

# *Ncam2* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Ncam2*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ncam2* gene. The schematic diagram is as follows:



- The *Ncam2* gene has 4 transcripts. According to the structure of *Ncam2* gene, exon2-exon6 of *Ncam2-202* (ENSMUST00000067602.4) transcript is recommended as the knockout region. The region contains 682bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ncam2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, A gene trap insertion into an intron of this gene results in no obvious phenotype. Mice homozygous for a knock-out allele exhibit increased proliferation rate and clonogenic frequency in spinal cord-derived neurospheres.
- The *Ncam2* gene is located on the Chr16. 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)

## Ncam2 neural cell adhesion molecule 2 [Mus musculus (house mouse)]

Gene ID: 17968, updated on 31-Jan-2019

### Summary



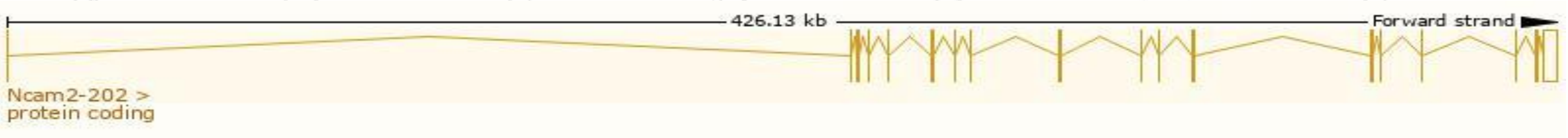
<b>Official Symbol</b>	Ncam2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	neural cell adhesion molecule 2 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:97282</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000022762</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	Ncam-2, Ocam, RNCAM
<b>Expression</b>	Biased expression in cortex adult (RPKM 3.2), frontal lobe adult (RPKM 3.0) and 6 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

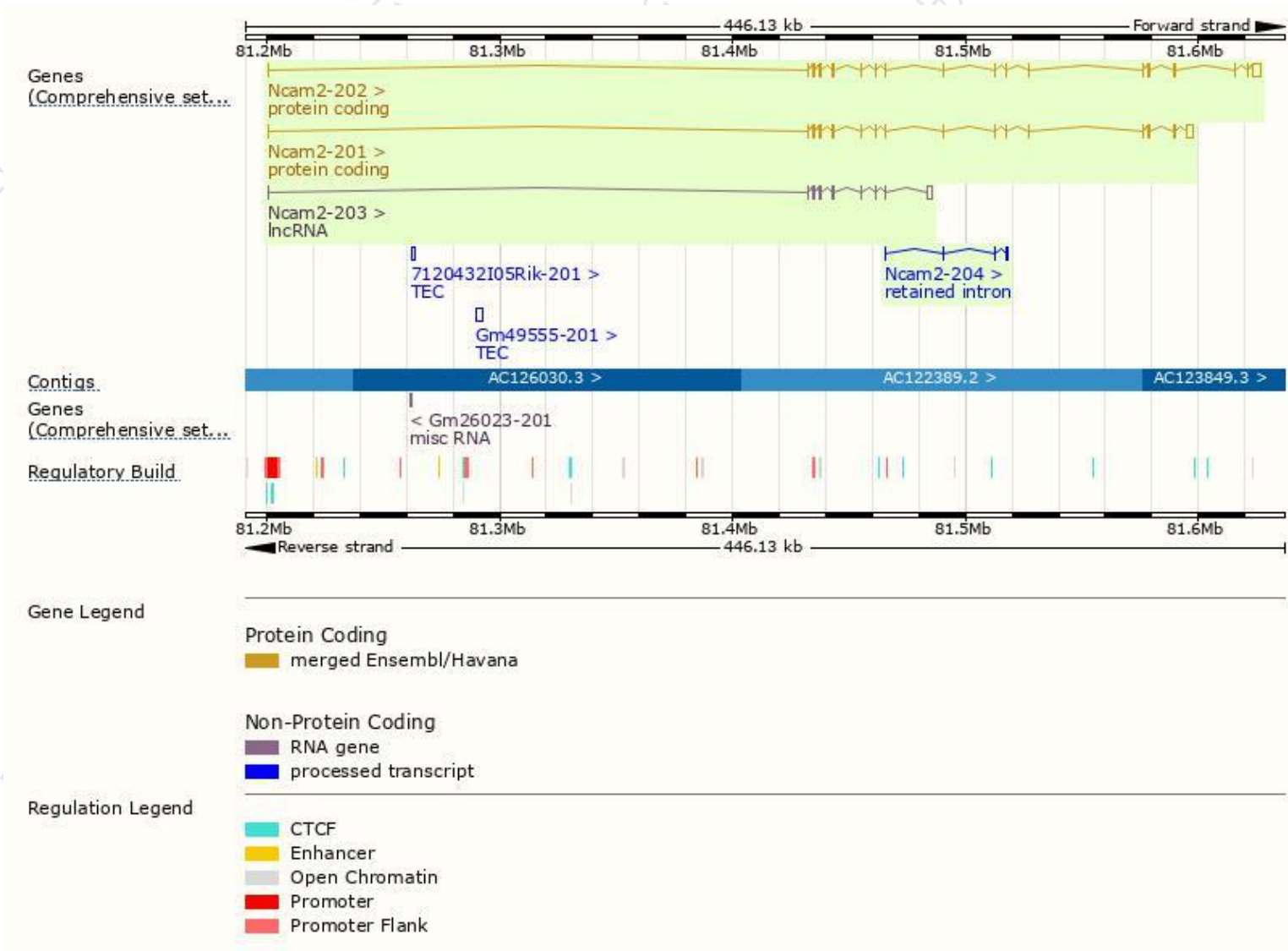
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ncam2-202	<a href="#">ENSMUST00000067602.4</a>	6106	<a href="#">837aa</a>	Protein coding	<a href="#">CCDS49888</a>	<a href="#">Q35136</a>	TSL:1 GENCODE basic APPRIS ALT2
Ncam2-201	<a href="#">ENSMUST00000037785.13</a>	4893	<a href="#">727aa</a>	Protein coding	<a href="#">CCDS28281</a>	<a href="#">Q35136</a>	TSL:1 GENCODE basic APPRIS P3
Ncam2-204	<a href="#">ENSMUST00000232550.1</a>	931	No protein	Retained intron	-	-	
Ncam2-203	<a href="#">ENSMUST00000231687.1</a>	3413	No protein	lncRNA	-	-	

