

Casp3 Cas9-CKO Strategy

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Project Overview

Project Name

Casp3

Project type

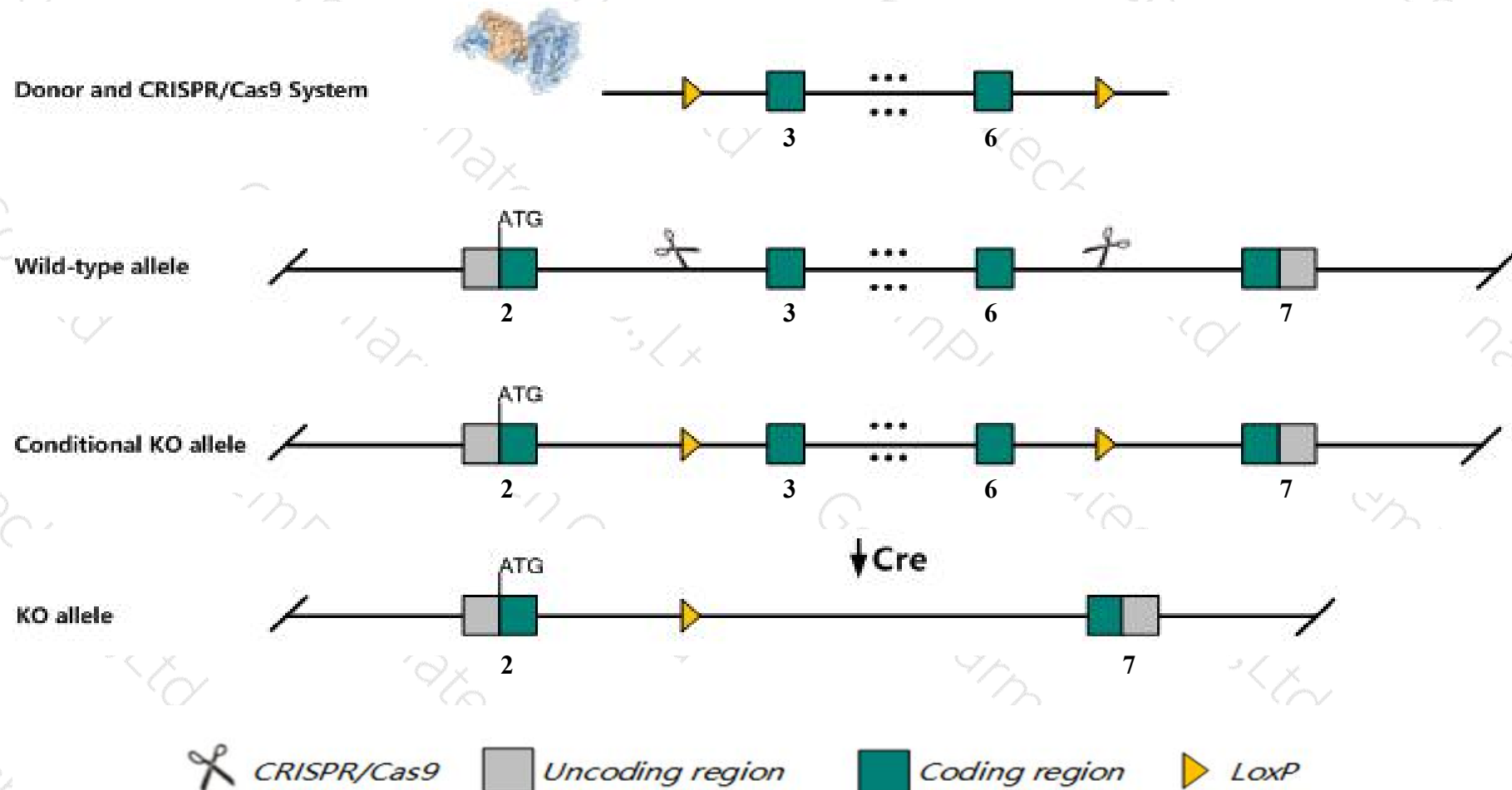
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Casp3* gene. The schematic diagram is as follows:



- The *Casp3* gene has 4 transcripts. According to the structure of *Casp3* gene, exon3-exon6 of *Casp3*-204 (ENSMUST00000211115.1) transcript is recommended as the knockout region. The region contains 551bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Casp3* 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- 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.

