

# *Nrcam* Cas9-KO Strategy

**Designer:**

**Yang Zeng**

**Reviewer:**

**Xiaojing Li**

**Design Date:**

**2019-11-26**

# Project Overview

**Project Name**

*Nrcam*

**Project type**

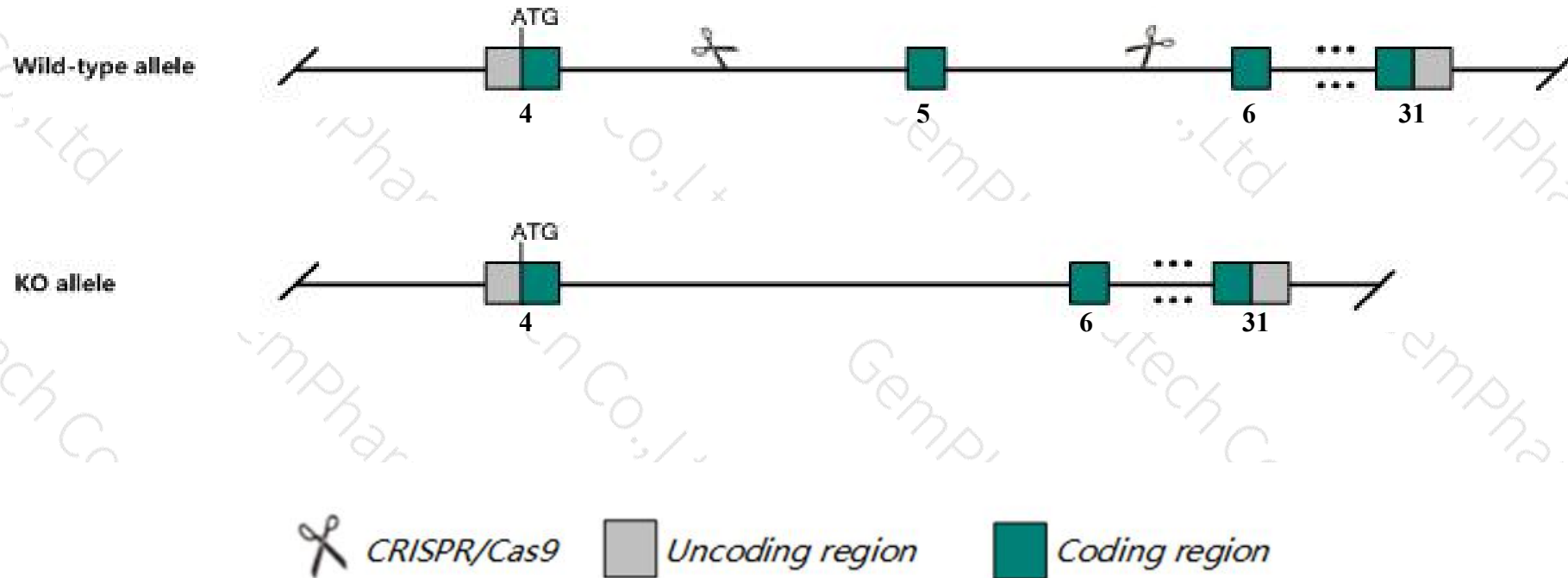
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Nrcam* gene has 17 transcripts. According to the structure of *Nrcam* gene, exon5 of *Nrcam-201* (ENSMUST00000020939.15) transcript is recommended as the knockout region. The region contains 106bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nrcam* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for targeted null mutations exhibit disorganization of lens fibers, cellular disintegration, and accumulation of cellular debris resulting in cataracts. Mutants show mild reductions in cerebellar lobe size.
- Transcript *Nrcam*-205/214 CDS are incomplete, whether they will be affected is unknown.
- The *Nrcam* gene is located on the Chr12. 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.



