

# *Cnbp* Cas9-KO Strategy

**Designer:**

**Huan Wang**

**Reviewer:**

**Huan Fan**

**Design Date:**

**2020-1-4**

# Project Overview

---

**Project Name**

*Cnbp*

---

**Project type**

**Cas9-KO**

---

**Strain background**

**C57BL/6JGpt**

---

# Knockout strategy

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



- The *Cnbp* gene has 9 transcripts. According to the structure of *Cnbp* gene, exon2-exon5 of *Cnbp-201* (ENSMUST00000032138.14) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cnbp* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a retroviral insertion die around E10.5 showing abnormal anterior visceral endoderm formation, reduced embryonic neuroepithelial cell proliferation, lack of anterior definitive endoderm and anterior neuroectoderm, absent diencephalon and telencephalon, and forebrain truncation.
- The *Cnbp* gene is located on the Chr6. 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)

## Cnbp cellular nucleic acid binding protein [Mus musculus (house mouse)]

Gene ID: 12785, updated on 31-Jan-2019

### Summary



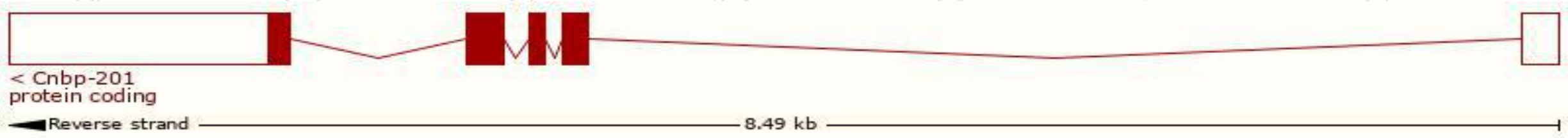
<b>Official Symbol</b>	Cnbp provided by <a href="#">MGI</a>
<b>Official Full Name</b>	cellular nucleic acid binding protein provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:88431</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000030057</a>
<b>Gene type</b>	protein coding
<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>	AA408710, Cnbp1, Znf9
<b>Expression</b>	Ubiquitous expression in placenta adult (RPKM 105.5), liver E14 (RPKM 104.7) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

