

# *Ncam1* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview



**Project Name**

***Ncam1***

**Project type**

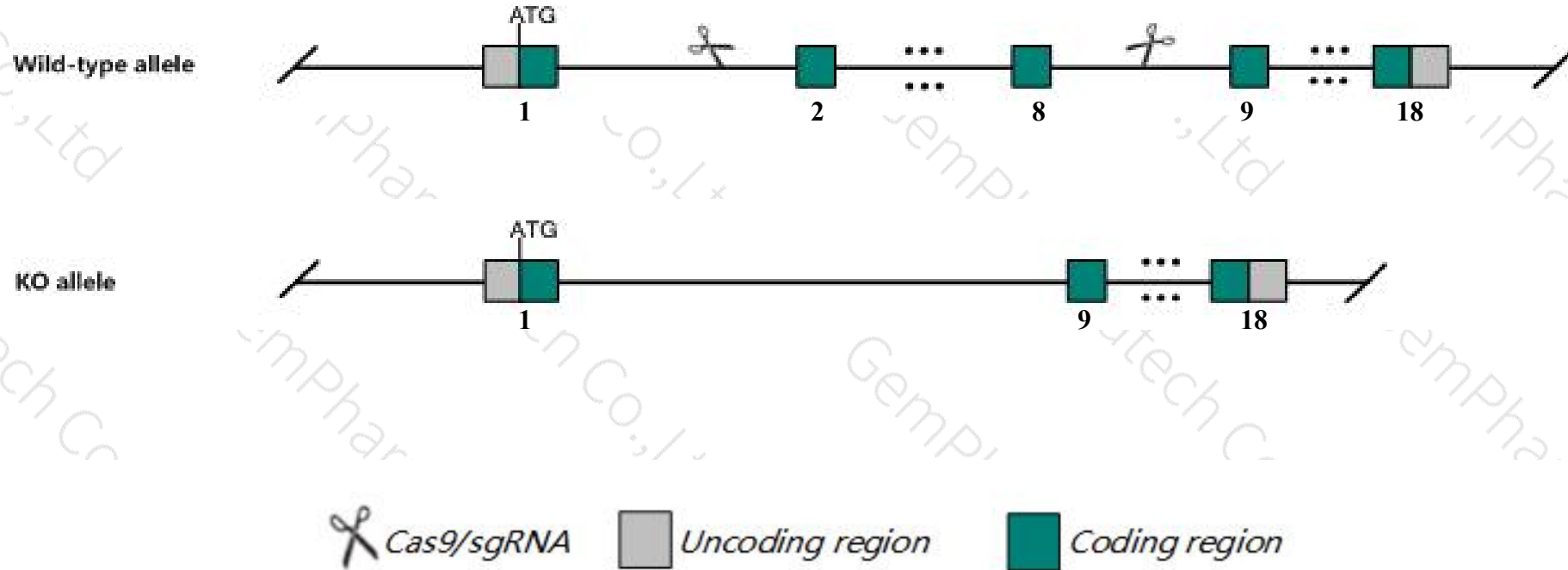
**Cas9-KO**

**Strain background**

**C57BL/6J**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ncam1* gene. The schematic diagram is as follows:



- The *Ncam1* gene has 7 transcripts. According to the structure of *Ncam1* gene, exon2-exon8 of *Ncam1-204* (ENSMUST00000193547.5) transcript is recommended as the knockout region. The region contains 1010bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ncam1* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, Homozygous mutants show impairment in Morris water maze test, reduced brain and olfactory bulb size, hypoplastic corticospinal tract, abnormally distributed anterior pituitary cell types, and morphological and functional defects of neuromuscular junctions.
- The *Ncam1* gene is located on the Chr9. 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)

