Casp2 Cas9-CKO Strategy

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Project Overview

Project Name	***Casp2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6J**

Conditional Knockout strategy

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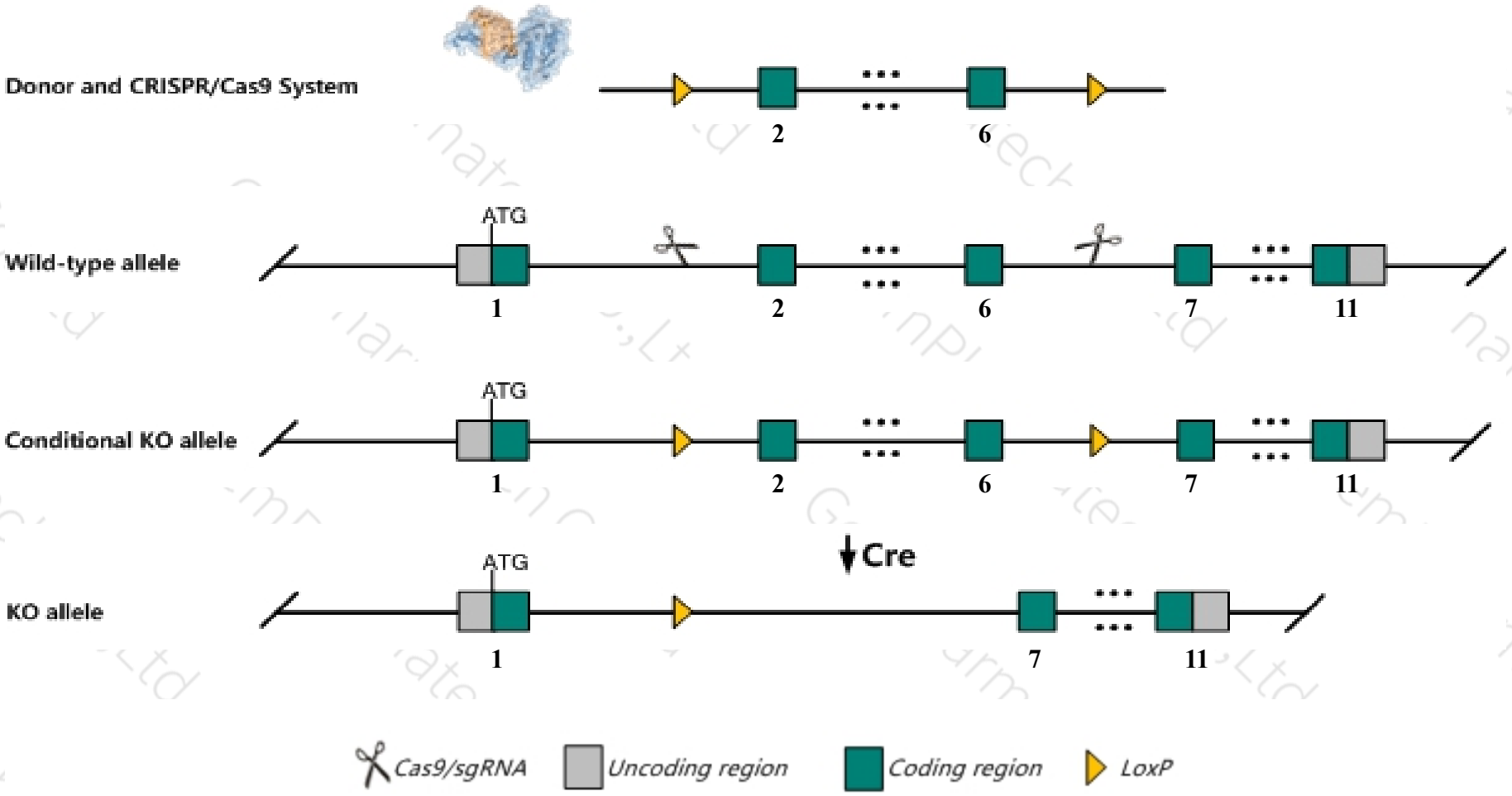
This model will use CRISPR/Cas9 technology to edit the *Casp2* gene. The schematic diagram is as follows:



Technical routes

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- The *Casp2* gene has 10 transcripts. According to the structure of *Casp2* gene, exon2-exon6 of *Casp2-201* (ENSMUST00000031895.12) transcript is recommended as the knockout region.The region contains 673bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Casp2* gene. The brief process is as follows:sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA and Donor were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- The flox mice was 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.