The strategy is based on the design of *Ncam2-202* transcript,The transcription is shown below

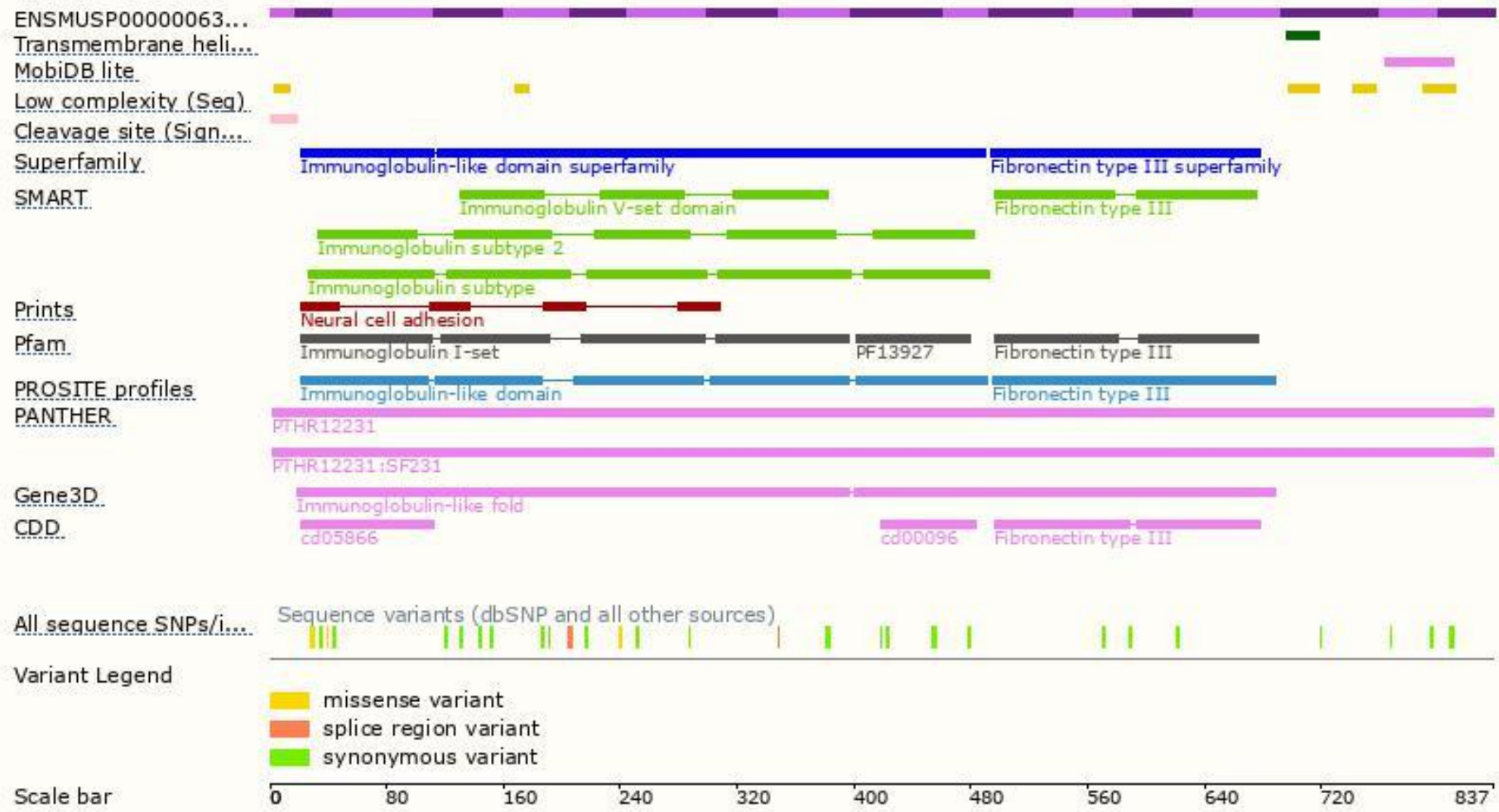


# Genomic location distribution

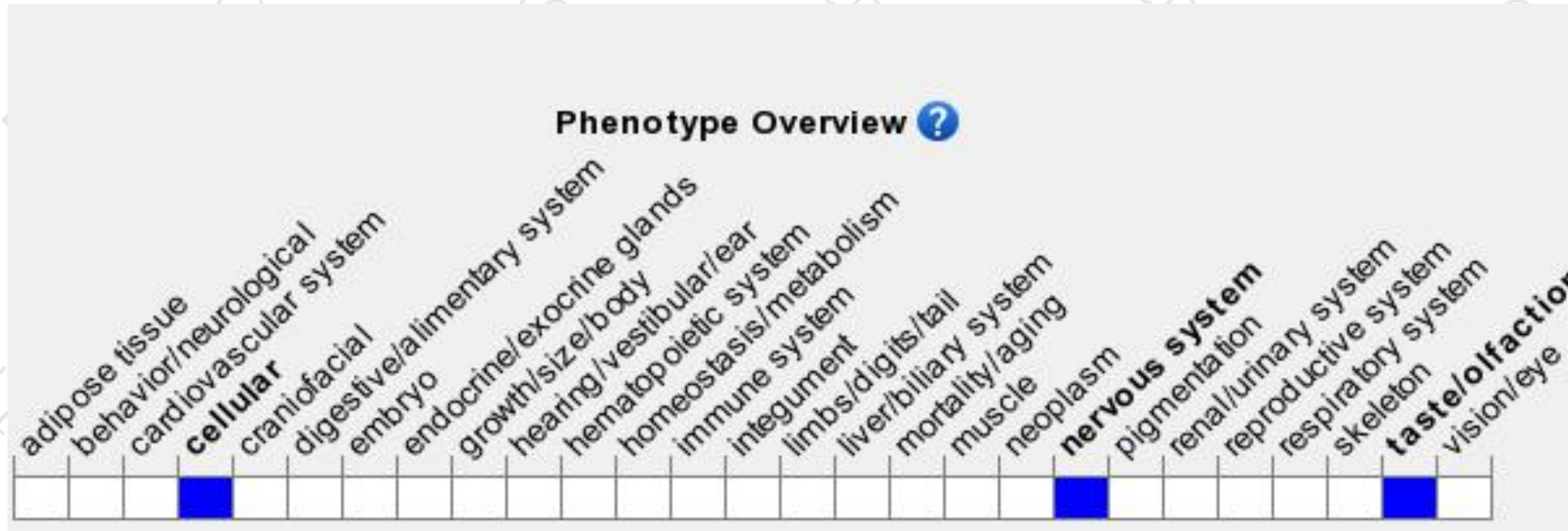




# Protein domain



# 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, A gene trap insertion into an intron of this gene results in no obvious phenotype.

Mice homozygous for a knock-out allele exhibit increased proliferation rate and clonogenic frequency in spinal cord-derived neurospheres.

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

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