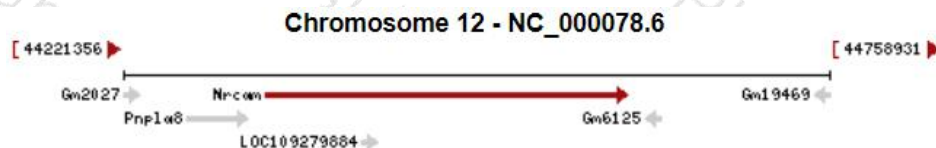
# Gene information (NCBI)

## Nrcam neuronal cell adhesion molecule [ *Mus musculus* (house mouse) ]

Gene ID: 319504, updated on 12-Aug-2019

### Summary

<b>Official Symbol</b>	Nrcam provided by MGI
<b>Official Full Name</b>	neuronal cell adhesion molecule provided by MGI
<b>Primary source</b>	MGI:MGI:104750
<b>See related</b>	Ensembl:ENSMUSG00000020598
<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>	Bravo; mKIAA0343; C030017F07Rik; C130076O07Rik
<b>Expression</b>	Biased expression in cortex adult (RPKM 15.8), frontal lobe adult (RPKM 14.8) and 6 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

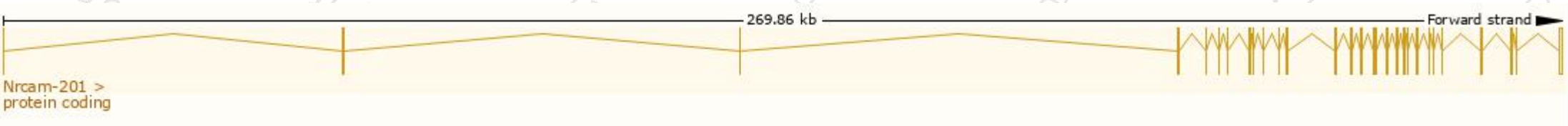


# Transcript information (Ensembl)

The gene has 17 transcripts,all transcripts are shown below:

