

# *Casp2* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Casp2*

**Project type**

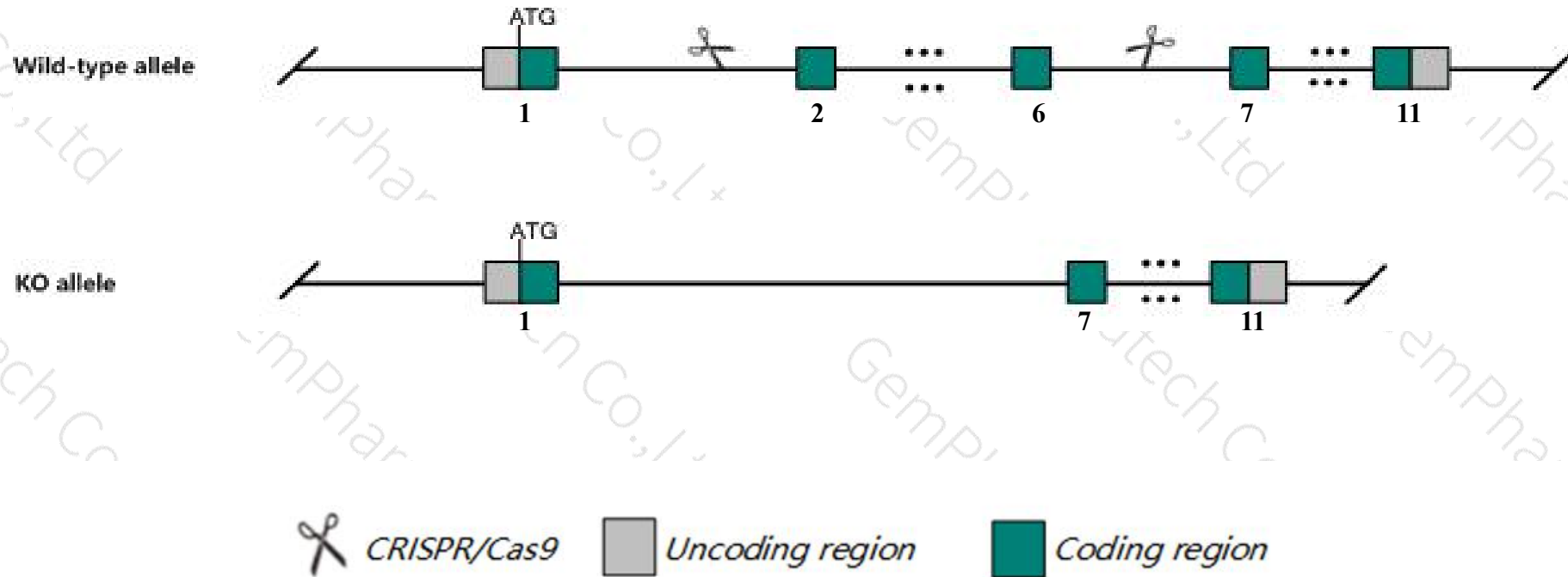
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- 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: CRISPR/Cas9 system

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## 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 by [MGI](#)