- According to the existing MGI data, Some homozygous animals show defects in brain development by embryonic day 12, reduced neuronal apoptosis causing hyperplasias, and pre- and postnatal lethality. Other homozygous animals exhibit only hearing loss, inner ear defects and degeneration of spiral ganglion neurons.
- The *Casp3* gene is located on the Chr8. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Casp3 caspase 3 [Mus musculus (house mouse)]

Gene ID: 12367, updated on 9-Apr-2019

Summary

Official Symbol Casp3 provided by [MGI](#)

Official Full Name caspase 3 provided by [MGI](#)

Primary source [MGI:MGI:107739](#)

See related [Ensembl:ENSMUSG000000031628](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

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

Also known as A830040C14Rik, AC-3, CASP-3, CC3, CPP-32, CPP32, Caspase-3, Lice, SCA-1, Yama, mldy

Summary This gene encodes a protein that belongs to a highly conserved family of cysteinyl aspartate-specific proteases that function as essential regulators of programmed cell death through apoptosis. Members of this family contain an N-terminal pro-domain and require cleavage at specific aspartate residues to become mature. The protein encoded by this gene belongs to a subgroup of cysteinyl aspartate-specific proteases that are activated by initiator caspases and that perform the proteolytic cleavage of apoptotic target proteins. Mice defective for this gene exhibit a variety of phenotypes including reduced neuronal apoptosis resulting in hyperplasias, hearing loss, attenuated osteogenic differentiation of bone marrow stromal stem cells, and pre- and post-natal lethality. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Sep 2015]

Expression Broad expression in CNS E18 (RPKM 54.1), CNS E14 (RPKM 37.8) and 16 other tissues [See more](#)

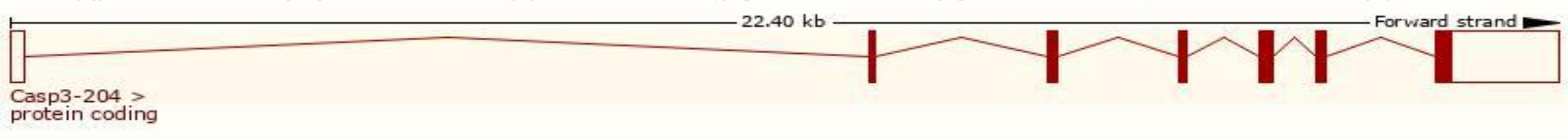
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

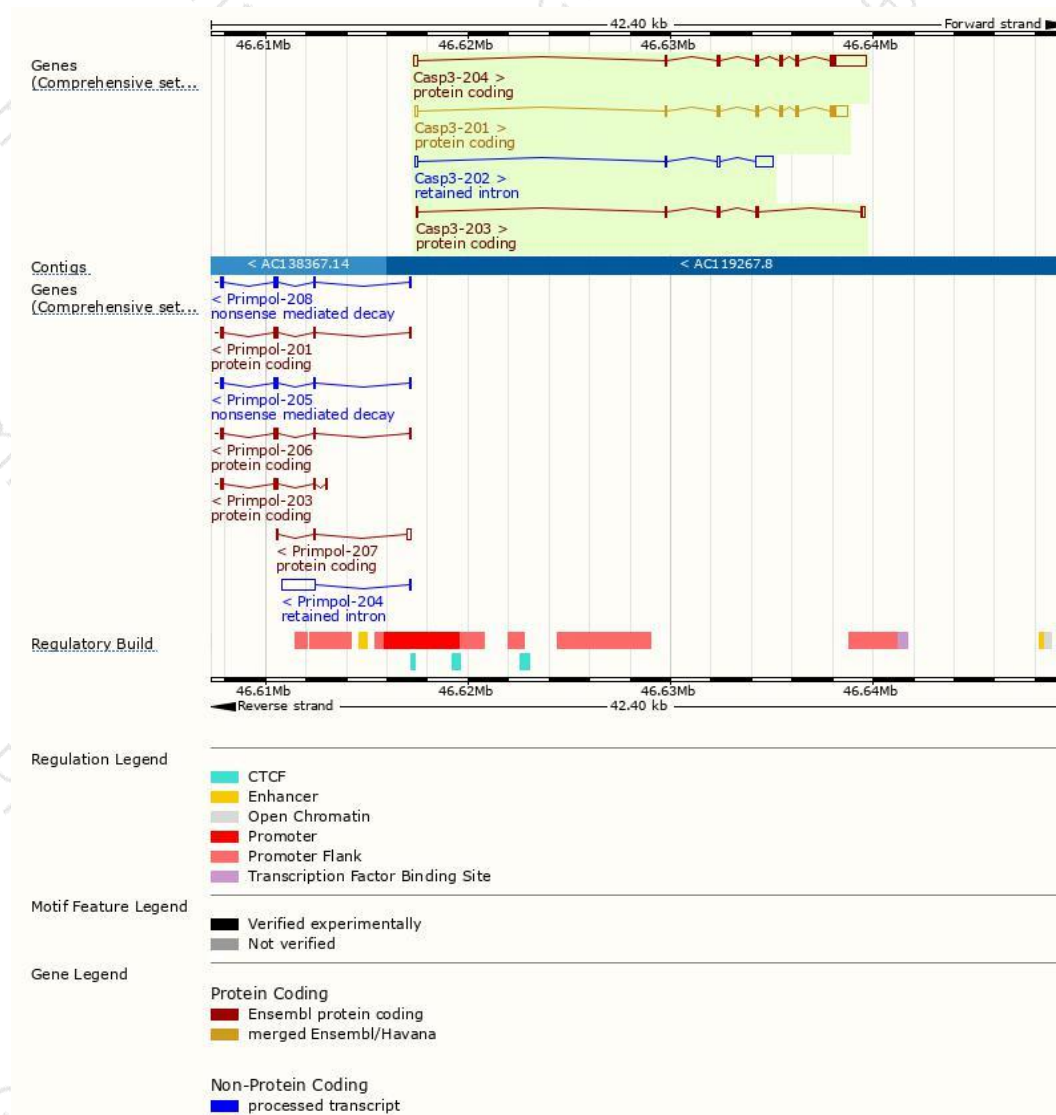
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Casp3-204	ENSMUST00000211115.1	2601	277aa	Protein coding	CCDS22294	P70677	TSL:1 GENCODE basic APPRIS P1
Casp3-201	ENSMUST00000093517.6	1520	277aa	Protein coding	CCDS22294	P70677	TSL:1 GENCODE basic APPRIS P1
Casp3-203	ENSMUST00000210534.1	583	133aa	Protein coding	-	A0A1B0GRX1	TSL:5 GENCODE basic
Casp3-202	ENSMUST00000209668.1	1173	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Casp3-204* transcript,The transcription is shown below



