

# *Cecr2* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Cecr2*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cecr2* gene. The schematic diagram is as follows:



- The *Cecr2* gene has 8 transcripts. According to the structure of *Cecr2* gene, exon2 of *Cecr2-202* (ENSMUST00000112686.7) transcript is recommended as the knockout region. The region contains 95bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cecr2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutant mice display varied penetrance of exencephaly depending on genetic background.
- Transcript *Cecr2-204,206* may not be affected.
- The *Cecr2* 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)

## Cecr2 CECR2, histone acetyl-lysine reader [Mus musculus (house mouse)]

Gene ID: 330409, updated on 21-Feb-2019

### Summary



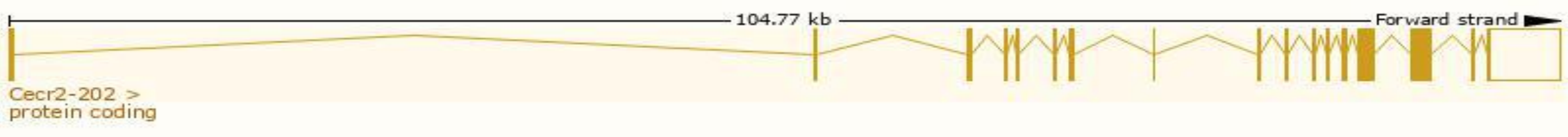
<b>Official Symbol</b>	Cecr2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	CECR2, histone acetyl-lysine reader provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1923799</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000071226</a>
<b>Gene type</b>	protein coding
<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>	2610101O16Rik, 2810409N01Rik, Gtl4
<b>Expression</b>	Ubiquitous expression in testis adult (RPKM 4.5), CNS E11.5 (RPKM 4.0) and 23 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

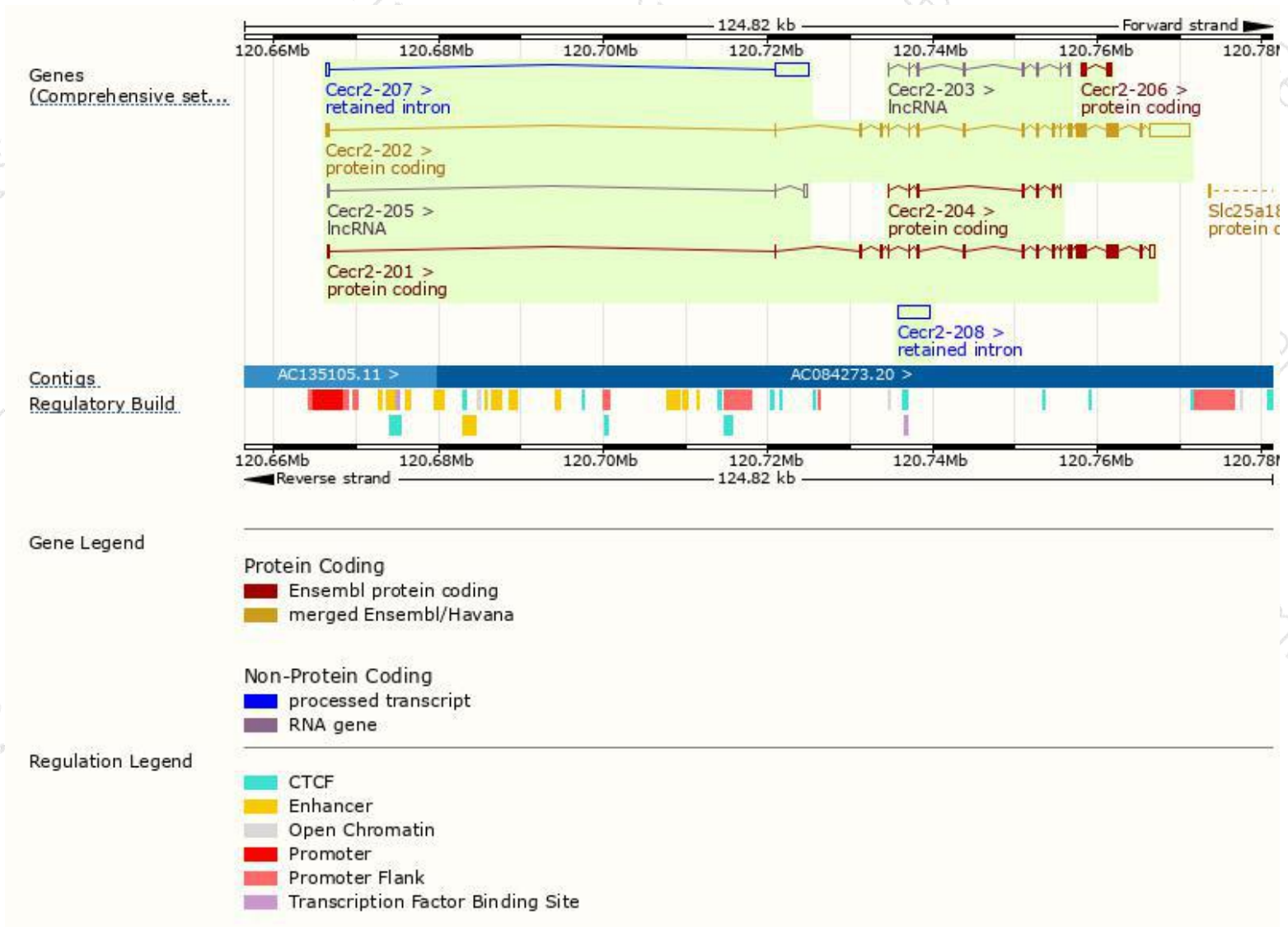
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cecr2-202	<a href="#">ENSMUST00000112686.7</a>	9212	<a href="#">1425aa</a>	Protein coding	<a href="#">CCDS51890</a>	<a href="#">E9Q2Z1</a>	TSL:5 GENCODE basic APPRIS P2
Cecr2-201	<a href="#">ENSMUST00000100993.8</a>	4849	<a href="#">1453aa</a>	Protein coding	-	<a href="#">E9Q2Z1</a>	TSL:5 GENCODE basic APPRIS ALT2
Cecr2-206	<a href="#">ENSMUST00000143563.1</a>	1071	<a href="#">357aa</a>	Protein coding	-	-	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:2
Cecr2-204	<a href="#">ENSMUST00000129803.1</a>	704	<a href="#">234aa</a>	Protein coding	-	-	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
Cecr2-207	<a href="#">ENSMUST00000148346.1</a>	4392	No protein	Retained intron	-	-	TSL:1
Cecr2-208	<a href="#">ENSMUST00000204732.1</a>	3996	No protein	Retained intron	-	-	TSL:NA
Cecr2-203	<a href="#">ENSMUST00000124634.1</a>	946	No protein	lncRNA	-	-	TSL:5
Cecr2-205	<a href="#">ENSMUST00000135109.1</a>	641	No protein	lncRNA	-	-	TSL:3

