

Capns1 Cas9-CKO Strategy

Designer:

Ruirui Zhang

Reviewer:

Huimin Su

Design Date:

2020-1-22

Project Overview

Project Name

Capns1

Project type

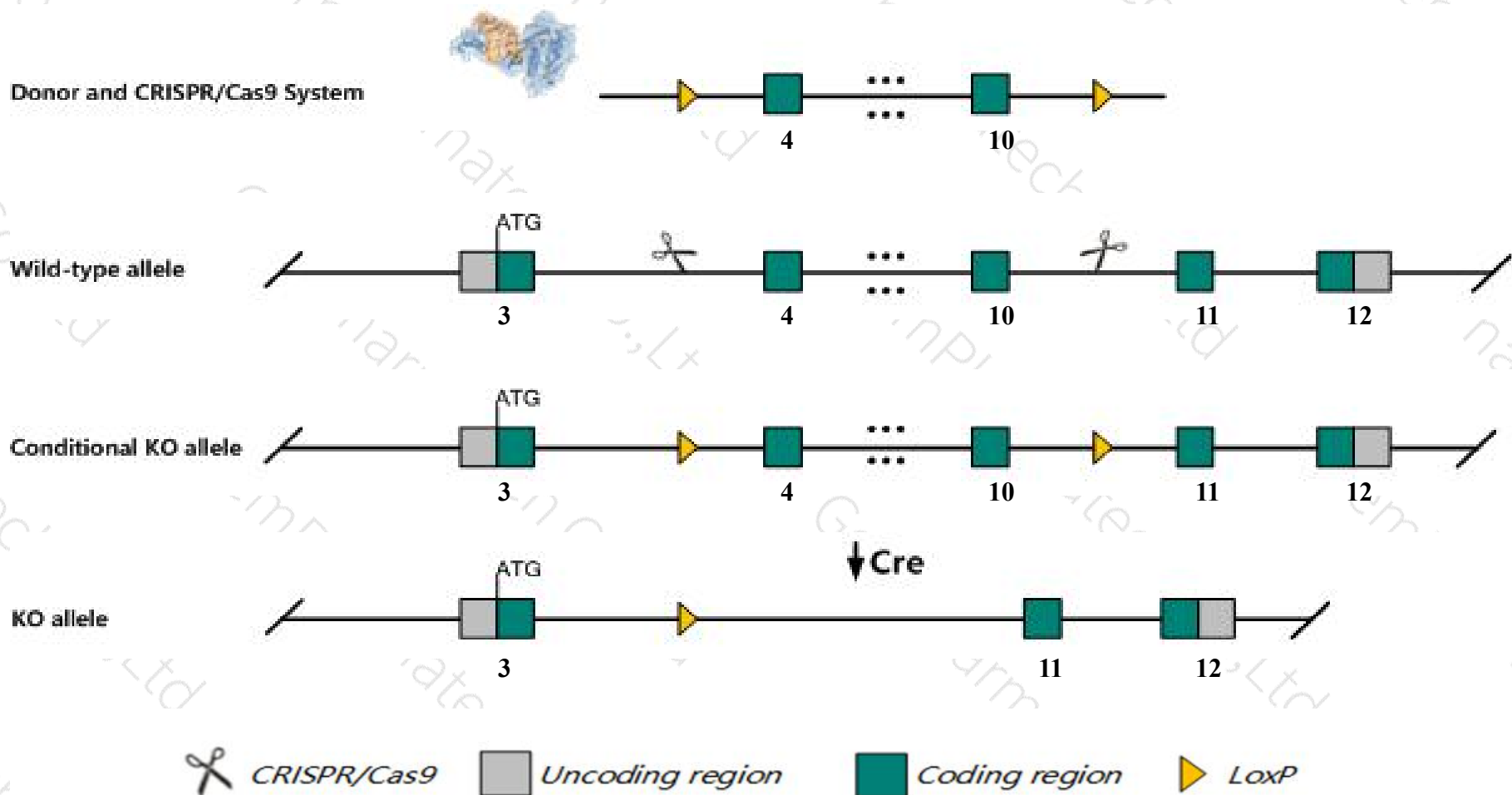
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Capns1* gene. The schematic diagram is as follows:



- The *Capns1* gene has 8 transcripts. According to the structure of *Capns1* gene, exon4-exon10 of *Capns1-201* (ENSMUST000000001845.12) transcript is recommended as the knockout region. The region contains 512bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Capns1* 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, Homozygous mutation of this gene results in embryonic lethality around E11.5. Mutant embryos exhibit cardiac developmental defects, reduced yolk sac vasculature, hemorrhaging in the area between the embryo and amnion, and accumulation of nucleated erythroid cells in the heart chambers, blood vessels, and developing liver.
- This strategy may affect the 5-terminal regulation function of *Gm26810* gene.
- The *Capns1* gene is located on the Chr7. 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)

Capns1 calpain, small subunit 1 [*Mus musculus* (house mouse)]

Gene ID: 12336, updated on 24-Sep-2019

Summary



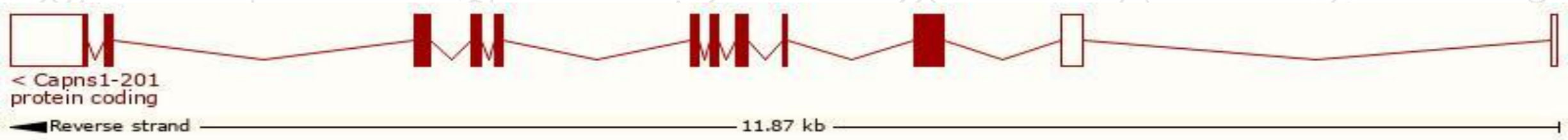
Official Symbol	Capns1 provided by MGI
Official Full Name	calpain, small subunit 1 provided by MGI
Primary source	MGI:MGI:88266
See related	Ensembl:ENSMUSG000000001794
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cdps; Css1; Capa4; Capn4; Capa-4; D7Ert146e
Expression	Ubiquitous expression in adrenal adult (RPKM 274.2), mammary gland adult (RPKM 214.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

