Casp3 Cas9-KO Strategy

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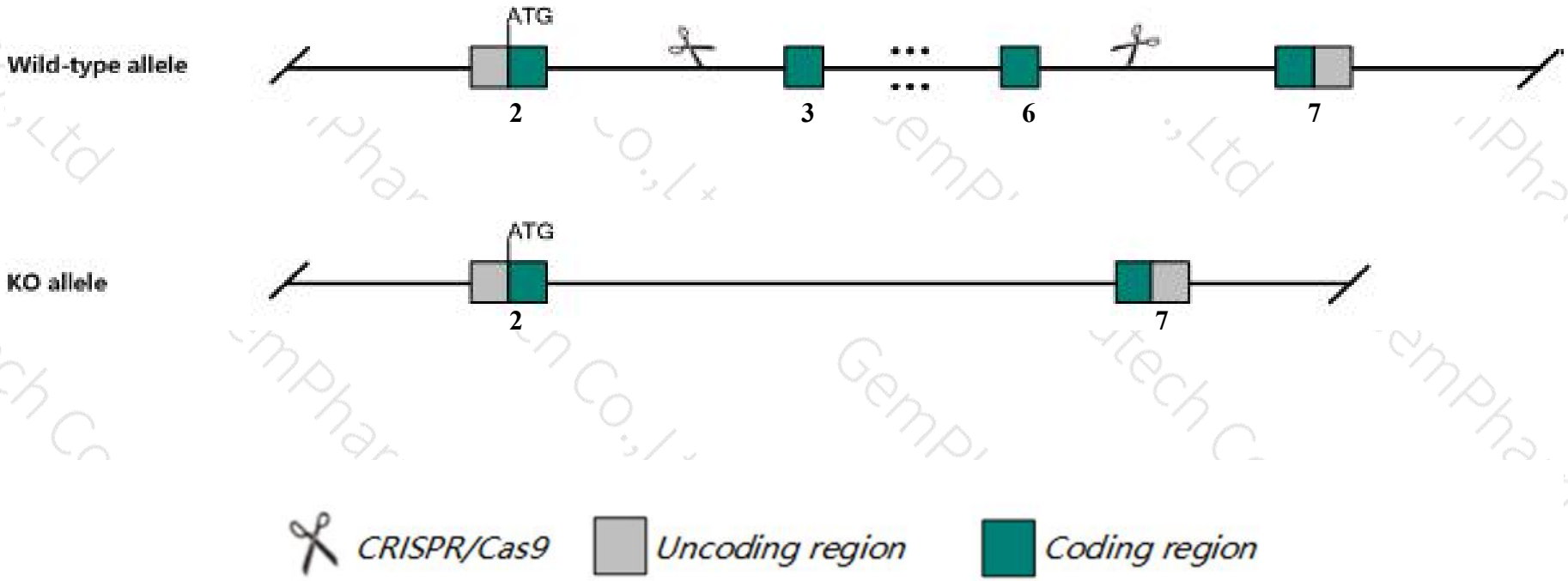
Project Overview

Project Name	***Casp3***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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



Technical routes

➢ 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

Notice

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

Gene information（NCBI）

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Casp3 caspase 3 [Mus musculus (house mouse)]

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

Summary

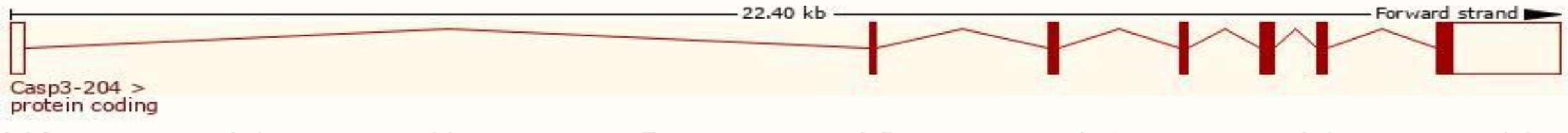
Official Symbol	Casp3 provided by MGI
Official Full Name	caspase 3 provided by MGI
Primary source	MGI:MGI:107739
See related	Ensembl:ENSMUSG00000031628
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; 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 tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