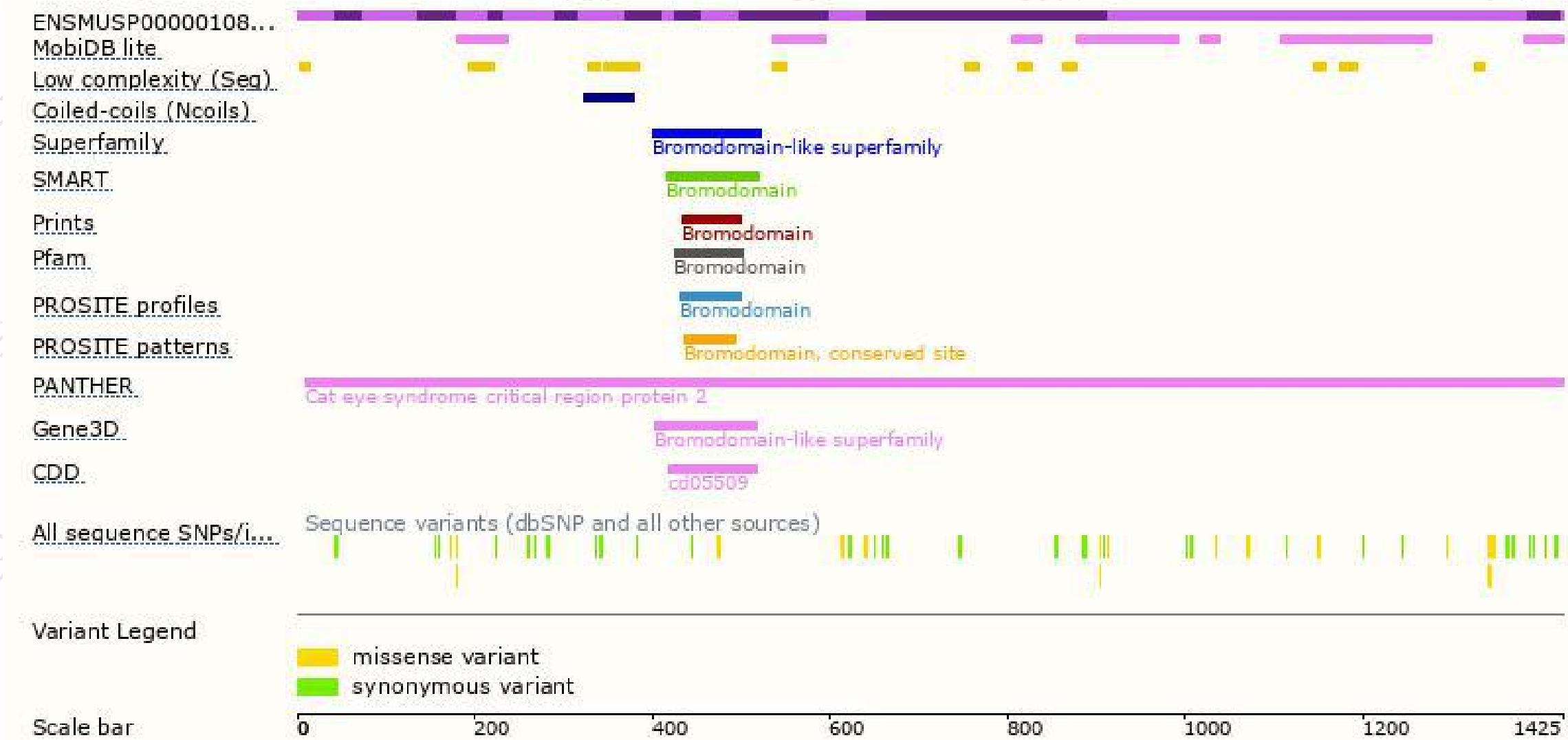
The strategy is based on the design of *Cecr2-202* transcript,The transcription is shown below



