

# ***Crabp1* Cas9-KO Strategy**

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# Project Overview

**Project Name**

***Crabp1***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Crabp1* gene. The schematic diagram is as follows:



- The *Crabp1* gene has 1 transcript. According to the structure of *Crabp1* gene, exon1-exon3 of *Crabp1-201* (ENSMUST00000034830.8) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Crabp1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for targeted null mutations are phenotypically normal and fertile.
- The *Crabp1* 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)

## Crabp1 cellular retinoic acid binding protein I [ *Mus musculus* (house mouse) ]

Gene ID: 12903, updated on 14-Aug-2019

### Summary

- Official Symbol** Crabp1 provided by [MGI](#)
- Official Full Name** cellular retinoic acid binding protein I provided by [MGI](#)
- Primary source** [MGI:MGI:88490](#)
- See related** [Ensembl:ENSMUSG00000032291](#)
- 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** Rbp-5; Crabpl; CRABP-I; Crabp-1; AI326249
- Expression** Biased expression in CNS E11.5 (RPKM 232.5), limb E14.5 (RPKM 196.0) and 3 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

### Genomic context

**Location:** 9 A5.3; 9 29.76 cM See Crabp1 in [Genome Data Viewer](#)

**Exon count:** 4

Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	9	NC_000075.6 (54764748..54773110)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	9	NC_000075.5 (54612615..54620916)

# Transcript information (Ensembl)

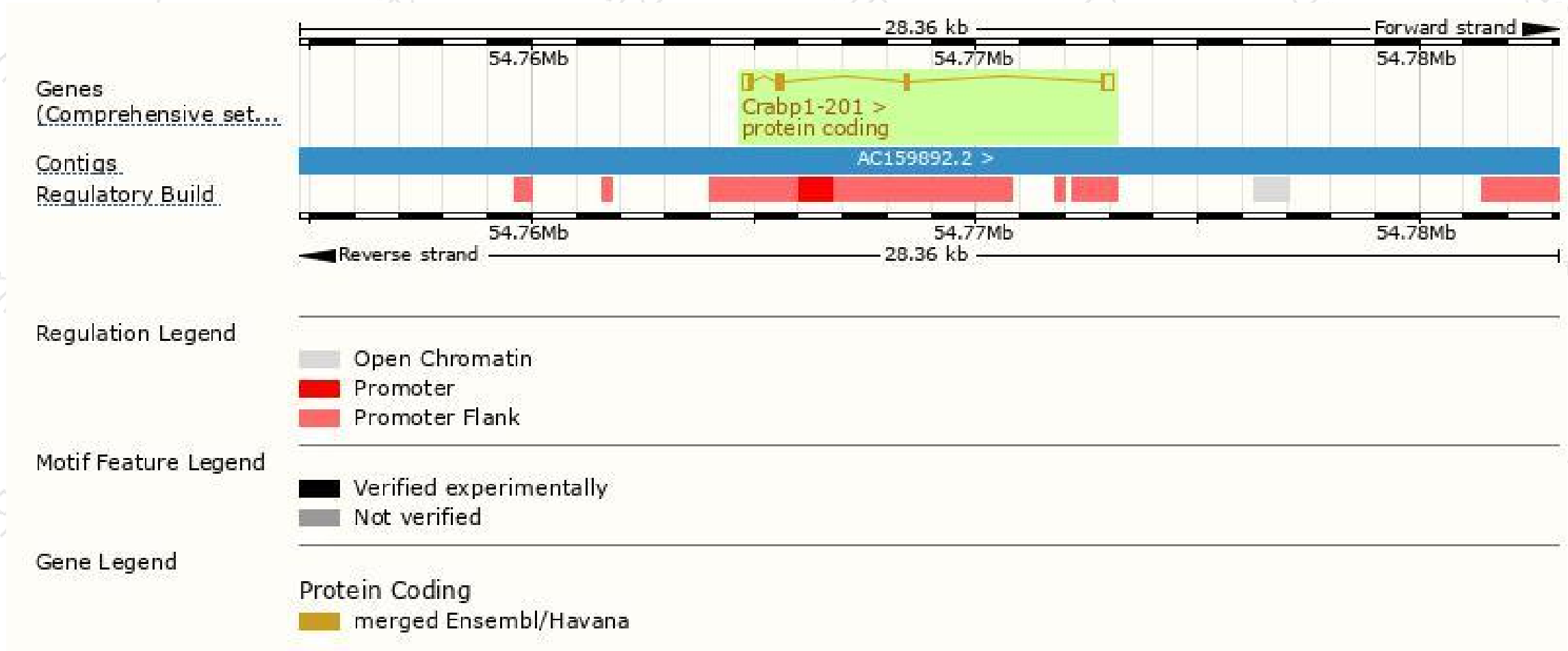
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Crabp1-201	<a href="#">ENSMUST00000034830.8</a>	802	<a href="#">137aa</a>	Protein coding	<a href="#">CCDS23195</a>	<a href="#">P62965</a>	TSL:1 GENCODE basic APPRIS P1