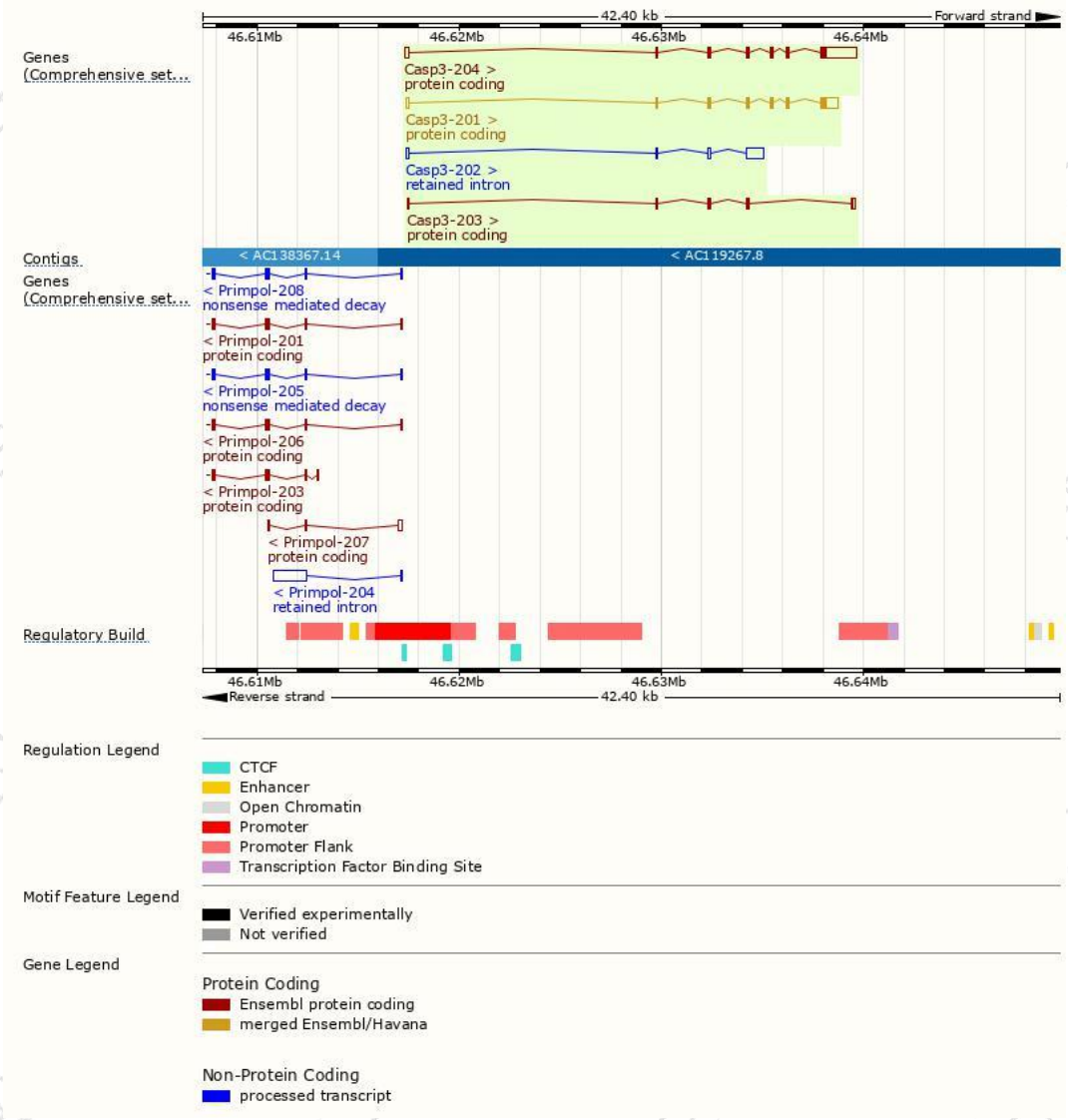
The gene has 4 transcripts,all transcripts are shown below:

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

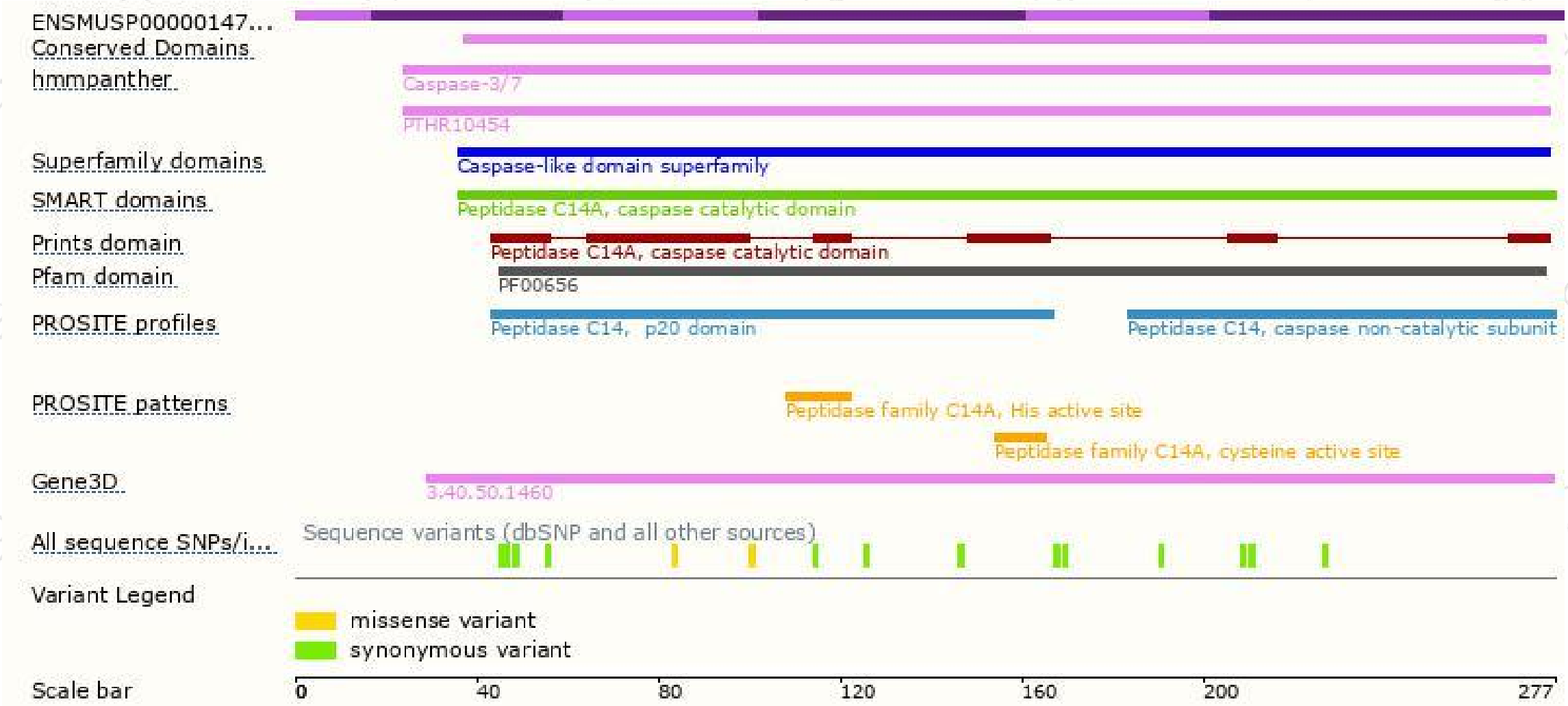
The strategy is based on the design of *Casp3-204* transcript,The transcription is shown below



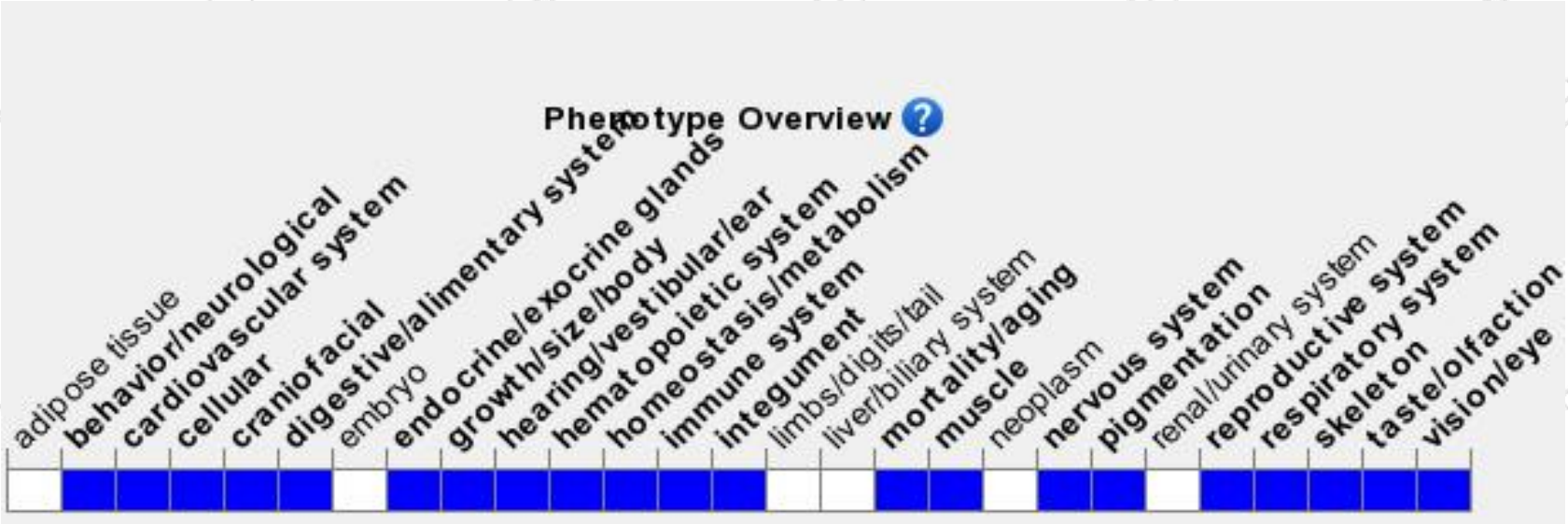
Genomic location distribution



Protein domain



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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