

# *Nrxn2* Cas9-KO Strategy

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**Reviewer: Daohu Xu**

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# Project Overview

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**Project Name**

*Nrxn2*

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**Project type**

**Cas9-KO**

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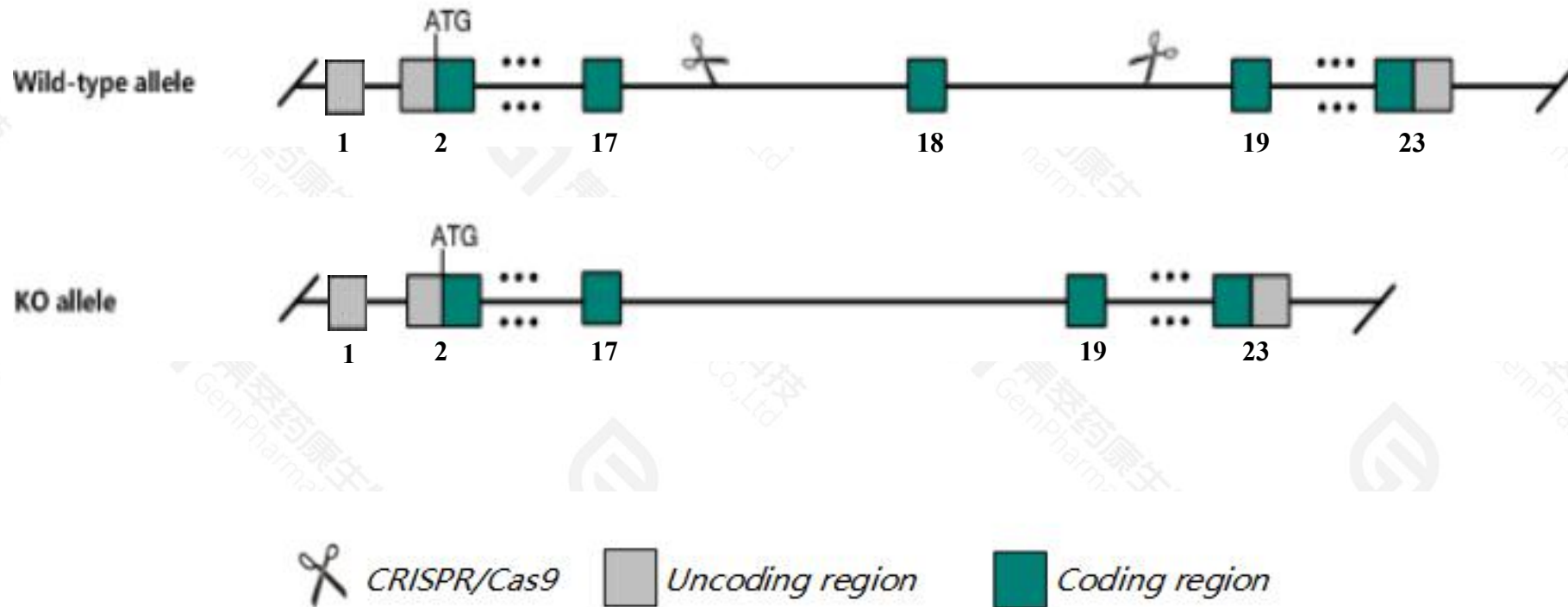
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nrxn2* gene. The schematic diagram is as follows:



- The *Nrxn2* gene has 18 transcripts. According to the structure of *Nrxn2* gene, exon18 of *Nrxn2*-205(ENSMUST00000113462.8) transcript is recommended as the knockout region. The region contains 182bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nrxn2* gene. The brief process is as follows: CRISPR/Cas9 system 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, mice homozygous for a knock-out allele are generally non-viable; surviving homozygotes show a 30-40% decrease in body weight and their inhibitory postsynaptic currents (IPSCs) are decreased in cortical slice cultures.
- The effect on *Nrxn2-209* transcript is unknown.
- The *Nrxn2* gene is located on the Chr19. 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.

## Nrxn2 neurexin II [Mus musculus (house mouse)]

Gene ID: 18190, updated on 25-Sep-2020

### Summary



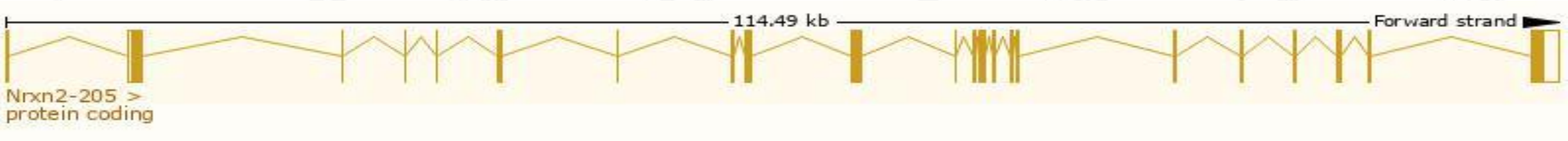
<b>Official Symbol</b>	Nrxn2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	neurexin II provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1096362</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000033768</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<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>	6430591O13Rik, mKIAA0921
<b>Expression</b>	Biased expression in cerebellum adult (RPKM 41.2), frontal lobe adult (RPKM 37.4) and 7 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

