

# *Creb3l2* Cas9-CKO Strategy

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# Overview

## Target Gene Name

- Creb3l2

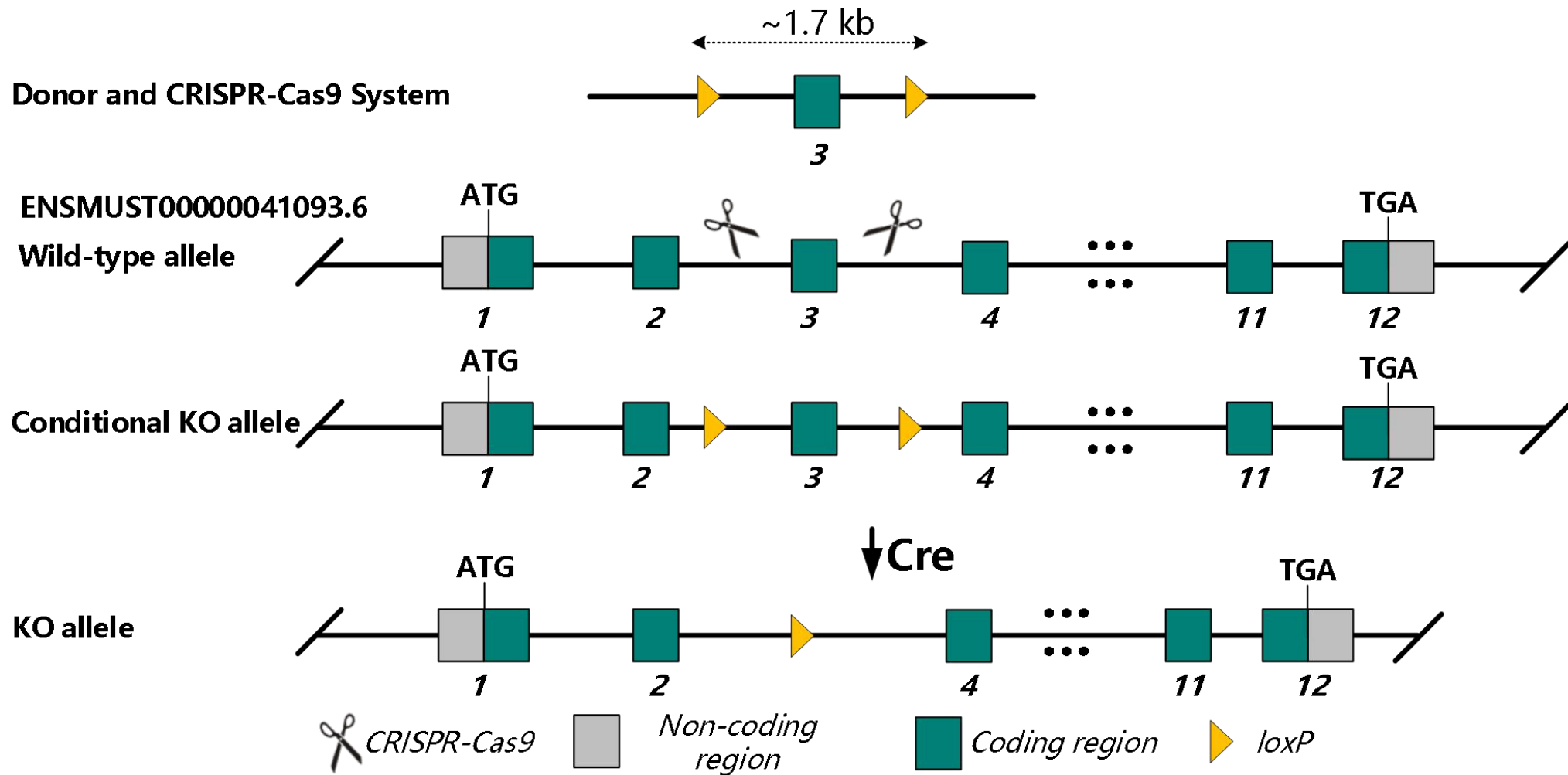
## Project Type

- Cas9-CKO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Creb3l2* gene.

# Technical Information

- The *Creb3l2* gene has 2 transcripts. According to the structure of *Creb3l2* gene, exon 3 of *Creb3l2*-201 (ENSMUST00000041093.6) transcript is recommended as the knockout region. The region contains 176 bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Creb3l2* gene. The brief process is as follows: CRISPR-Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

# Gene Information

**Creb3l2** cAMP responsive element binding protein 3-like 2 [ *Mus musculus* (house mouse) ]

[Download Datasets](#)