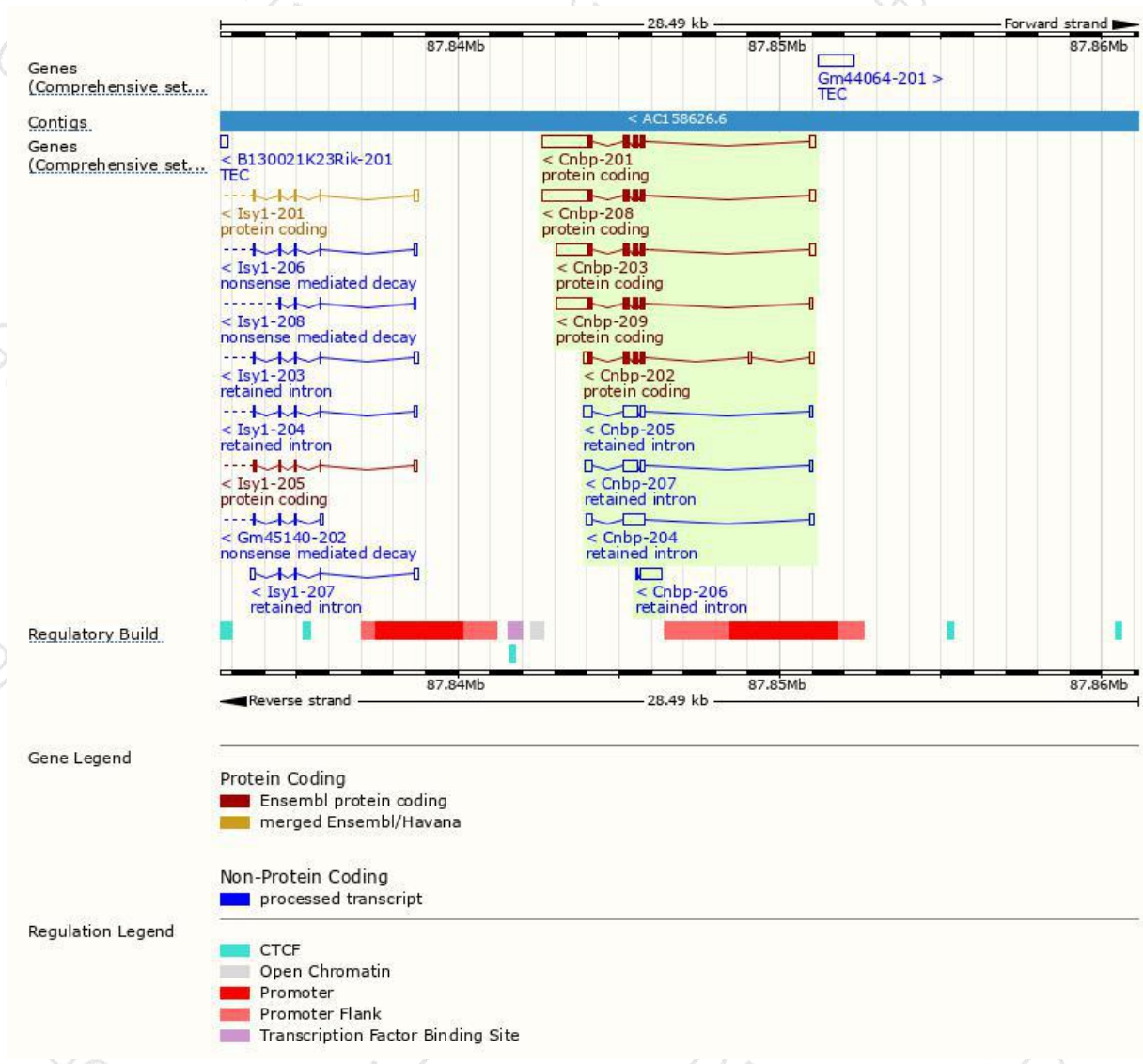
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cnbp-201	<a href="#">ENSMUST00000032138.14</a>	2178	<a href="#">178aa</a>	Protein coding	<a href="#">CCDS51841</a>	<a href="#">P53996 Q5QJQ9</a>	TSL:1 GENCODE basic APPRIS P3
Cnbp-208	<a href="#">ENSMUST00000204653.2</a>	2175	<a href="#">177aa</a>	Protein coding	<a href="#">CCDS85091</a>	<a href="#">P53996 Q3ULK8</a>	TSL:1 GENCODE basic APPRIS ALT1
Cnbp-203	<a href="#">ENSMUST00000113619.7</a>	1661	<a href="#">170aa</a>	Protein coding	<a href="#">CCDS85092</a>	<a href="#">P53996 Q3U935</a>	TSL:1 GENCODE basic APPRIS ALT1
Cnbp-202	<a href="#">ENSMUST00000113617.2</a>	952	<a href="#">177aa</a>	Protein coding	<a href="#">CCDS85091</a>	<a href="#">P53996 Q3ULK8</a>	TSL:5 GENCODE basic APPRIS ALT1
Cnbp-209	<a href="#">ENSMUST00000204890.2</a>	1614	<a href="#">171aa</a>	Protein coding	-	<a href="#">A0A0N4SVS6</a>	TSL:1 GENCODE basic APPRIS ALT1
Cnbp-204	<a href="#">ENSMUST00000134851.2</a>	985	No protein	Retained intron	-	-	TSL:5
Cnbp-205	<a href="#">ENSMUST00000141961.3</a>	915	No protein	Retained intron	-	-	TSL:3
Cnbp-207	<a href="#">ENSMUST00000204596.1</a>	911	No protein	Retained intron	-	-	TSL:5
Cnbp-206	<a href="#">ENSMUST00000204104.1</a>	690	No protein	Retained intron	-	-	TSL:3

