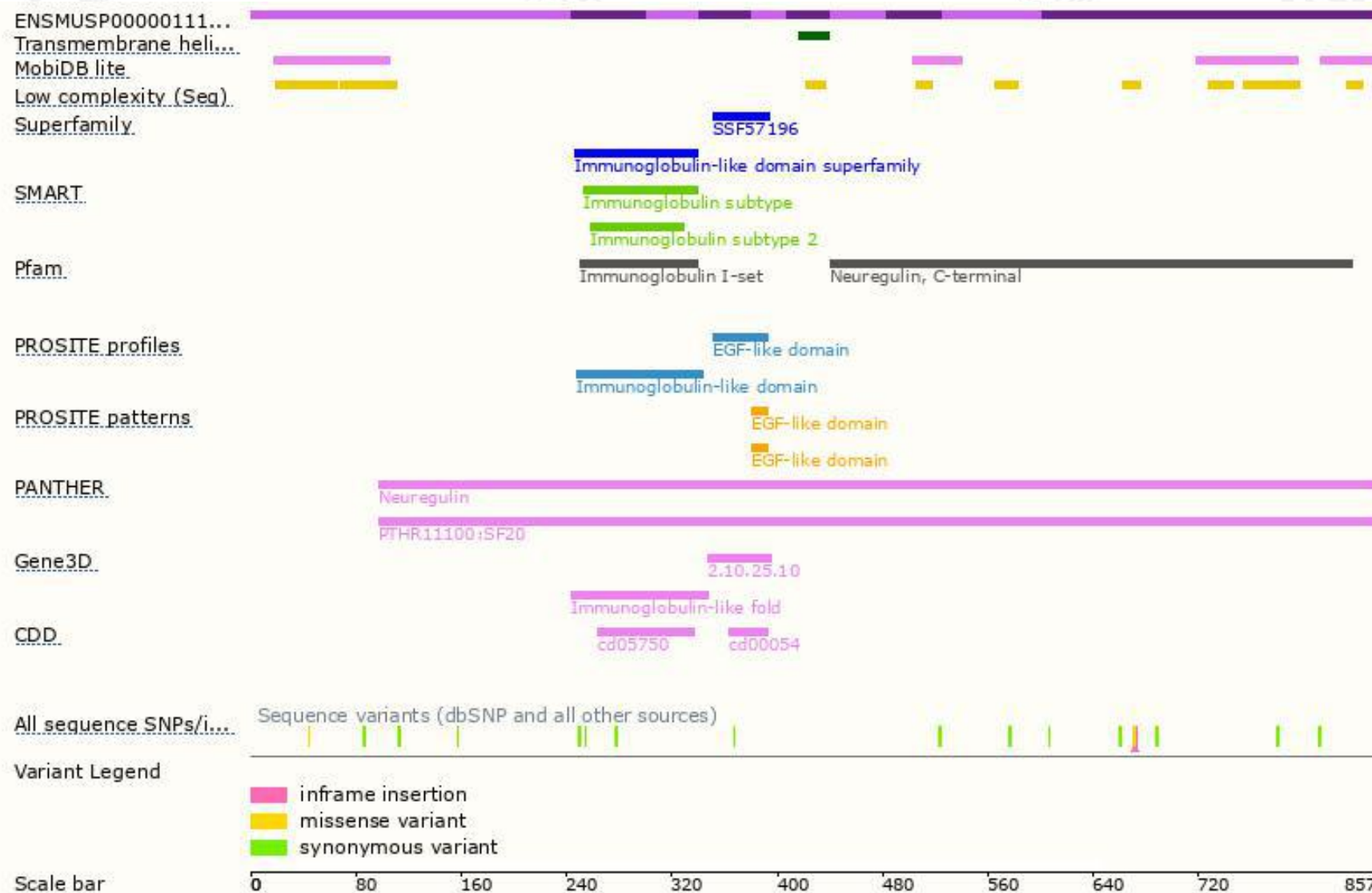
The strategy is based on the design of *Nrg2-203* transcript,the transcription is shown below:



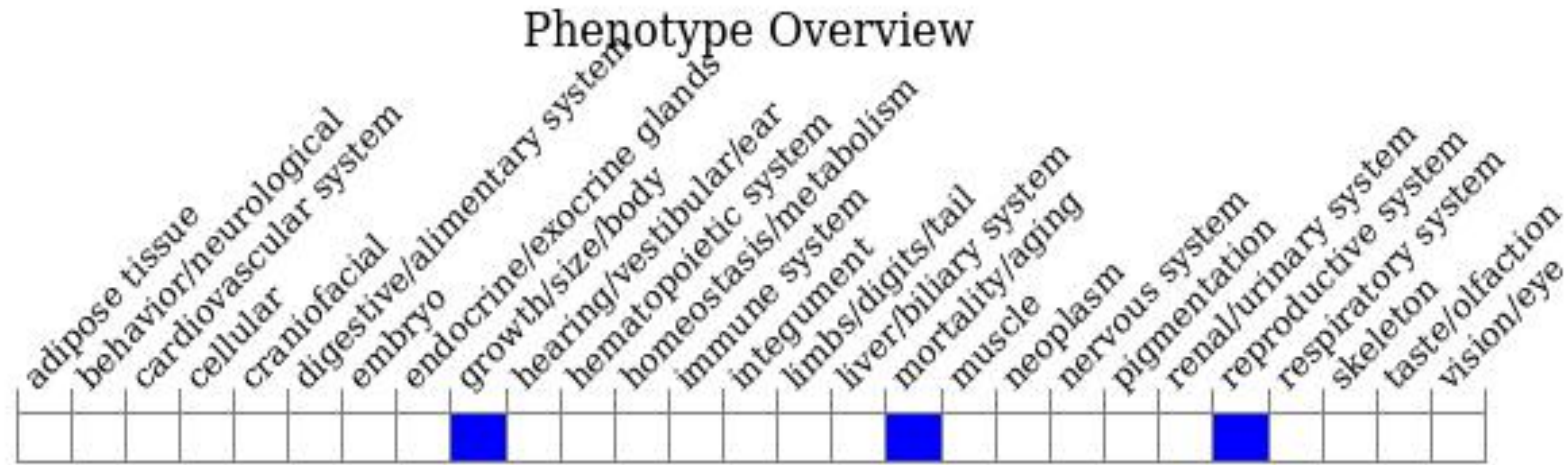
Genomic location distribution



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, about one third of mice homozygous for a knock-out allele die prior to weaning in the absence of cardiac defects or other morphological abnormalities. Homozygotes display an early but transient postnatal growth deficit and reduced reproductive capacity.

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

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