Adam12 Cas9-CKO Strategy

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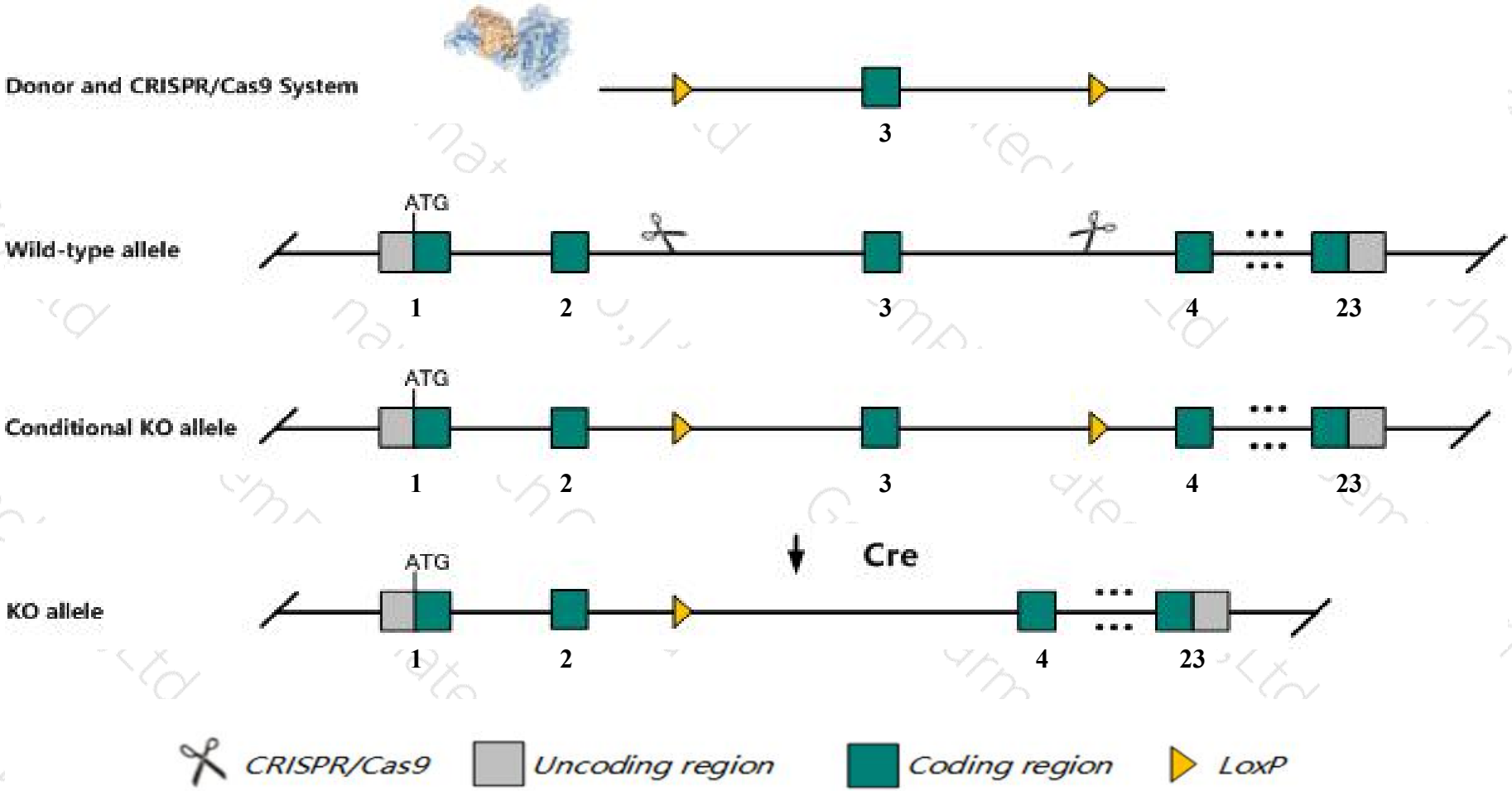
Project Overview

Project Name	***Adam12***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Adam12* gene. The schematic diagram is as follows:



Technical routes

➢ The *Adam12* gene has 7 transcripts. According to the structure of *Adam12* gene, exon3 of *Adam12-201*(ENSMUST00000067680.10) transcript is recommended as the knockout region.The region contains 74bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Adam12* 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.

Notice

➢ According to the existing MGI data,homozygous null mice display partial postnatal lethality, decreased brown fat, and impaired formation of neck and interscapular muscles.