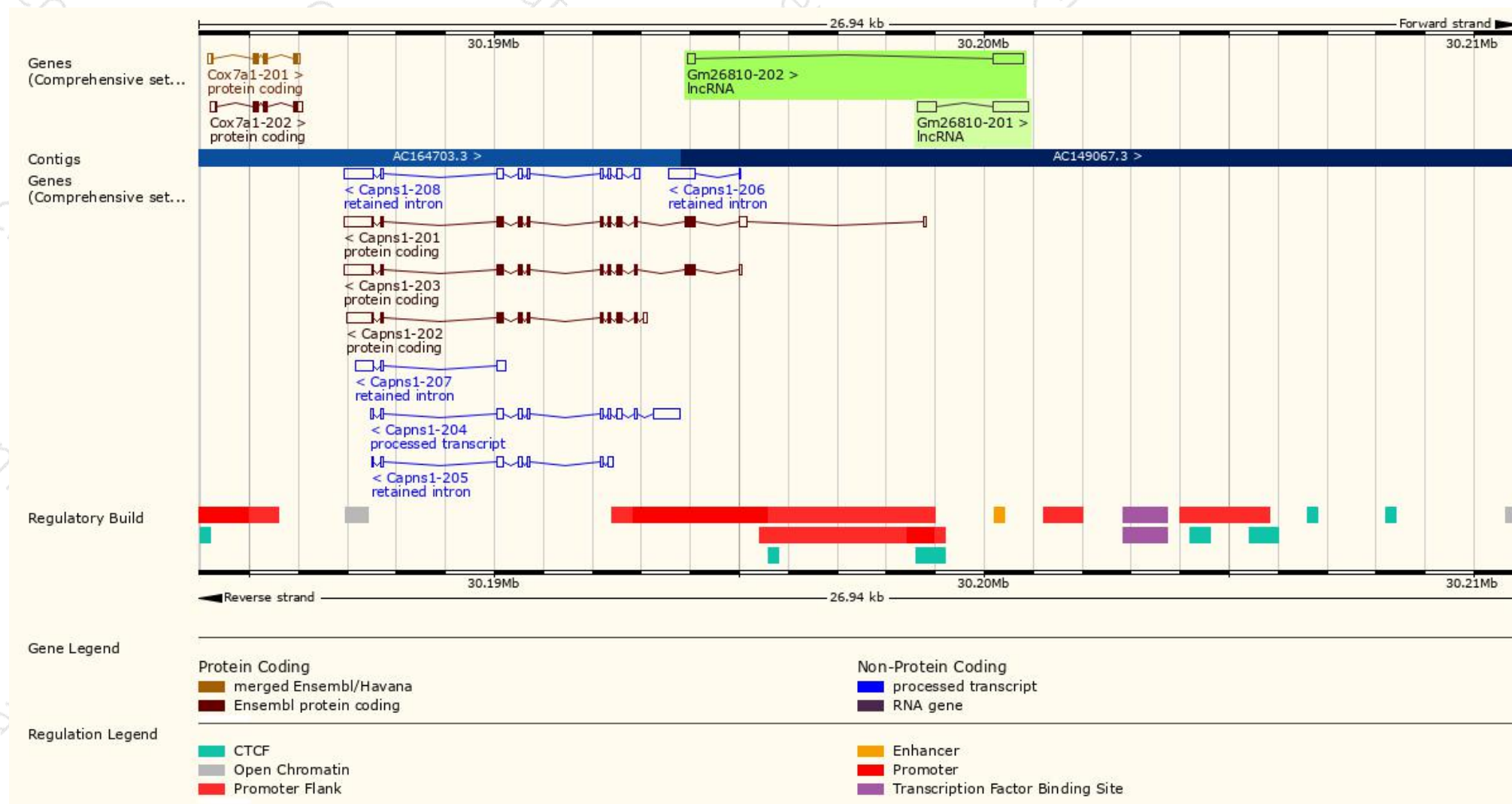
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Capns1-201	ENSMUST00000001845.12	1600	268aa	Protein coding	CCDS21082	A0A0R4IZW8	TSL:5 GENCODE basic APPRIS P2
Capns1-203	ENSMUST00000126116.2	1429	268aa	Protein coding	CCDS21082	A0A0R4IZW8	TSL:1 GENCODE basic APPRIS P2
Capns1-202	ENSMUST00000108196.7	1192	200aa	Protein coding	-	A0A0R4J1C2	TSL:1 GENCODE basic APPRIS ALT2
Capns1-204	ENSMUST00000129761.7	1157	No protein	Processed transcript	-	-	TSL:5
Capns1-208	ENSMUST00000207082.1	1241	No protein	Retained intron	-	-	TSL:1
Capns1-207	ENSMUST00000148973.7	600	No protein	Retained intron	-	-	TSL:2
Capns1-206	ENSMUST00000146852.1	587	No protein	Retained intron	-	-	TSL:2
Capns1-205	ENSMUST00000141851.1	507	No protein	Retained intron	-	-	TSL:2

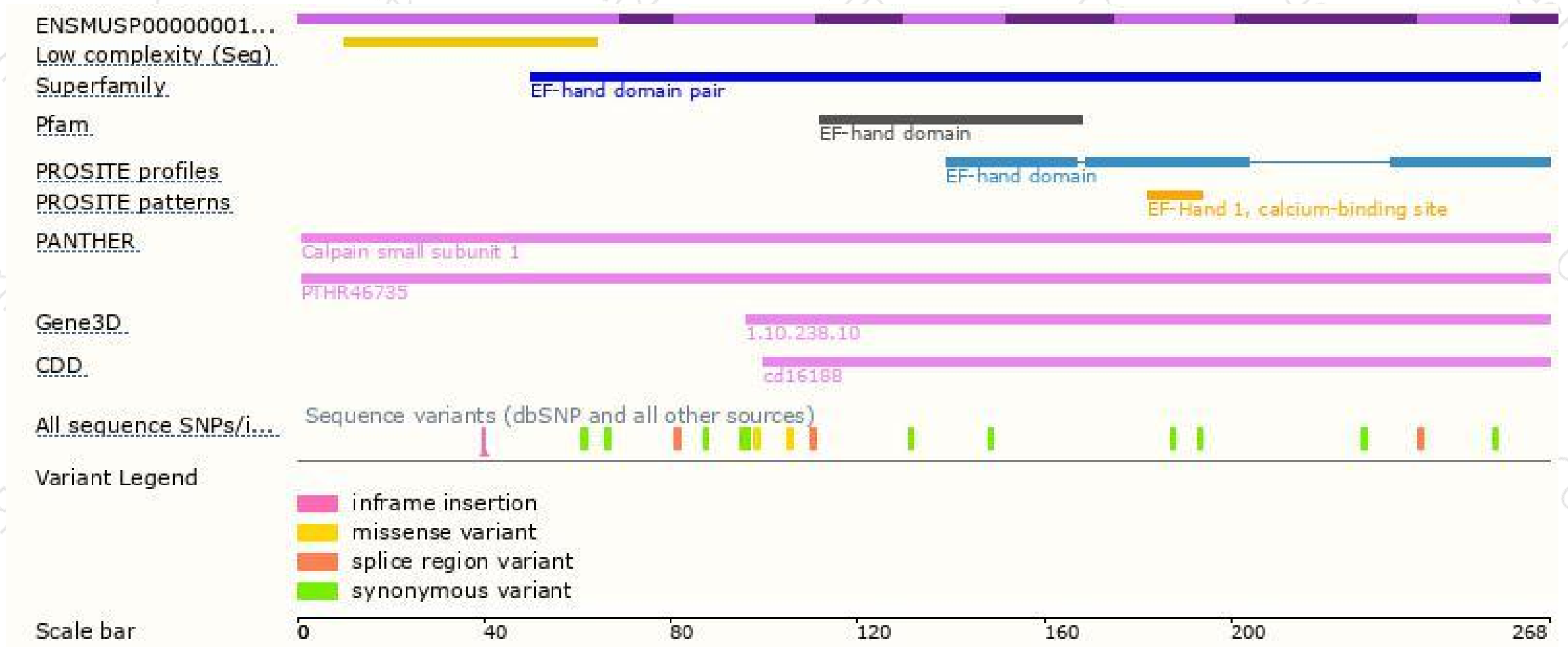
The strategy is based on the design of *Capns1-201* transcript,The transcription is shown below