## Ncam1 neural cell adhesion molecule 1 [Mus musculus (house mouse)]

Gene ID: 17967, updated on 7-Apr-2019

### Summary

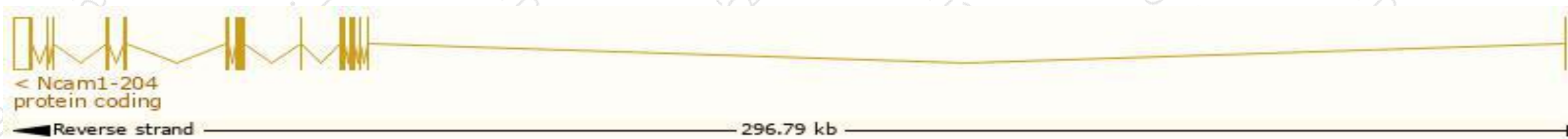
<b>Official Symbol</b>	Ncam1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	neural cell adhesion molecule 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:97281</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000039542</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	CD56, E-NCAM, NCAM-1, Ncam
<b>Expression</b>	Biased expression in CNS E18 (RPKM 29.9), whole brain E14.5 (RPKM 28.6) and 10 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

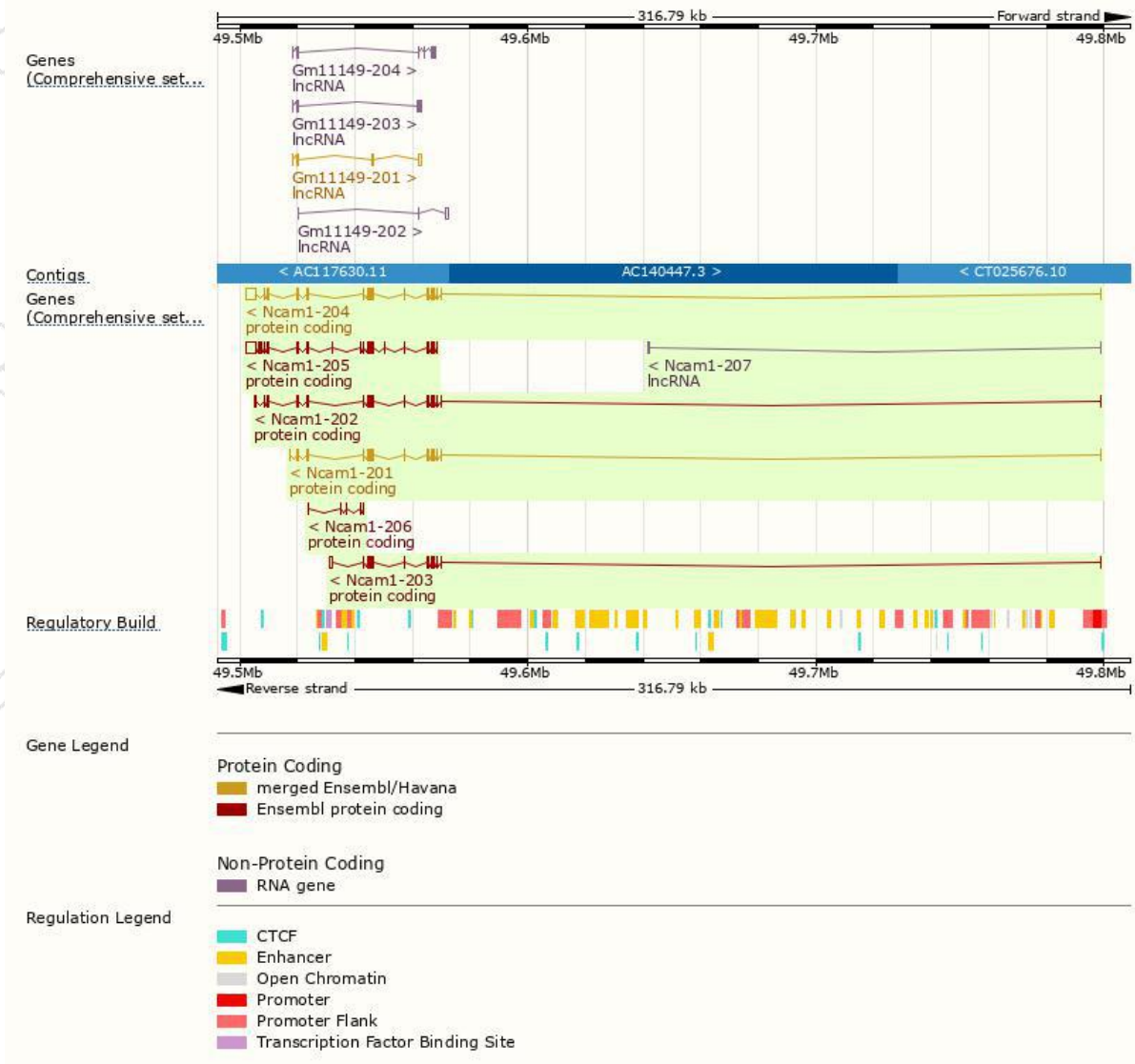
The gene has 7 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ncam1-204	<a href="#">ENSMUST00000193547.5</a>	6050	<a href="#">848aa</a>	Protein coding	<a href="#">CCDS40617</a>	<a href="#">A0A0A6YY47</a>	TSL:1 GENCODE basic APPRIS P4
Ncam1-202	<a href="#">ENSMUST00000166811.8</a>	3088	<a href="#">849aa</a>	Protein coding	<a href="#">CCDS80993</a>	<a href="#">E9QB01</a>	TSL:1 GENCODE basic APPRIS ALT2
Ncam1-201	<a href="#">ENSMUST00000114476.7</a>	2567	<a href="#">725aa</a>	Protein coding	<a href="#">CCDS40618</a>	<a href="#">E9Q589</a>	TSL:1 GENCODE basic APPRIS ALT2
Ncam1-205	<a href="#">ENSMUST00000194252.5</a>	6564	<a href="#">1089aa</a>	Protein coding	-	<a href="#">A0A0A6YY91</a>	CDS 5' incomplete TSL:5
Ncam1-203	<a href="#">ENSMUST00000192584.1</a>	2525	<a href="#">605aa</a>	Protein coding	-	<a href="#">A0A0A6YWU2</a>	TSL:1 GENCODE basic
Ncam1-206	<a href="#">ENSMUST00000194844.1</a>	146	<a href="#">49aa</a>	Protein coding	-	<a href="#">A0A0A6YWW5</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Ncam1-207	<a href="#">ENSMUST00000217121.1</a>	914	No protein	lncRNA	-	-	TSL:1