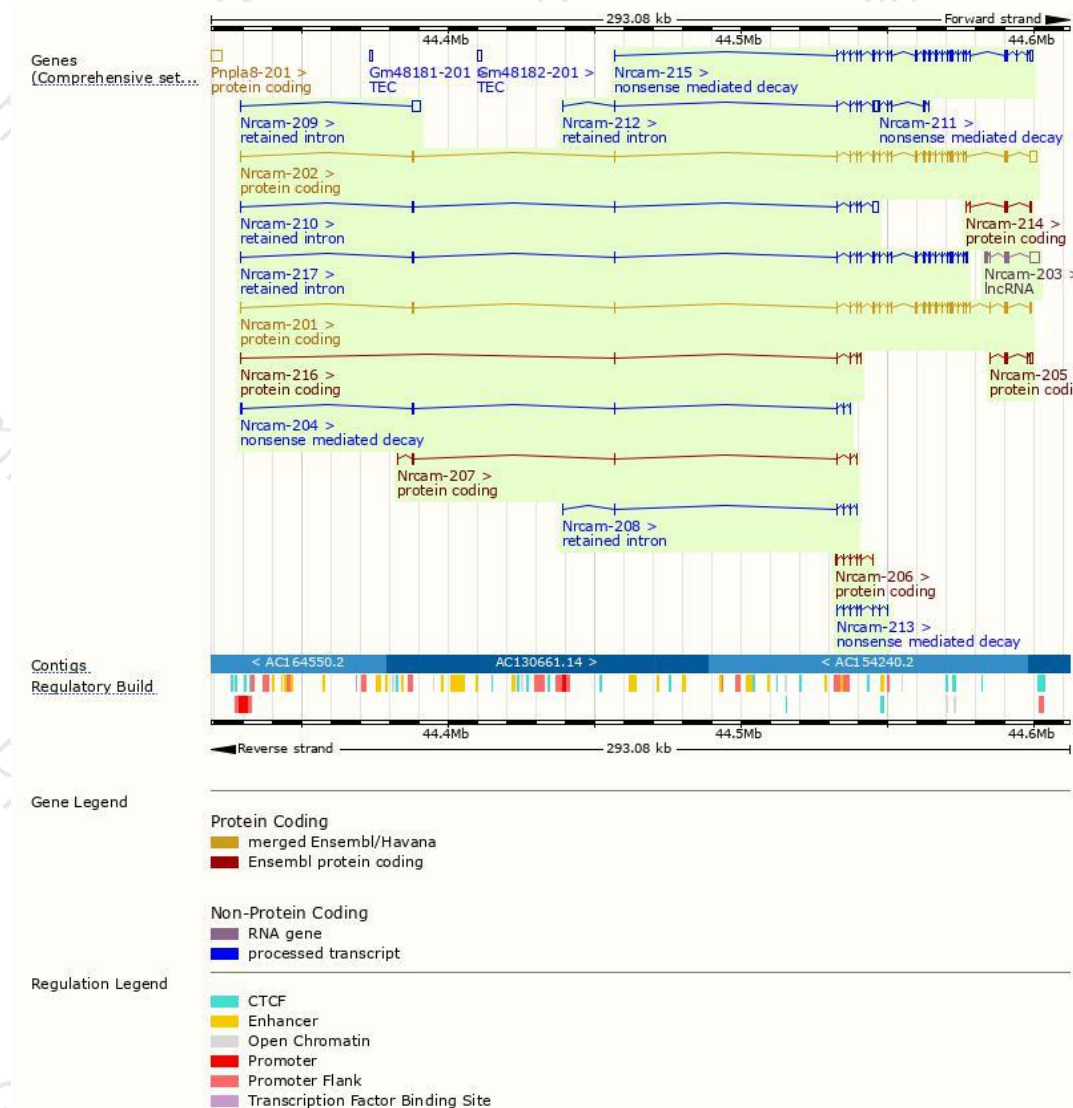
Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Nrcam-202	<a href="#">ENSMUST00000110748.3</a>	6275	<a href="#">1186aa</a>	<a href="#">ENSMUSP00000106376.2</a>	Protein coding	<a href="#">CCDS49057</a>	<a href="#">Q810U4</a>	TSL:1 GENCODE basic APPRIS P1
Nrcam-201	<a href="#">ENSMUST0000020939.15</a>	4469	<a href="#">1256aa</a>	<a href="#">ENSMUSP0000020939.8</a>	Protein coding	<a href="#">CCDS49056</a>	<a href="#">Q810U4</a>	TSL:1 GENCODE basic
Nrcam-205	<a href="#">ENSMUST00000218062.1</a>	1586	<a href="#">168aa</a>	<a href="#">ENSMUSP00000151475.1</a>	Protein coding	-	<a href="#">A0A1W2P6Z1</a>	CDS 5' incomplete TSL:1
Nrcam-214	<a href="#">ENSMUST00000220082.1</a>	916	<a href="#">220aa</a>	<a href="#">ENSMUSP00000151824.1</a>	Protein coding	-	<a href="#">A0A1W2P7X4</a>	CDS 5' incomplete TSL:1
Nrcam-206	<a href="#">ENSMUST00000218431.1</a>	823	<a href="#">232aa</a>	<a href="#">ENSMUSP00000151873.1</a>	Protein coding	-	<a href="#">A0A1W2P814</a>	CDS 3' incomplete TSL:3
Nrcam-216	<a href="#">ENSMUST00000220126.1</a>	736	<a href="#">175aa</a>	<a href="#">ENSMUSP00000151296.1</a>	Protein coding	-	<a href="#">A0A1W2P6P3</a>	CDS 3' incomplete TSL:5
Nrcam-207	<a href="#">ENSMUST00000218540.1</a>	625	<a href="#">81aa</a>	<a href="#">ENSMUSP00000151732.1</a>	Protein coding	-	<a href="#">A0A1W2P7R6</a>	CDS 3' incomplete TSL:3
Nrcam-215	<a href="#">ENSMUST00000220123.1</a>	4943	<a href="#">1134aa</a>	<a href="#">ENSMUSP00000151844.1</a>	Nonsense mediated decay	-	<a href="#">A0A1W2P7Y9</a>	TSL:1
Nrcam-213	<a href="#">ENSMUST00000219939.1</a>	939	<a href="#">30aa</a>	<a href="#">ENSMUSP00000152002.1</a>	Nonsense mediated decay	-	<a href="#">A0A1W2P8F5</a>	CDS 5' incomplete TSL:5
Nrcam-204	<a href="#">ENSMUST00000217907.1</a>	682	<a href="#">59aa</a>	<a href="#">ENSMUSP00000151419.1</a>	Nonsense mediated decay	-	<a href="#">A0A1W2P6V1</a>	CDS 5' incomplete TSL:5
Nrcam-211	<a href="#">ENSMUST00000219906.1</a>	546	<a href="#">41aa</a>	<a href="#">ENSMUSP00000151243.1</a>	Nonsense mediated decay	-	<a href="#">A0A1W2P6F8</a>	CDS 5' incomplete TSL:3
Nrcam-217	<a href="#">ENSMUST00000220130.1</a>	4176	No protein	-	Retained intron	-	-	TSL:1
Nrcam-210	<a href="#">ENSMUST00000219592.1</a>	3159	No protein	-	Retained intron	-	-	TSL:5
Nrcam-209	<a href="#">ENSMUST00000218940.1</a>	2610	No protein	-	Retained intron	-	-	TSL:1
Nrcam-212	<a href="#">ENSMUST00000219928.1</a>	2433	No protein	-	Retained intron	-	-	TSL:2
Nrcam-208	<a href="#">ENSMUST00000218805.1</a>	677	No protein	-	Retained intron	-	-	TSL:3
Nrcam-203	<a href="#">ENSMUST00000217796.1</a>	4487	No protein	-	lncRNA	-	-	TSL:5

