GemPharmatech™

Crabp2 Cas9-CKO Strategy

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Overview

Target Gene Name

- *Crabp2*

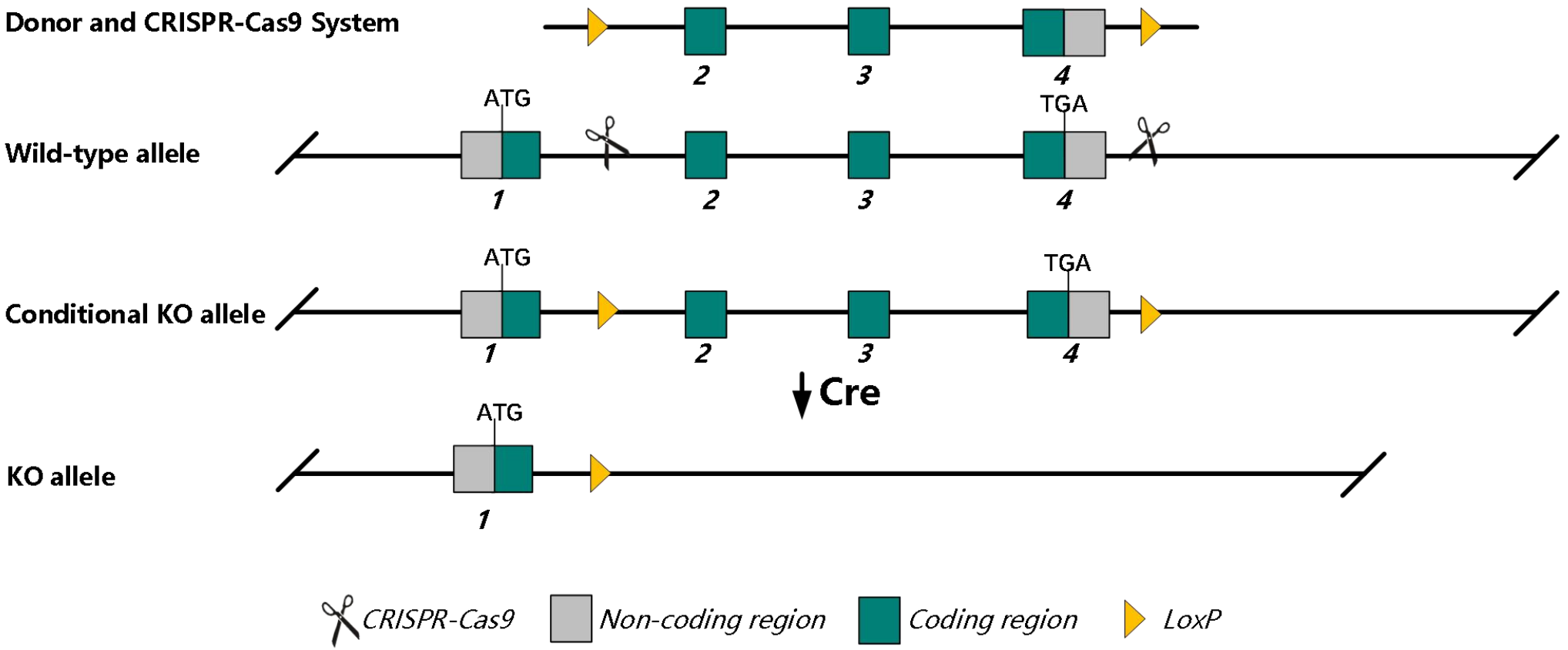
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Crabp2* gene.

Technical Information

- The *Crabp2* gene has 2 transcripts. According to the structure of *Crabp2* gene, exon2-4 of *Crabp2*-201 (ENSMUST00000005019.6) transcript is recommended as the knockout region. The region contains 347bp of coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Crabp2* 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

Crabp2 cellular retinoic acid binding protein II [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 12904, updated on 5-Aug-2023

Summary

Official Symbol	Crabp2 provided by MGI
Official Full Name	cellular retinoic acid binding protein II provided by MGI
Primary source	MGI:MGI:88491
See related	Ensembl:ENSMUSG00000004885 AllianceGenome:MGI:88491
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Crabp-2; Crabpll
Summary	Enables retinoic acid binding activity. Acts upstream of or within embryonic forelimb morphogenesis; positive regulation of collateral sprouting; and retinoic acid metabolic process. Located in endoplasmic reticulum and nucleus. Is expressed in several structures, including alimentary system; central nervous system; embryo mesenchyme; heart and pericardium; and sensory organ. Orthologous to human CRABP2 (cellular retinoic acid binding protein 2). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Biased expression in CNS E11.5 (RPKM 125.3), limb E14.5 (RPKM 55.3) and 3 other tissues See more
Orthologs	human all

NEW Try the new Gene table
Try the new Transcript table

Genomic context

Location: 3 F1; 3 38.78 cM — See Crabp2 in Genome Data Viewer

Exon count: 4

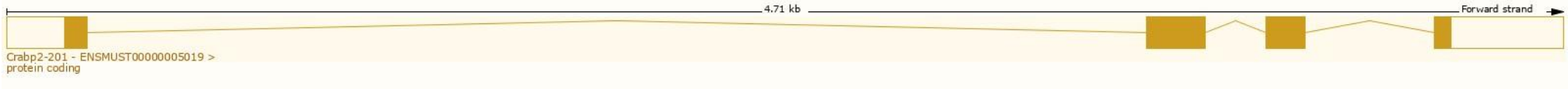
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

