



Aimp2 Cas9-CKO Strategy

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Reviewer: Xiaojing Li

Design Date: 2020-8-3

Project Overview

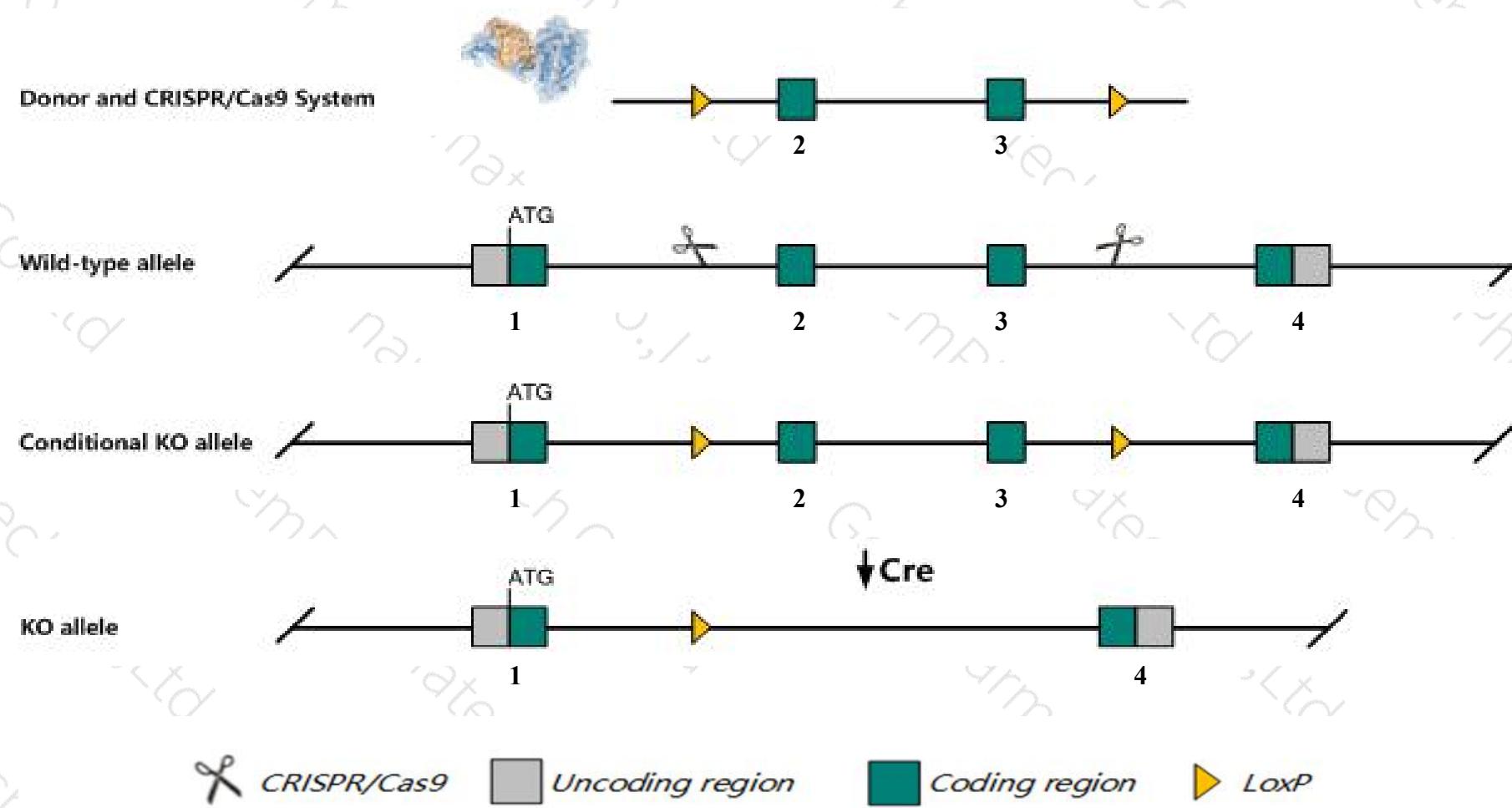
Project Name*Aimp2*

Project type**Cas9-CKO**

Strain background**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Aimp2* gene. The schematic diagram is as follows:



Technical routes

- The *Aimp2* gene has 4 transcripts. According to the structure of *Aimp2* gene, exon2-exon3 of *Aimp2*-201(ENSMUST00000031613.10) transcript is recommended as the knockout region. The region contains 439bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Aimp2* 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.