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





# Genomic location distribution

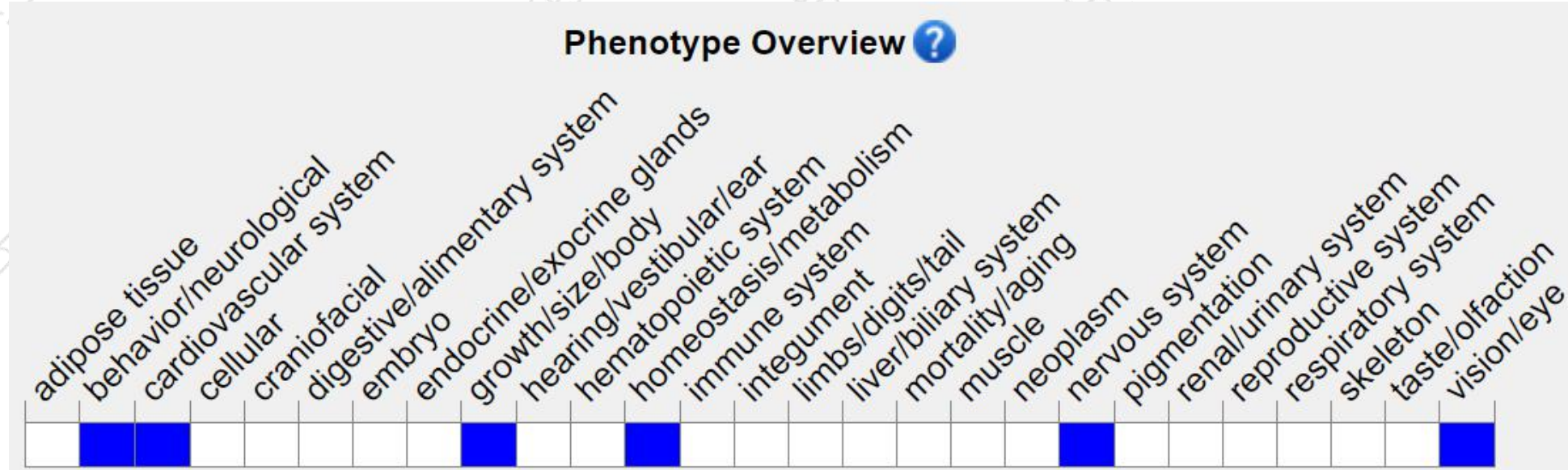




# Protein domain



# 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, Homozygotes for targeted null mutations exhibit disorganization of lens fibers, cellular disintegration, and accumulation of cellular debris resulting in cataracts. Mutants show mild reductions in cerebellar lobe size.

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

Tel: 400-9660890