**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 tissues [See more](#)

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

# Transcript information (Ensembl)

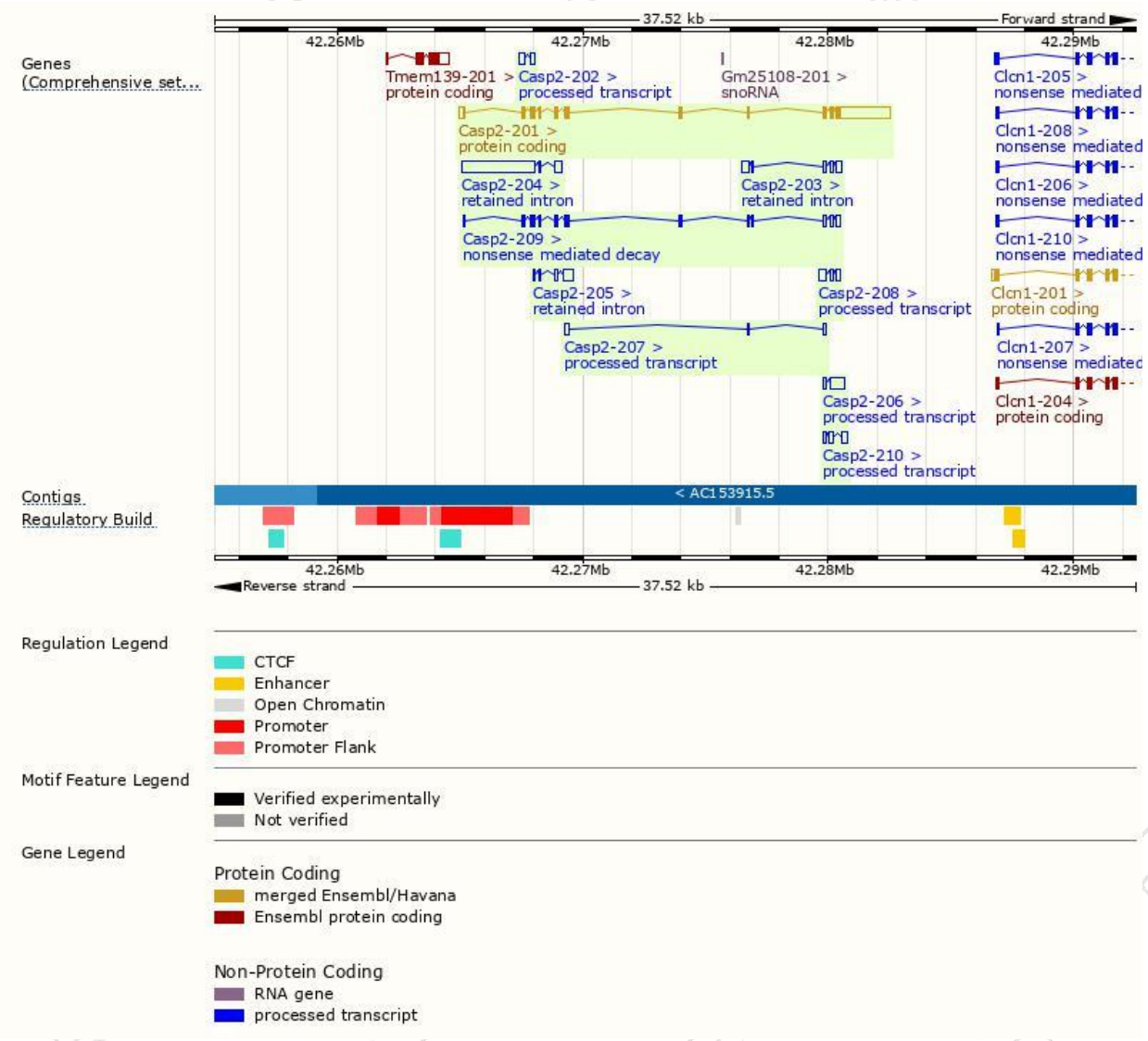
The gene has 10 transcripts,all transcripts are shown below:

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

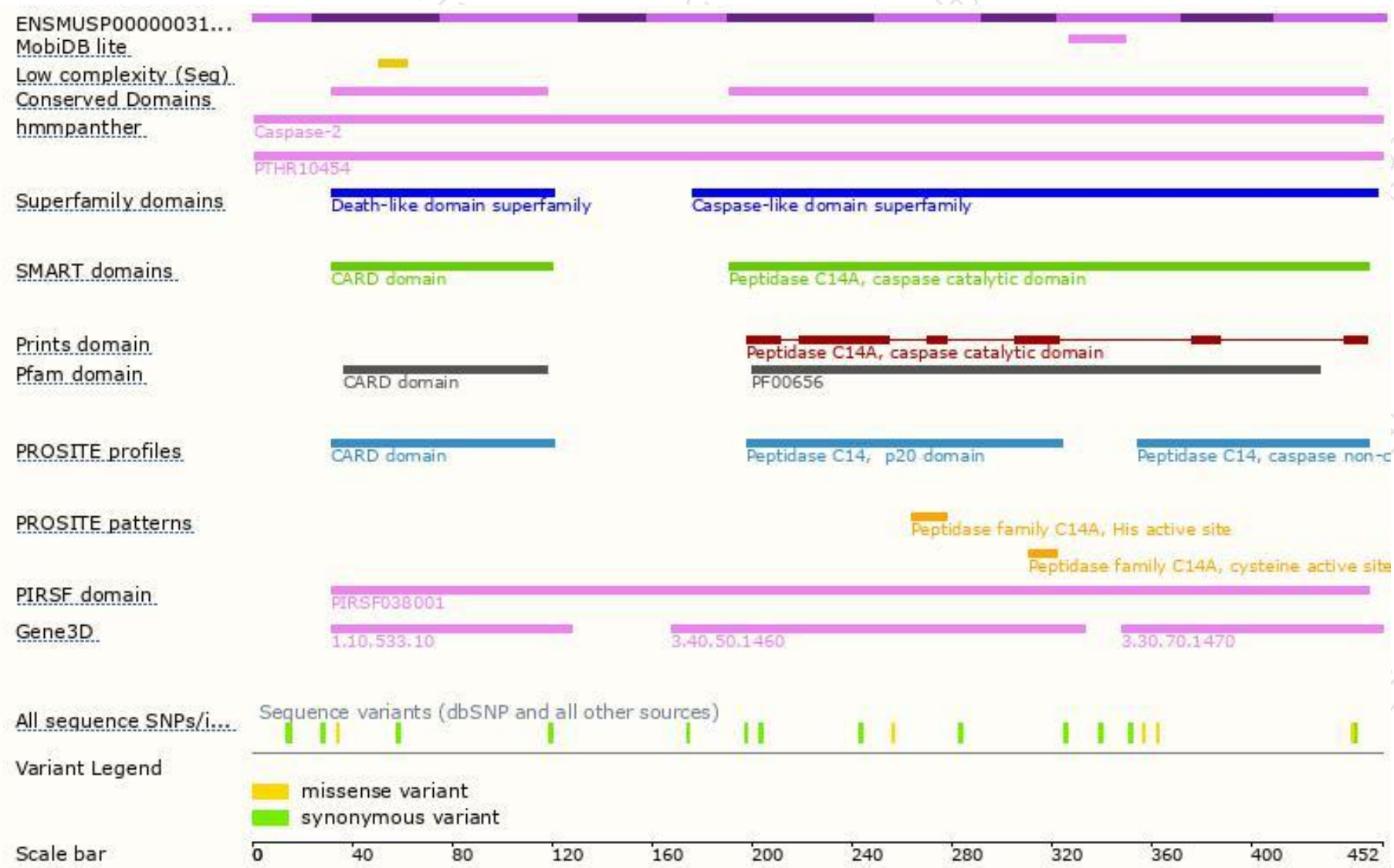




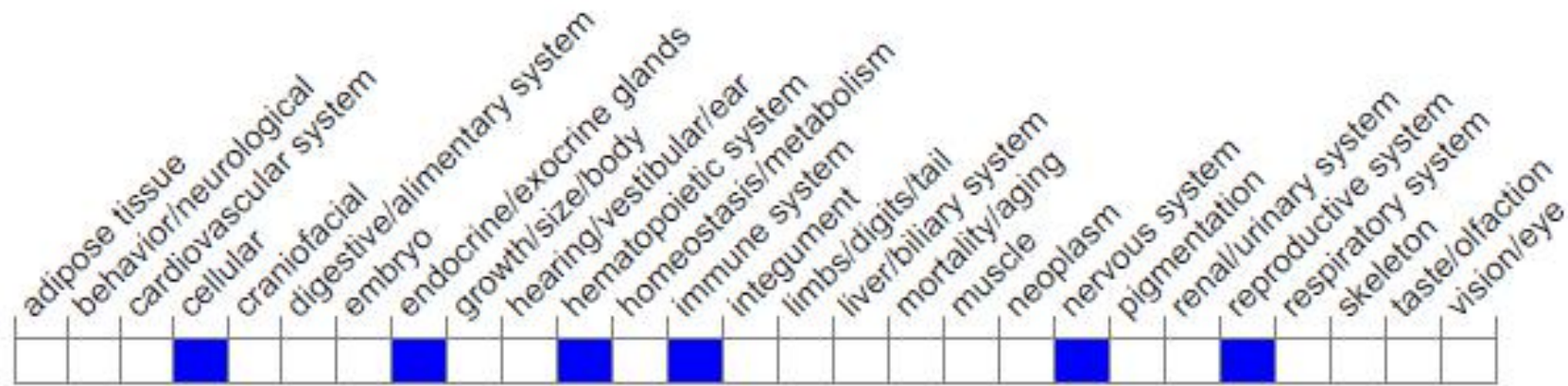
# Protein domain



集萃药康  
GemPharmatech



# 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, Homozygous mutation of this gene results in abnormal apoptosis. Apoptosis is reduced in the female germline, but is increased in sympathetic neurons during development.

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

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