Notice

- According to the existing MGI data,Homozygous mutation of this gene results in abnormal apoptosis. Apoptosis is reduced in the female germline, but is increased in sympathetic neurons during development.

- The *Casp2* gene is located on the Chr6. 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）

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Casp2 caspase 2 [Mus musculus (house mouse)]

Gene ID: 12366, updated on 9-Apr-2019

Summary

Official Symbol	Casp2 provided by MGI
Official Full Name	caspase 2 provided byMGI
Primary source	MGI:MGI:97295
See related	Ensembl:ENSMUSG00000029863
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	CASP-2, ICH-1, NEDD-2, Nedd2
Summary	This gene encodes the evolutionarily ancient and most conserved member of the cysteine proteases that plays important role in stress-induced apoptosis, DNA repair and tumor suppression. Mice lacking the encoded protein develop normally but display cell type-specific apoptotic defects. Germ cells and oocytes from such mice were found to be resistant to cell death after treatment with chemotherapeutic drugs. [provided by RefSeq, Apr 2015]
Expression	Ubiquitous expression in thymus adult (RPKM 27.3), limb E14.5 (RPKM 22.2) and 27 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

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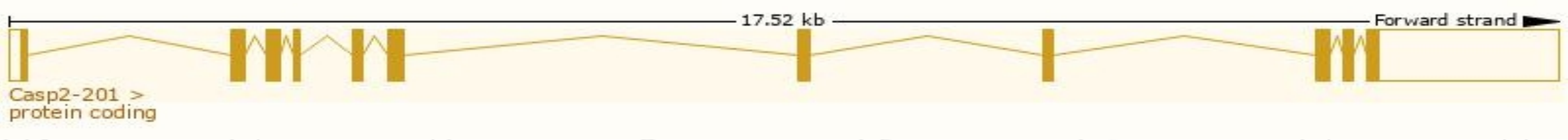
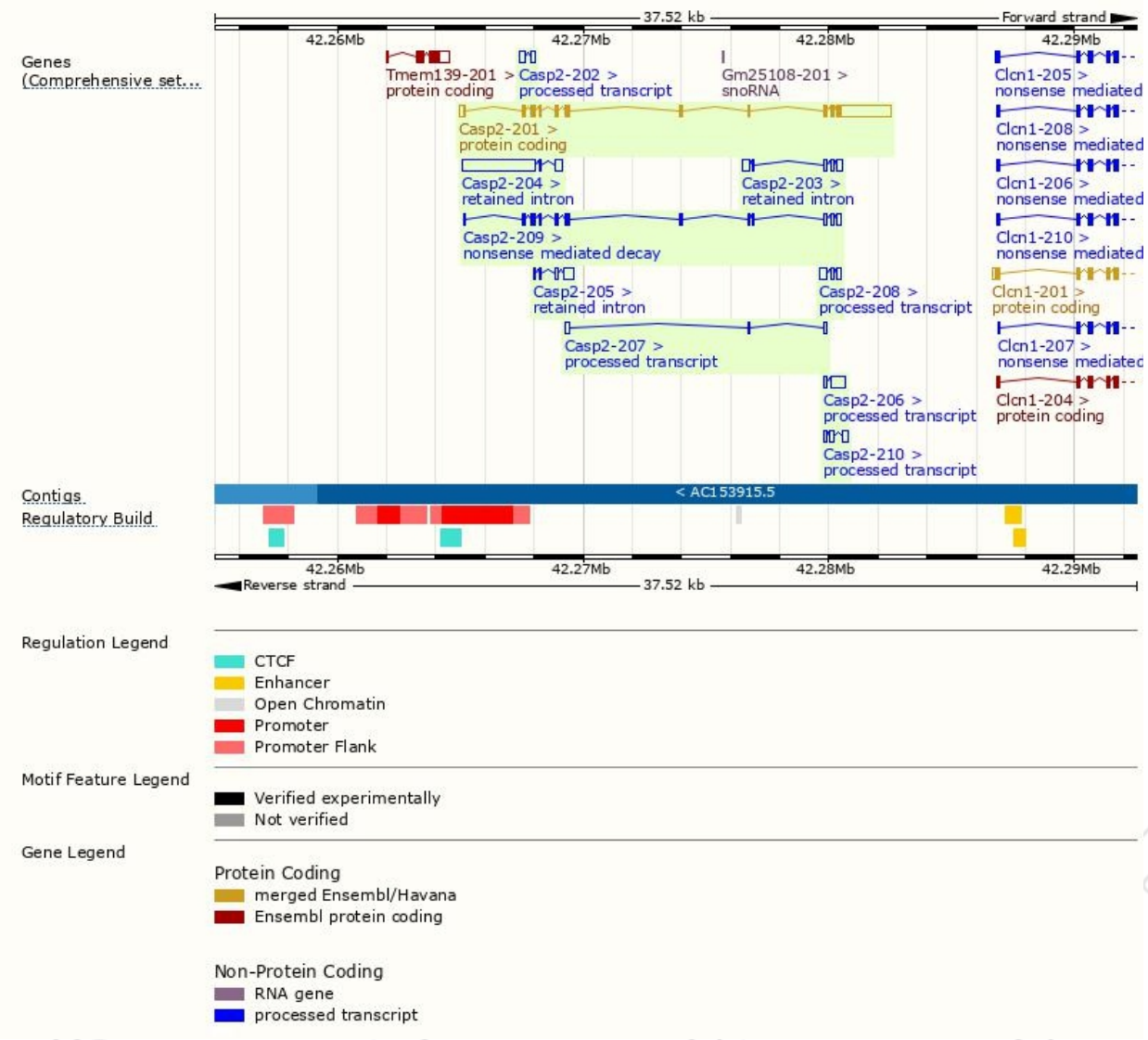
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Casp2-201	ENSMUST00000031895.12	3529	452aa	Protein coding	CCDS20064	P29594	TSL:1 GENCODE basic APPRIS P1
Casp2-209	ENSMUST00000156829.7	1439	343aa	Nonsense mediated decay	-	D6RFN6	TSL:5
Casp2-204	ENSMUST00000139930.7	3325	No protein	Retained intron	-	-	TSL:2
Casp2-203	ENSMUST00000132398.7	808	No protein	Retained intron	-	-	TSL:3
Casp2-205	ENSMUST00000141669.1	615	No protein	Retained intron	-	-	TSL:3
Casp2-206	ENSMUST00000141727.1	704	No protein	lncRNA	-	-	TSL:2
Casp2-208	ENSMUST00000152893.1	545	No protein	lncRNA	-	-	TSL:2
Casp2-210	ENSMUST00000203089.1	494	No protein	lncRNA	-	-	TSL:5
Casp2-202	ENSMUST00000132246.1	396	No protein	lncRNA	-	-	TSL:1
Casp2-207	ENSMUST00000144821.1	384	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Casp2-201* transcript,The transcription is shown below