Genomic location distribution



Protein domain

ENSMUSP00000147...

Conserved Domains

hmmpanther

Caspase-3/7

PTHR10454

Superfamily domains

Caspase-like domain superfamily

SMART domains

Peptidase C14A, caspase catalytic domain

Prints domain

Peptidase C14A, caspase catalytic domain

Pfam domain

PF00656

PROSITE profiles

Peptidase C14, p20 domain

Peptidase C14, caspase non-catalytic subunit

PROSITE patterns

Peptidase family C14A, His active site

Peptidase family C14A, cysteine active site

Gene3D

3:40.50.1460

All sequence SNPs/i...

Sequence variants (dbSNP and all other sources)

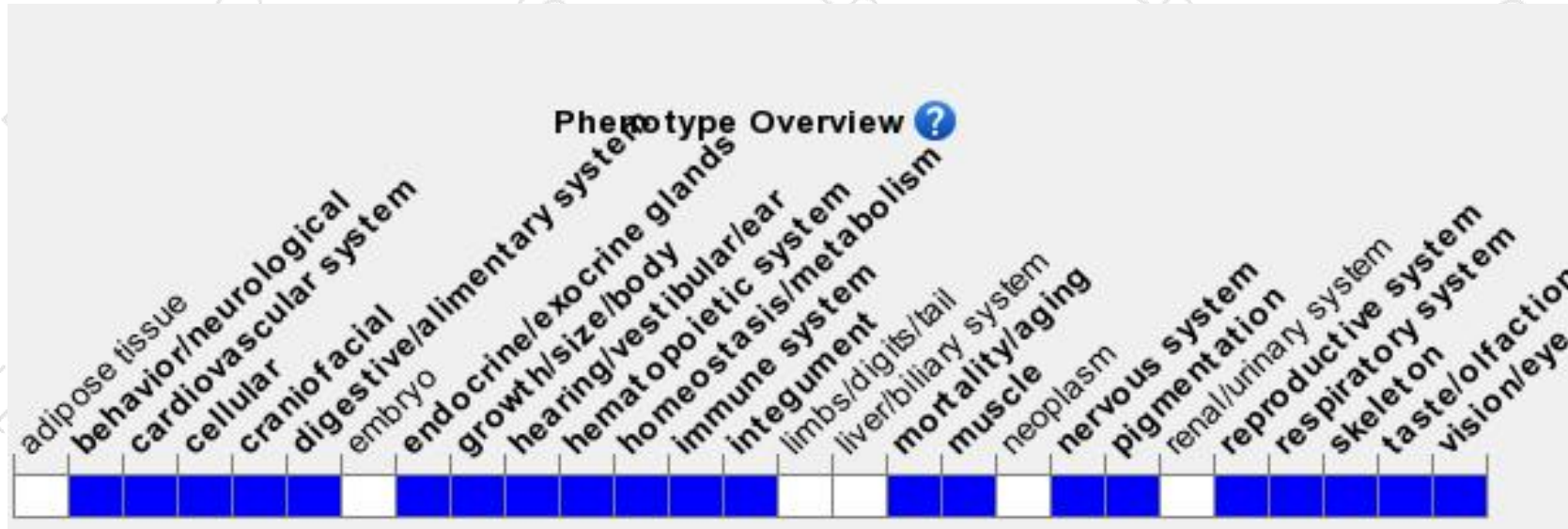
Variant Legend

- missense variant
- synonymous variant

Scale bar

0 40 80 120 160 200 277

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, Some homozygous animals show defects in brain development by embryonic day 12, reduced neuronal apoptosis causing hyperplasias, and pre- and postnatal lethality. Other homozygous animals exhibit only hearing loss, inner ear defects and degeneration of spiral ganglion neurons.

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

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