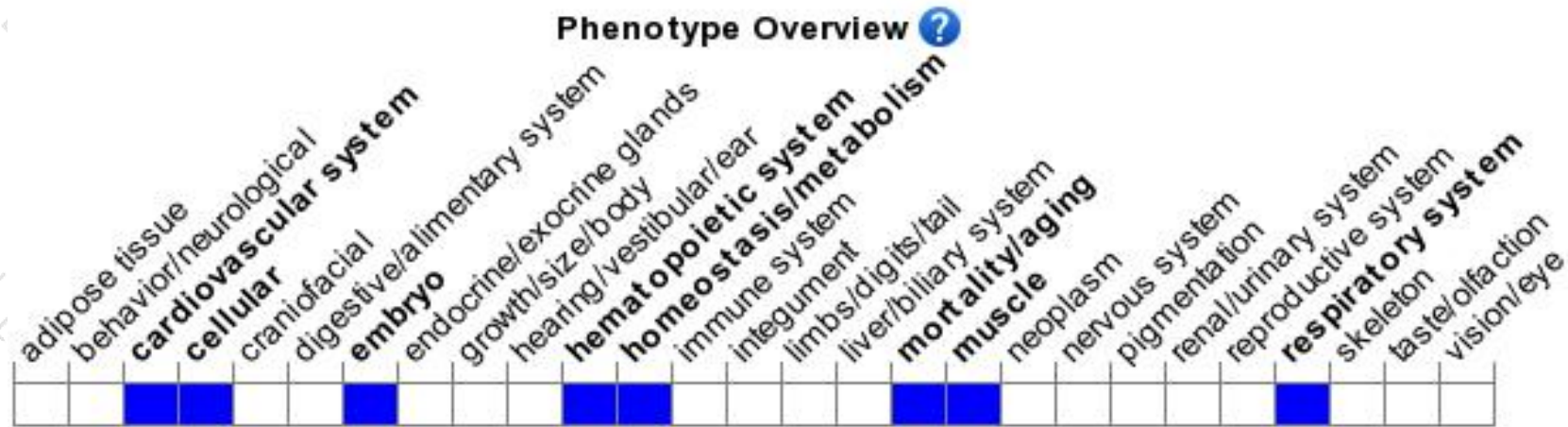
Genomic location distribution



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/>).

According to the existing MGI data, Homozygous mutation of this gene results in embryonic lethality around E11.5. Mutant embryos exhibit cardiac developmental defects, reduced yolk sac vasculature, hemorrhaging in the area between the embryo and amnion, and accumulation of nucleated erythroid cells in the heart chambers, blood vessels, and developing liver.

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

Tel: 400-9660890

