

Crip1 Cas9-KO Strategy

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Overview

Target Gene Name

• Crip1

Project Type

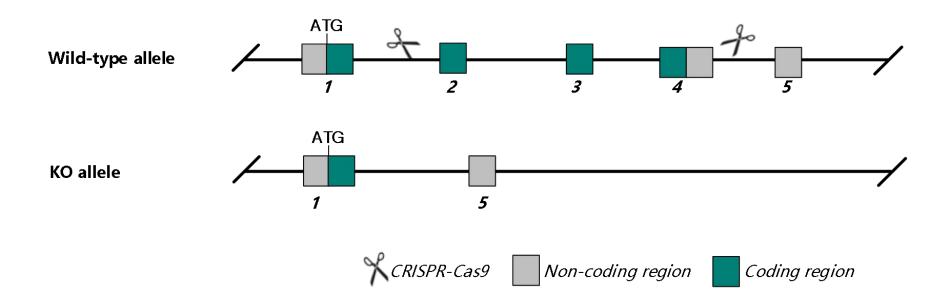
• Cas9-KO

Genetic Background

• C57BL/6JGpt



Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the Crip1 gene.



Technical Information

- The *Crip1* gene has 6 transcripts. According to the structure of *Crip1* gene, exon2-4 of *Crip1*-201 (ENSMUST0000006523.12) transcript is recommended as the knockout region. The region contains most of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Crip1* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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.



Gene Information

Crip1 cysteine-rich protein 1 (intestinal) [Mus musculus (house mouse)]

Gene ID: 12925, updated on 26-Sep-2022

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Official Symbol Crip1 provided by MGI

Official Full Name cysteine-rich protein 1 (intestinal) provided by MGI

Primary source MGI:MGI:88501

See related Ensembl:ENSMUSG00000006360 AllianceGenome:MGI:88501

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 CRHP; CRP1; Crip

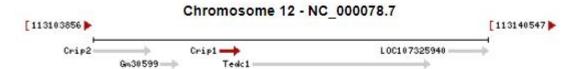
Summary Predicted to enable peptide binding activity and zinc ion binding activity. Predicted to be involved in several processes, including cellular response to UV-B; intrinsic apoptotic signaling

pathway in response to DNA damage; and response to zinc ion. Predicted to be located in cytoplasm. Is expressed in several structures, including genitourinary system; gut;

hemolymphoid system gland; integumental system; and limb segment. Orthologous to human CRIP1 (cysteine rich protein 1). [provided by Alliance of Genome Resources, Apr 2022]

Expression Biased expression in large intestine adult (RPKM 3684.4), small intestine adult (RPKM 2998.6) and 10 other tissues See more

Orthologs <u>human</u> <u>all</u>



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



Transcript Information

The gene has 6 transcripts, all transcripts are shown below:

Transcript ID	Name 🍦	bp 🖕	Protein 🍦	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000199089.5	Crip1-205	509	<u>128aa</u>	Protein coding		A0A0G2JEK2₺	Ensembl Canonical GENCODE basic TSL:3
ENSMUST00000200553.2	Crip1-206	516	<u>77aa</u>	Protein coding	CCDS26205₽	P63254 ₽	GENCODE basic APPRIS P1 TSL:2
ENSMUST00000006523.12	Crip1-201	445	<u>77aa</u>	Protein coding	CCDS26205₽	P63254₺	GENCODE basic APPRIS P1 TSL:1
ENSMUST00000198597.5	Crip1-203	552	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000196932.2	Crip1-202	1809	No protein	Retained intron		=	TSL:NA
ENSMUST00000198909.2	Crip1-204	1505	No protein	Retained intron		-	TSL:1

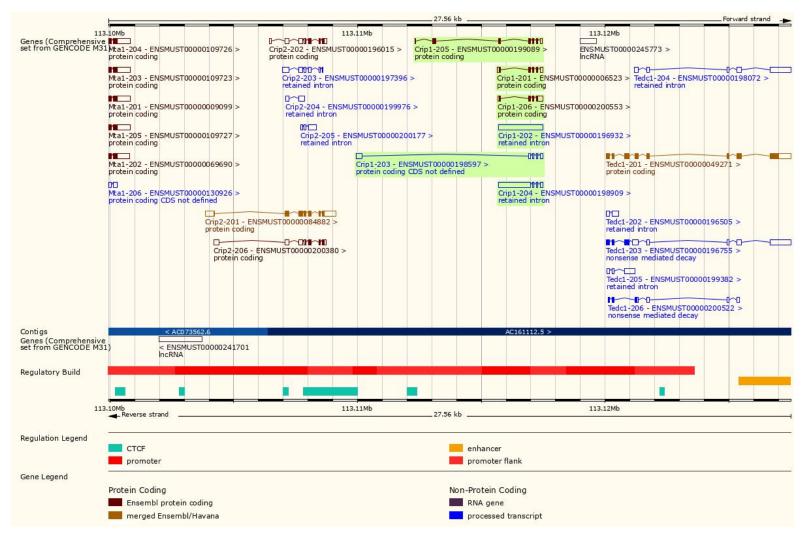
The strategy is based on the design of *Crip1*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org



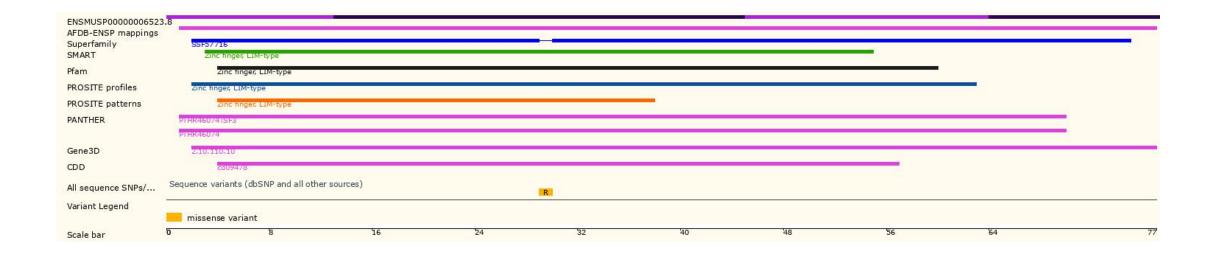
Genomic Information

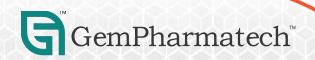




Source: : https://www.ensembl.org

Protein Information





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

Important Information

- The effect of *Tedc1*, ENSMUST00000245773.1 gene is unknown.
- *Crip1* is located on Chr 12. 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 risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