Gene ID: 208647, updated on 26-Sep-2022

**Summary**

**Official Symbol** Creb3l2 provided by [MGI](#)

**Official Full Name** cAMP responsive element binding protein 3-like 2 provided by [MGI](#)

**Primary source** [MGI:MGI:2442695](#)

**See related** [Ensembl:ENSMUSG00000038648](#) [AllianceGenome:MGI:2442695](#)

**Gene type** protein coding

**RefSeq status** VALIDATED

**Organism** [Mus musculus](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

**Also known as** BBF2H7; SCIRR69; C530025K05Rik

**Summary** Enables DNA-binding transcription activator activity, RNA polymerase II-specific and cAMP response element binding activity. Involved in chondrocyte differentiation; endoplasmic reticulum to Golgi vesicle-mediated transport; and positive regulation of transcription by RNA polymerase II. Predicted to be located in chromatin; nucleoplasm; and perinuclear endoplasmic reticulum. Is expressed in several structures, including brain; early conceptus; embryo mesenchyme; and genitourinary system. Orthologous to human CREB3L2 (cAMP responsive element binding protein 3 like 2). [provided by Alliance of Genome Resources, Apr 2022]

**Expression** Broad expression in limb E14.5 (RPKM 19.4), adrenal adult (RPKM 18.8) and 27 other tissues [See more](#)

**Orthologs** [human](#) [all](#)

**NEW**

Try the new [Gene table](#)  
Try the new [Transcript table](#)

**Genomic context**

**Location:** 6; 6 B1 [See Creb3l2 in Genome Data Viewer](#)

**Exon count:** 12

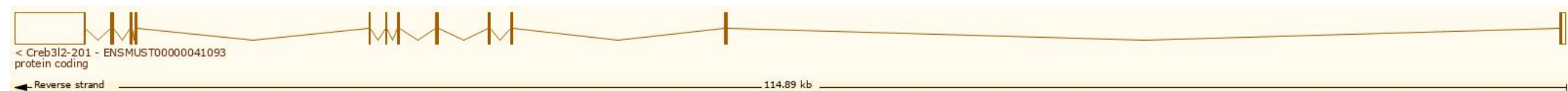
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

The gene has 2 transcripts, all transcripts are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
<a href="#">ENSMUST00000128534.2</a>	Creb3l2-202	648	No protein	Protein coding CDS not defined		-	TSL:2
<a href="#">ENSMUST00000041093.6</a>	Creb3l2-201	7082	<a href="#">521aa</a>	Protein coding	<a href="#">CCDS20006</a>	<a href="#">Q8BH52</a>	Ensembl Canonical Gencode basic APPRIS P1 TSL:1

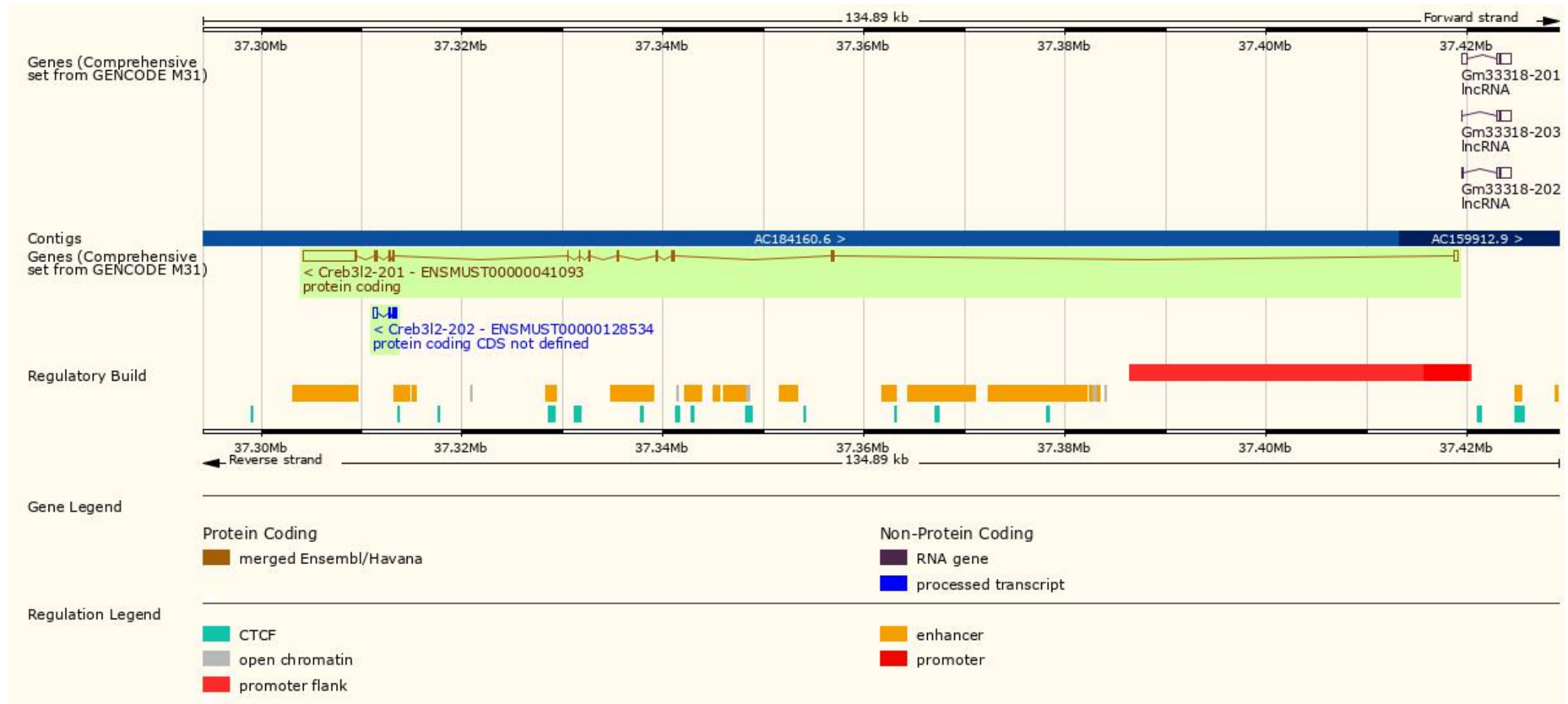
The strategy is based on the design of *Creb3l2*-201 transcript, the transcription is shown below:



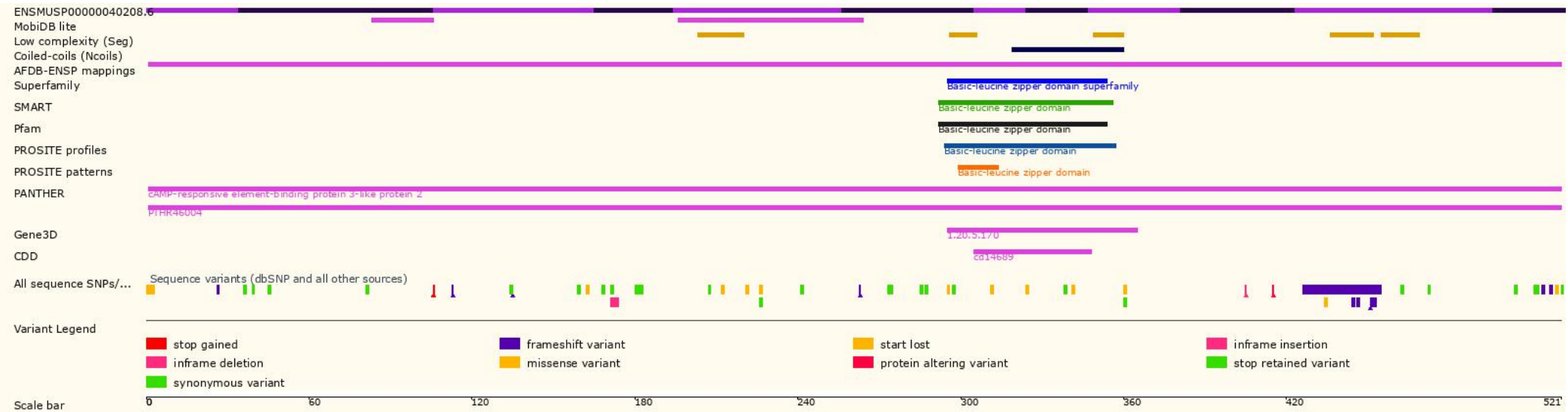
Source: <https://www.ensembl.org>



# Genomic Information

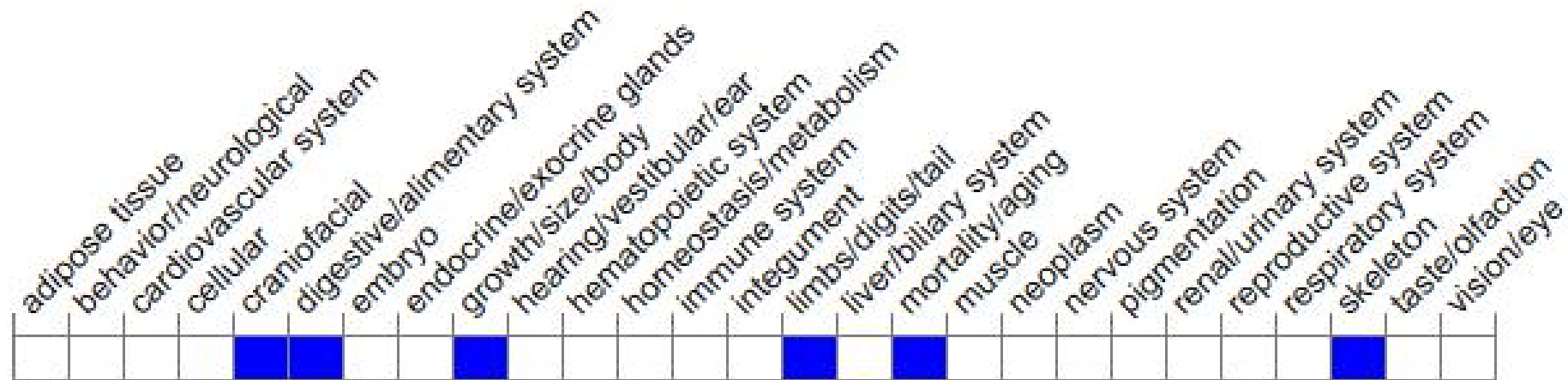


# Protein Information





# Mouse Phenotype Information (MGI)



# Important Information

- Mice homozygous for a knock-out allele exhibit severe chondrodysplasia and die shortly after first birth from suffocation.
- *Creb3l2* is located on Chr 6. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.