➢ The effect on transcript *Adam12*-204 is unknown.

➢ Transcript *Adam12*-205&206&207 may not be affected.

➢ The *Adam12* 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）

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Adam12 a disintegrin and metallopeptidase domain 12 (meltrin alpha) [Mus musculus (house mouse)]

Gene ID: 11489, updated on 13-Mar-2020

Summary

Official Symbol	Adam12 provided by MGI
Official Full Name	a disintegrin and metallopeptidase domain 12 (meltrin alpha) provided byMGI
Primary source	MGI:MGI:105378
See related	Ensembl:ENSMUSG00000054555
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	Mltna
Summary	This gene encodes a member of a disintegrin and metalloprotease (ADAM) family of endoproteases that play important roles in various biological processes including cell signaling, adhesion and migration. The encoded preproprotein undergoes proteolytic processing to generate a mature, functional protein that localizes to the cell surface. About a third of the mice lacking the encoded protein die before weaning. Overexpression of the encoded protein in a mouse model of Duchenne muscular dystrophy alleviates the muscle pathology by preventing cell necrosis and inflammation. [provided by RefSeq, May 2016]
Expression	Broad expression in subcutaneous fat pad adult (RPKM 12.7), mammary gland adult (RPKM 6.4) and 16 other tissuesSee more
Orthologs	human all