The strategy is based on the design of *Crabp1-201* transcript, The transcription is shown below

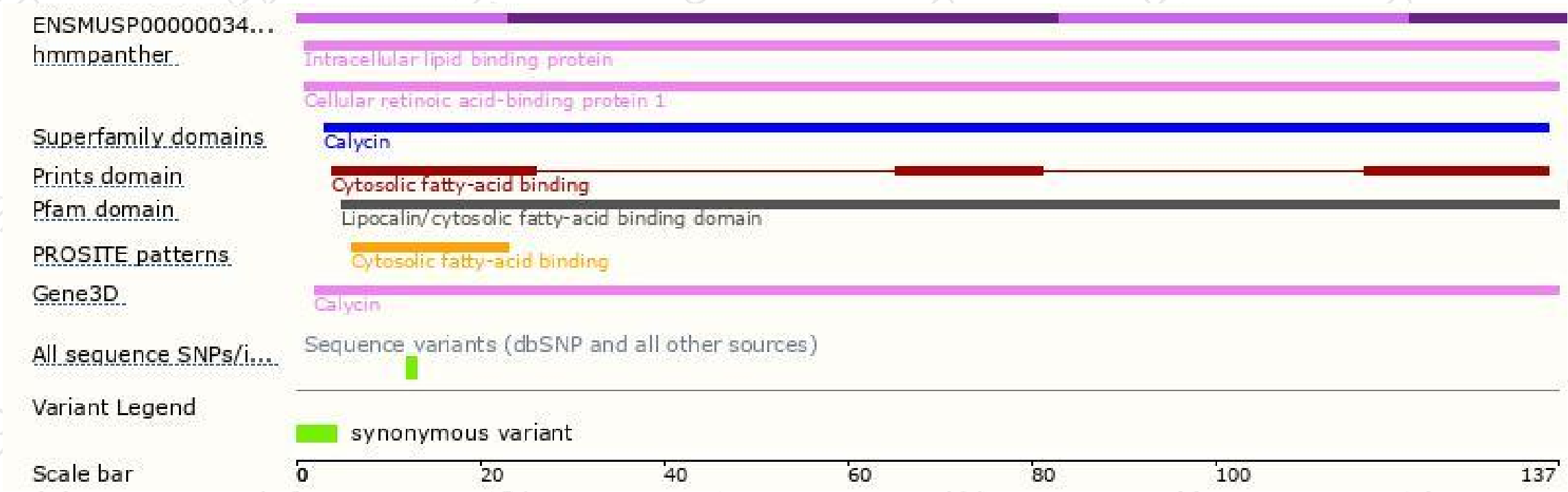


# Genomic location distribution

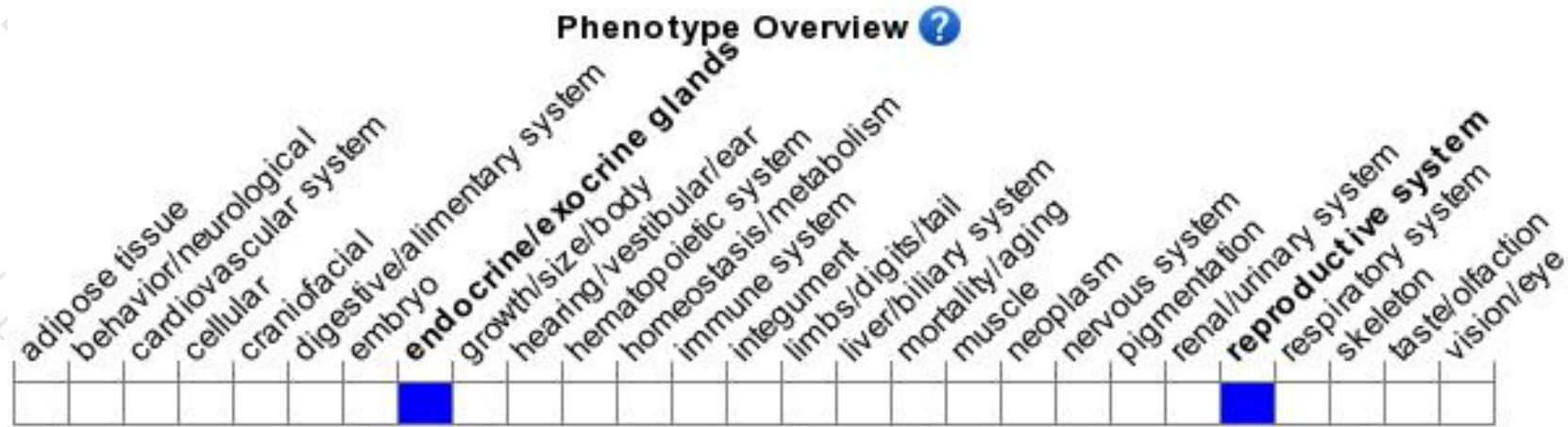




# Protein domain



# 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, Homozygotes for targeted null mutations are phenotypically normal and fertile.

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

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