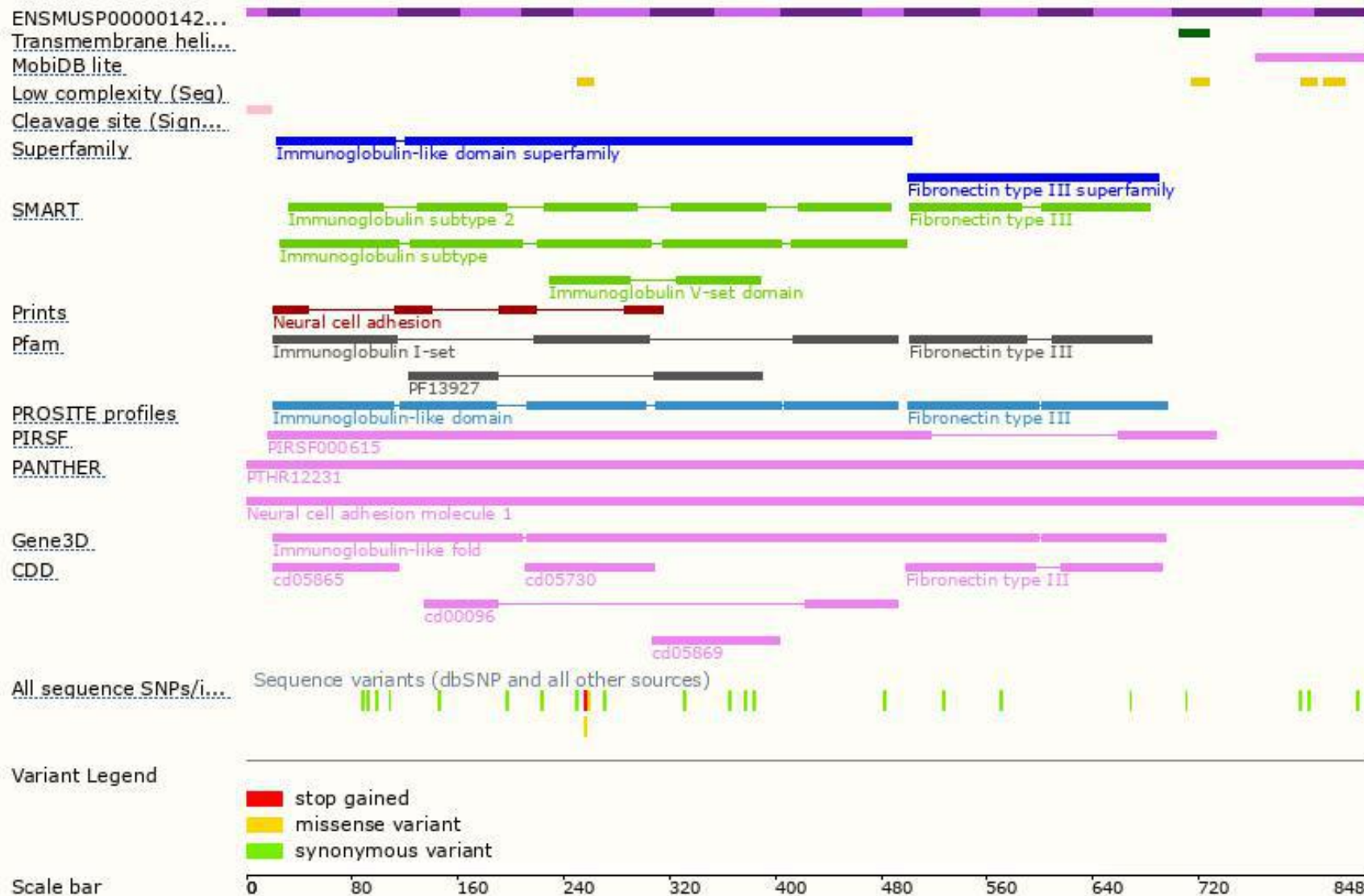
The strategy is based on the design of *Ncam1-204* transcript, The transcription is shown below