The gene has 18 transcripts,all transcripts are shown below:

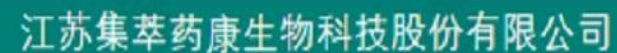
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nrxn2-205	<a href="#">ENSMUST00000113462.8</a>	6667	<a href="#">1703aa</a>	Protein coding	<a href="#">CCDS57132</a>		TSL:1 , GENCODE basic , APPRIS P4 ,
Nrxn2-201	<a href="#">ENSMUST00000077182.13</a>	6059	<a href="#">1503aa</a>	Protein coding	<a href="#">CCDS57133</a>		TSL:5 , GENCODE basic , APPRIS ALT2 ,
Nrxn2-216	<a href="#">ENSMUST00000235714.2</a>	5001	<a href="#">1503aa</a>	Protein coding	<a href="#">CCDS57133</a>		GENCODE basic , APPRIS ALT2 ,
Nrxn2-208	<a href="#">ENSMUST00000137166.8</a>	6314	<a href="#">1710aa</a>	Protein coding	-		TSL:5 , GENCODE basic ,
Nrxn2-204	<a href="#">ENSMUST00000113461.8</a>	5505	<a href="#">1640aa</a>	Protein coding	-		TSL:5 , GENCODE basic ,
Nrxn2-218	<a href="#">ENSMUST00000236635.2</a>	5118	<a href="#">1511aa</a>	Protein coding	-		GENCODE basic , APPRIS ALT2 ,
Nrxn2-202	<a href="#">ENSMUST00000113458.8</a>	3503	<a href="#">660aa</a>	Protein coding	-		TSL:5 , GENCODE basic ,
Nrxn2-203	<a href="#">ENSMUST00000113459.2</a>	3285	<a href="#">353aa</a>	Protein coding	-		TSL:2 , GENCODE basic ,
Nrxn2-209	<a href="#">ENSMUST00000137821.8</a>	648	<a href="#">216aa</a>	Protein coding	-		CDS 5' and 3' incomplete , TSL:3 ,
Nrxn2-206	<a href="#">ENSMUST00000124815.8</a>	818	No protein	Processed transcript	-		TSL:3 ,
Nrxn2-215	<a href="#">ENSMUST00000157014.8</a>	739	No protein	Processed transcript	-		TSL:3 ,
Nrxn2-217	<a href="#">ENSMUST00000236610.2</a>	725	No protein	Processed transcript	-		
Nrxn2-214	<a href="#">ENSMUST00000155158.3</a>	604	No protein	Processed transcript	-		TSL:5 ,
Nrxn2-213	<a href="#">ENSMUST00000154580.2</a>	576	No protein	Processed transcript	-		TSL:3 ,
Nrxn2-211	<a href="#">ENSMUST00000148391.2</a>	547	No protein	Processed transcript	-		TSL:5 ,
Nrxn2-207	<a href="#">ENSMUST00000128272.8</a>	4456	No protein	Retained intron	-		TSL:1 ,
Nrxn2-212	<a href="#">ENSMUST00000150792.8</a>	2748	No protein	Retained intron	-		TSL:5 ,
Nrxn2-210	<a href="#">ENSMUST00000140435.2</a>	1933	No protein	Retained intron	-		TSL:1 ,

The strategy is based on the design of *Nrxn2-205* transcript,the transcription is shown below:

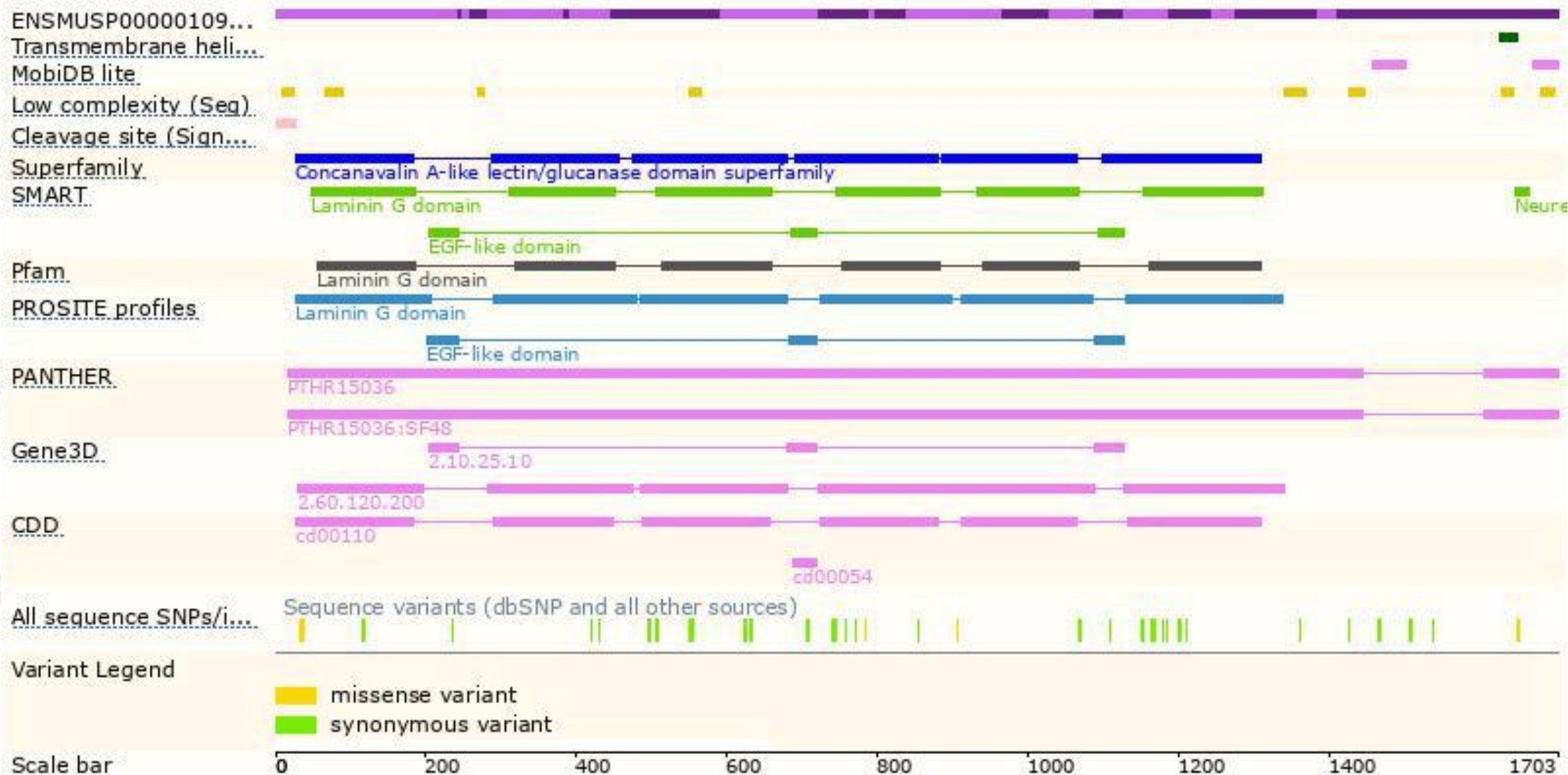




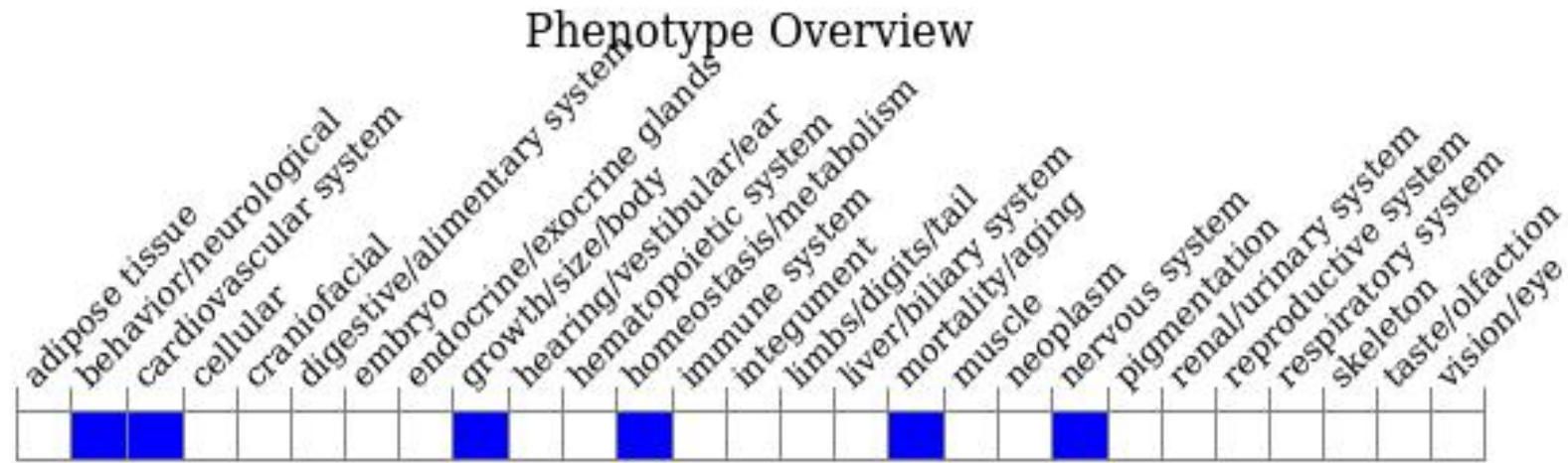
集萃药康  
GemPharmatech



# 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, mice homozygous for a knock-out allele are generally non-viable; surviving homozygotes show a 30-40% decrease in body weight and their inhibitory postsynaptic currents (IPSCs) are decreased in cortical slice cultures.

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