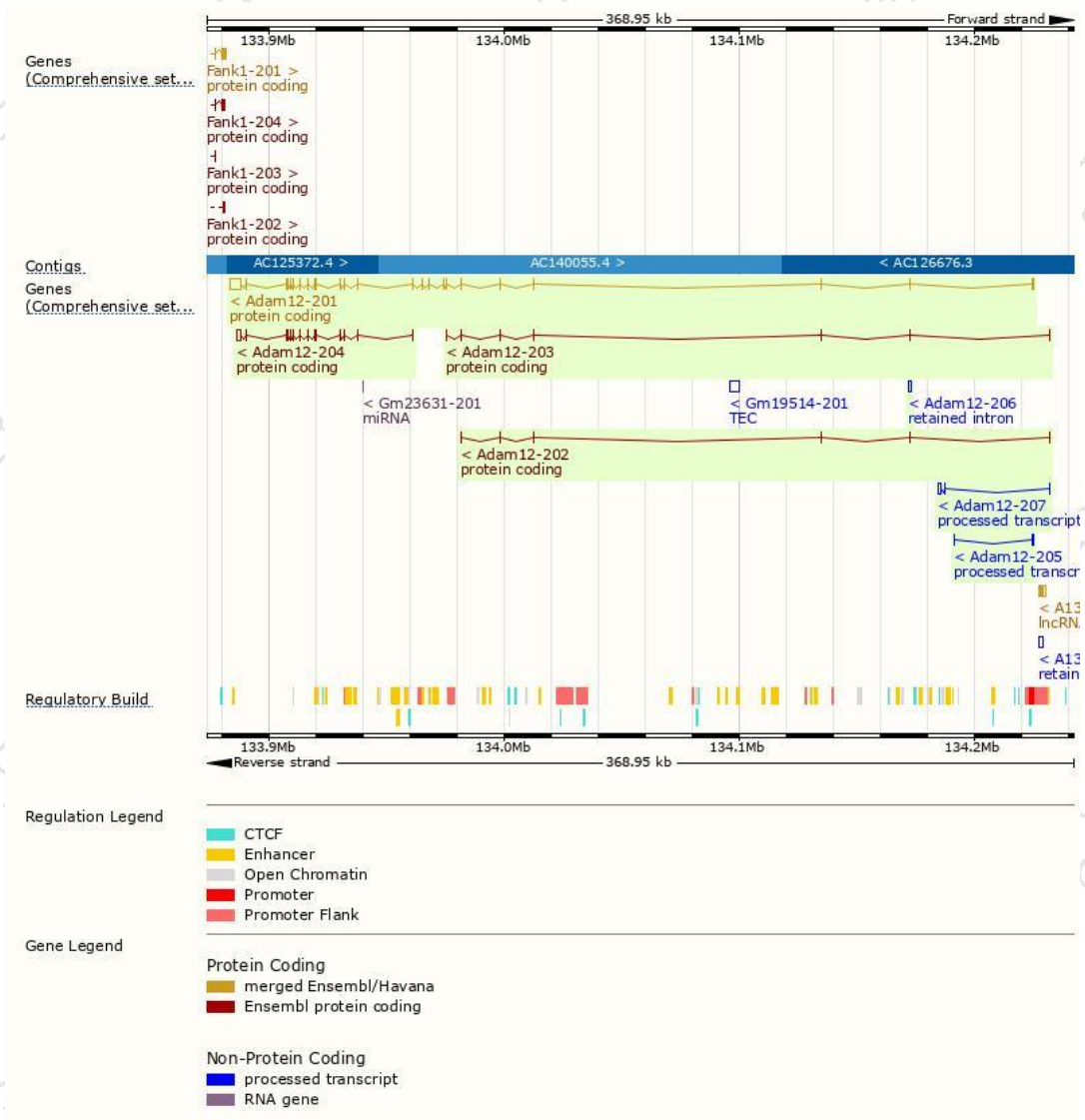
Transcript information（Ensembl）

The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Adam12-201	ENSMUST00000067680.10	7675	903aa	Protein coding	CCDS21938	Q61824	TSL:1 GENCODE basic APPRIS P1
Adam12-204	ENSMUST00000138363.1	3492	581aa	Protein coding	-	F6YWH6	CDS 5' incomplete TSL:1
Adam12-203	ENSMUST00000134504.7	647	189aa	Protein coding	-	D3Z117	CDS 3' incomplete TSL:5
Adam12-202	ENSMUST00000127524.1	630	168aa	Protein coding	-	D3YUK3	CDS 3' incomplete TSL:3
Adam12-207	ENSMUST00000206426.1	1463	No protein	Processed transcript	-	-	TSL:1
Adam12-205	ENSMUST00000154144.1	675	No protein	Processed transcript	-	-	TSL:3
Adam12-206	ENSMUST00000206313.1	1043	No protein	Retained intron	-	-	TSL:NA

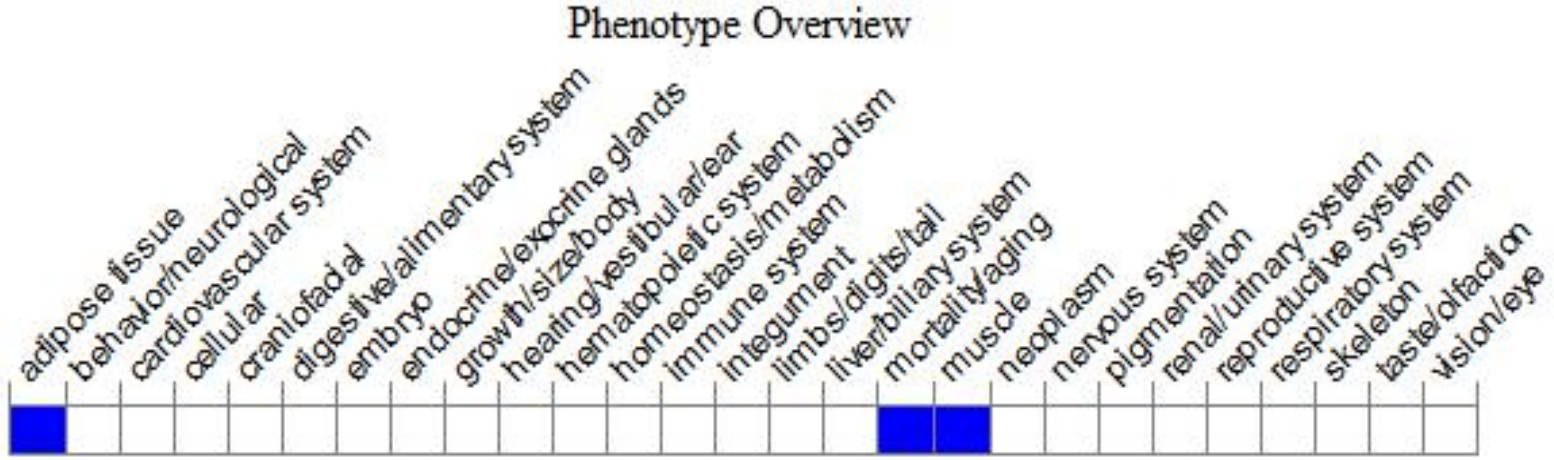
The strategy is based on the design of *Adam12-201* transcript,the transcription is shown below:

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 null mice display partial postnatal lethality, decreased brown fat, and impaired formation of neck and interscapular muscles.

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

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