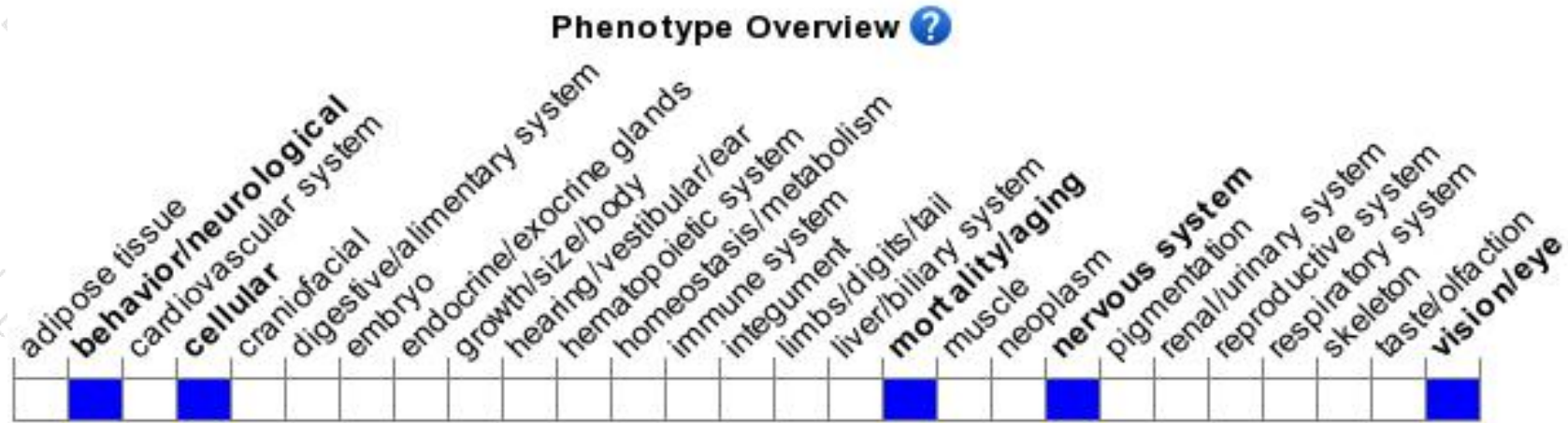
# Genomic location distribution



# 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 mutants show impairment in Morris water maze test, reduced brain and olfactory bulb size, hypoplastic corticospinal tract, abnormally distributed anterior pituitary cell types, and morphological and functional defects of neuromuscular junctions.

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

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