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

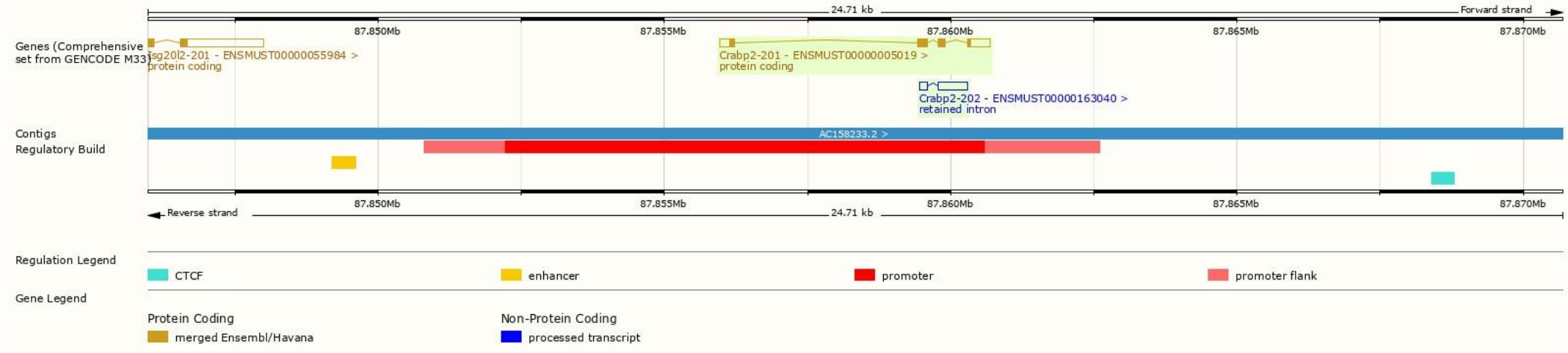
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000005019.6	Crabp2-201	931	138aa	Protein coding	CCDS17460	P22935	Ensembl Canonical, GENCODE basic, APPRIS P1, TSL:1
ENSMUST00000163040.2	Crabp2-202	658	No protein	Retained intron		-	TSL:2

The strategy is based on the design of *Crabp2*-201 transcript, the transcription is shown below:



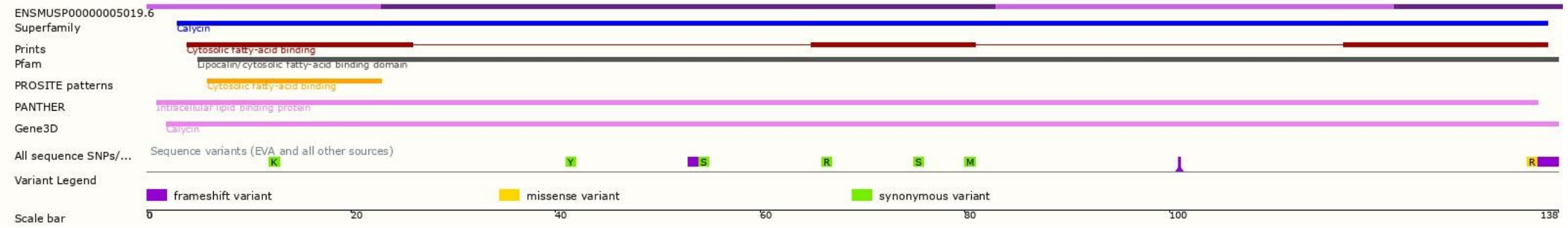
Source: https://www.ensembl.org

Genomic Information



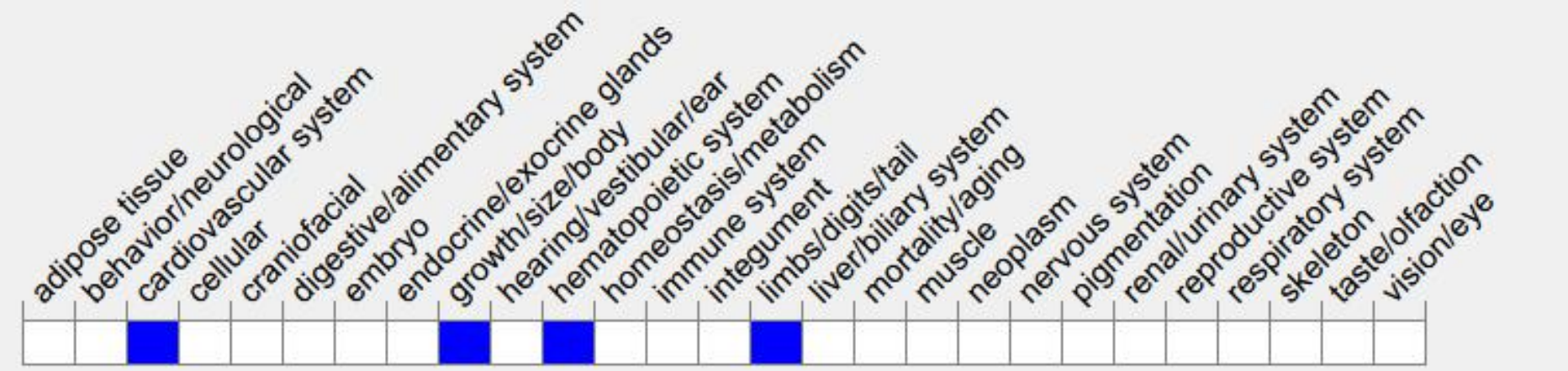
Source: https://www.ensembl.org

Protein Information



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

Mouse Phenotype Information (MGI)



Homozygotes for targeted null mutations may exhibit an additional postaxial digit, usually on a single forepaw. Penetrance is dependent on the genetic background.

Source: https://www.informatics.jax.org

Important Information

- According to the existing MGI data, homozygotes for targeted null mutations may exhibit an additional postaxial digit, usually on a single forepaw. Penetrance is dependent on the genetic background.
- *Crabp2* is located on Chr3. 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.