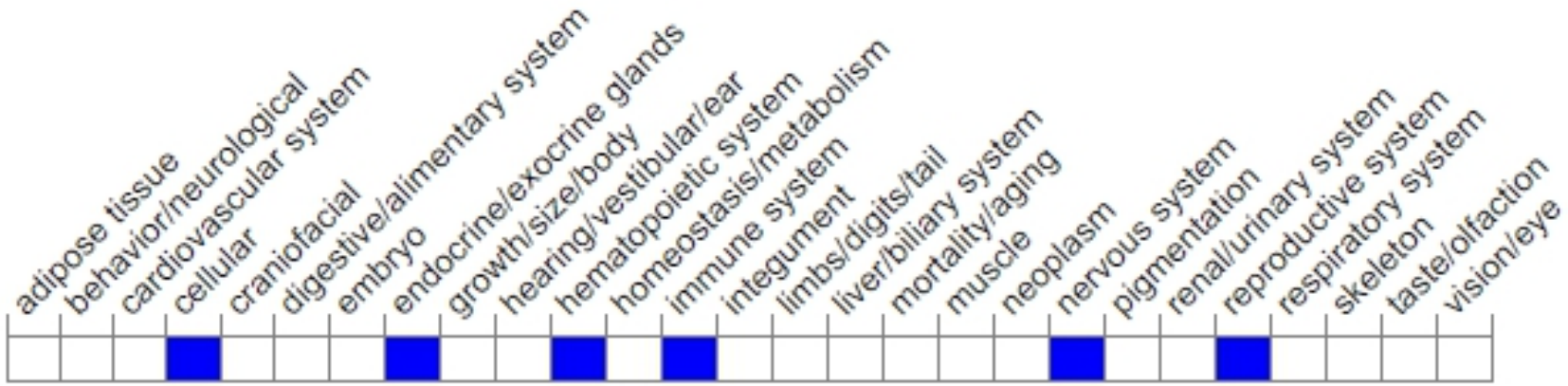


Genomic location distribution



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/).

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

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