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

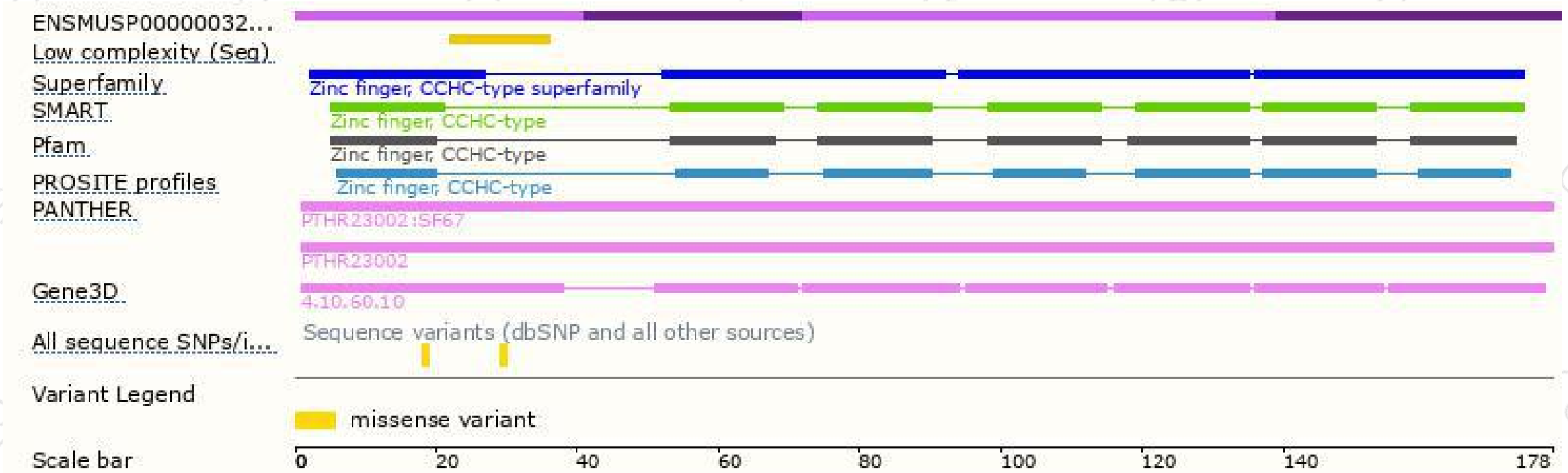


# Genomic location distribution

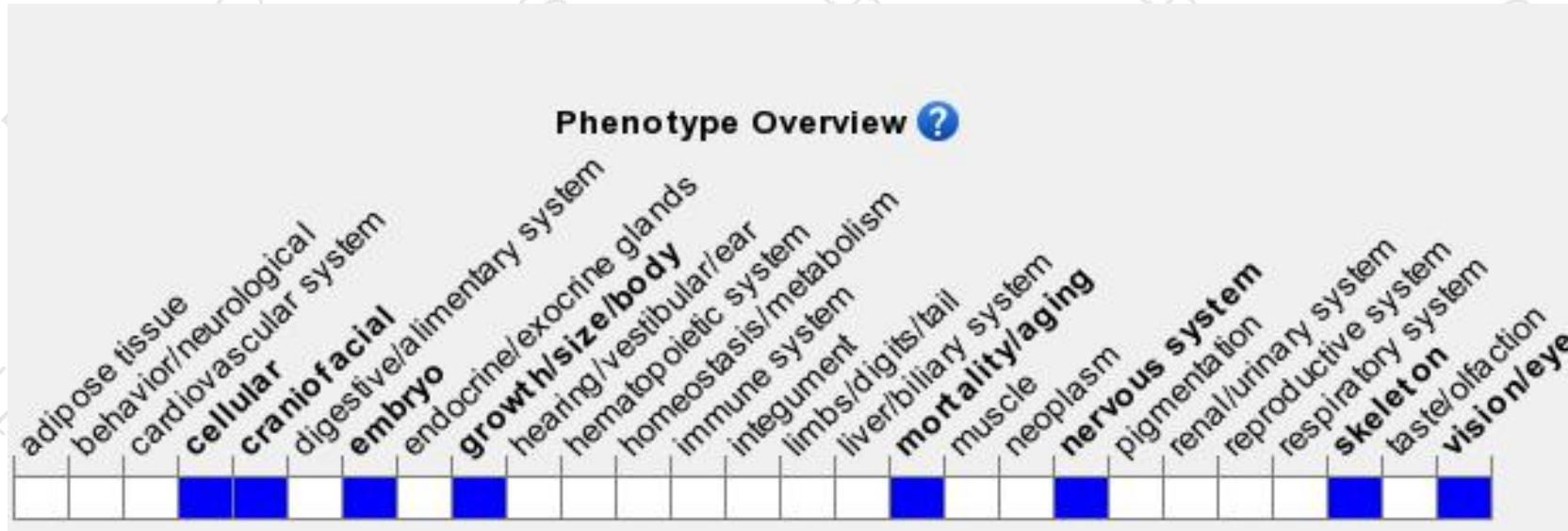




# Protein domain



# 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, Mice homozygous for a retroviral insertion die around E10.5 showing abnormal anterior visceral endoderm formation, reduced embryonic neuroepithelial cell proliferation, lack of anterior definitive endoderm and anterior neuroectoderm, absent diencephalon and telencephalon, and forebrain truncation.

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

Tel: 400-9660890