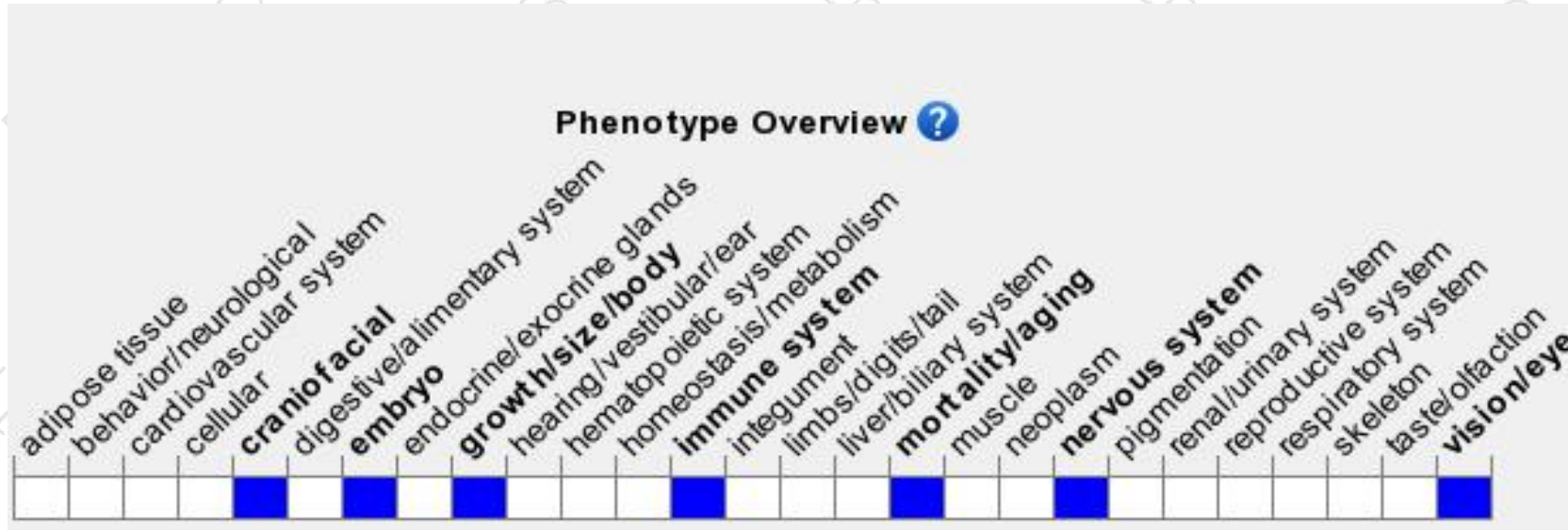
# Genomic location distribution



# 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, Homozygous mutant mice display varied penetrance of exencephaly depending on genetic background.

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

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