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Notice

- According to the existing MGI data, mice homozygous for a gene trapped allele are born with no apparent phenotype but die within 2 days of birth of unknown causes.
- The flox region is about 3 kb away from the 5th end of the Pms2 gene, which may affect the regulation of this gene.
- The flox region is about 300bp away from the 3th end of the Eif2ak1 gene, which may affect the regulation of this gene.
- The *Aimp2* gene is located on the Chr5. 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)

Aimp2 aminoacyl tRNA synthetase complex-interacting multifunctional protein 2 [Mus musculus (house mouse)]

Gene ID: 231872, updated on 13-Mar-2020

Summary



Official Symbol Aimp2 provided by [MGI](#)

Official Full Name aminoacyl tRNA synthetase complex-interacting multifunctional protein 2 provided by [MGI](#)

Primary source [MGI:MGI:2385237](#)

See related [Ensembl:ENSMUSG00000029610](#)

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 AA407136, AA407225, Aimp2(p38), Jtv1

Expression Ubiquitous expression in adrenal adult (RPKM 41.7), liver E14.5 (RPKM 30.1) and 28 other tissues [See more](#)

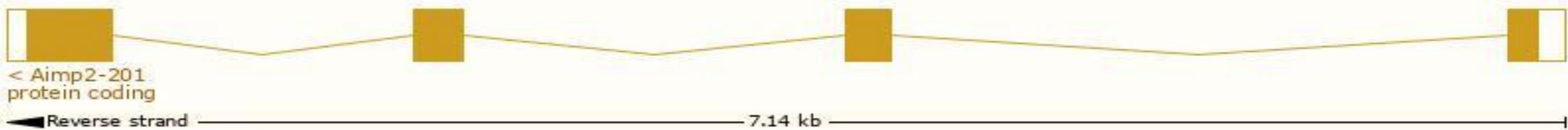
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Aimp2-201	ENSMUST0000031613.10	1185	320aa	Protein coding	CCDS51692	Q8R010	TSL:1 GENCODE basic APPRIS P1
Aimp2-202	ENSMUST00000100483.2	1073	280aa	Protein coding	CCDS39374	Q8R3V2	TSL:1 GENCODE basic
Aimp2-203	ENSMUST00000128440.1	752	No protein	Retained intron	-	-	TSL:2
Aimp2-204	ENSMUST00000149473.1	591	No protein	Retained intron	-	-	TSL:2

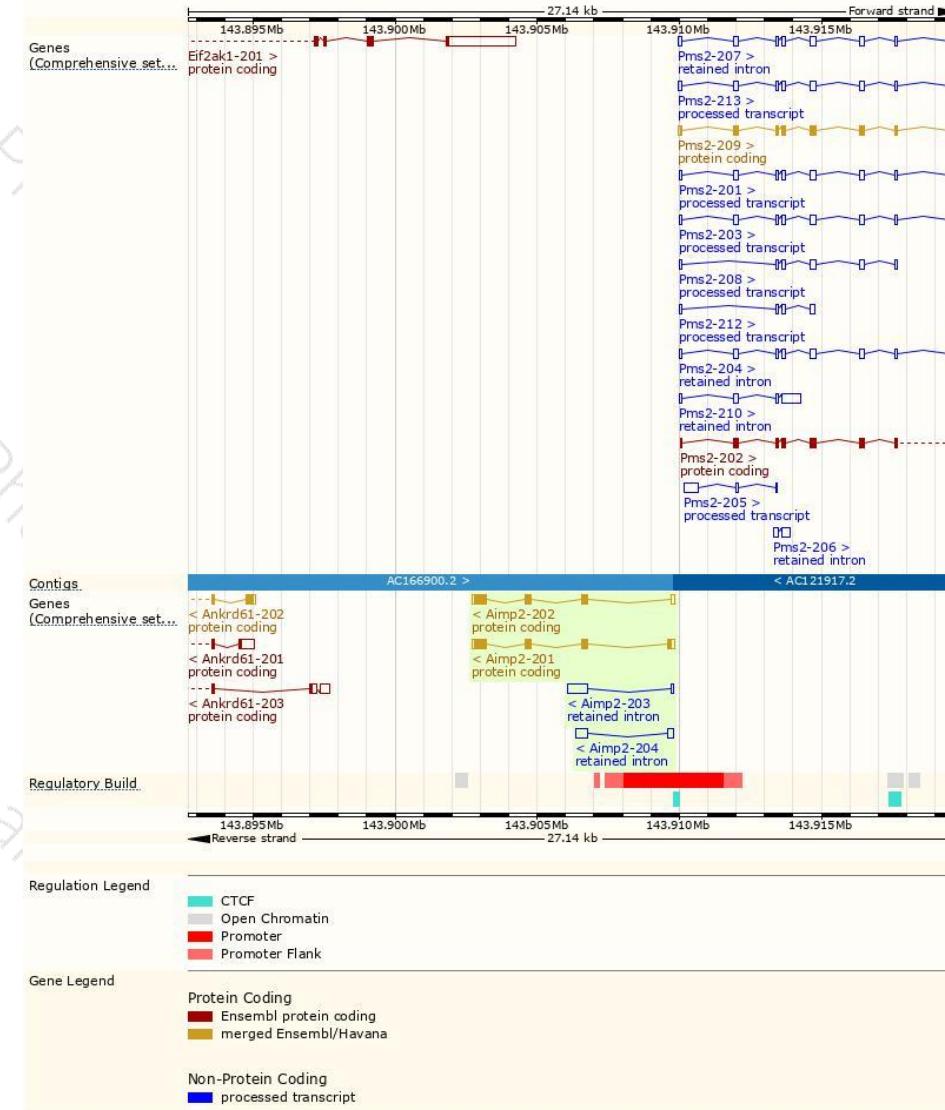
The strategy is based on the design of *Aimp2-201* transcript, the transcription is shown below:





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Genomic location distribution



Protein domain

ENSMUSP000000031...

Low complexity (Seq)

Superfamily

Pfam

AIMP2, lysyl-tRNA synthetase binding domain

AIMP2, thioredoxin-like domain

Glutathione S-transferase, C-terminal

Glutathione S-transferase, C-te

PANTHER

Aminoacyl tRNA synthetase complex-interacting multifunctional protein 2

Gene3D

1,20,1050,130

CDD

cd03200

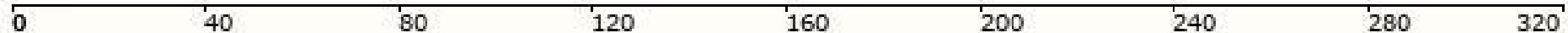
All sequence SNPs/i...

Sequence variants (dbSNP and all other sources)

Variant Legend

- missense variant
- splice region variant
- synonymous variant

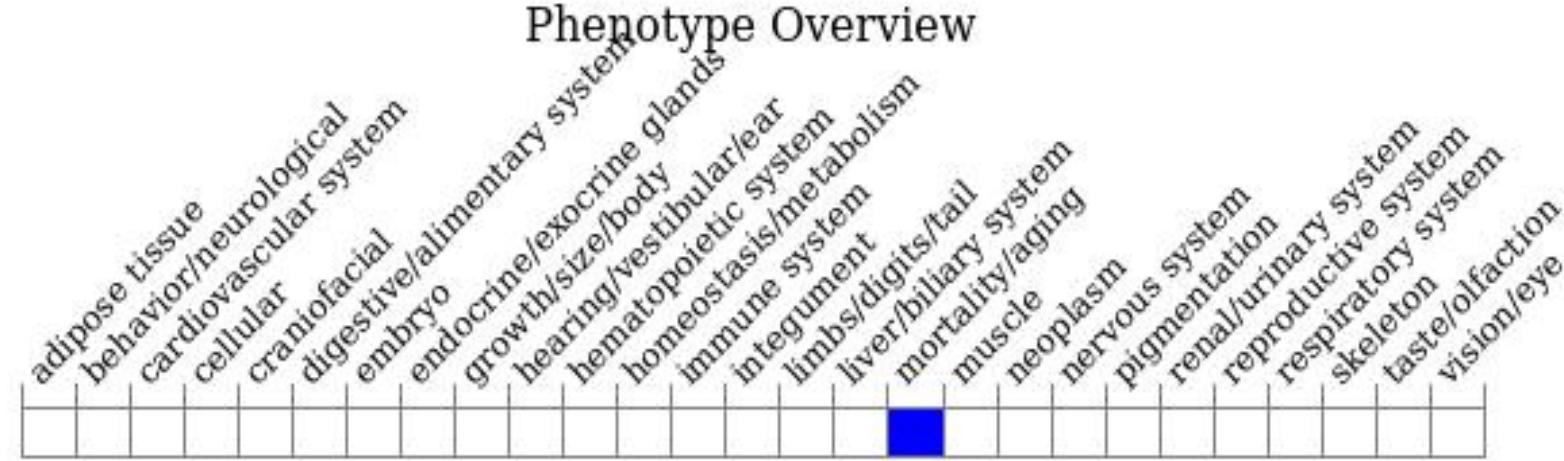
Scale bar





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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, mice homozygous for a gene trapped allele are born with no apparent phenotype but die within 2 days of birth of unknown causes.



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

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