Adamts7 Cas9-KO Strategy

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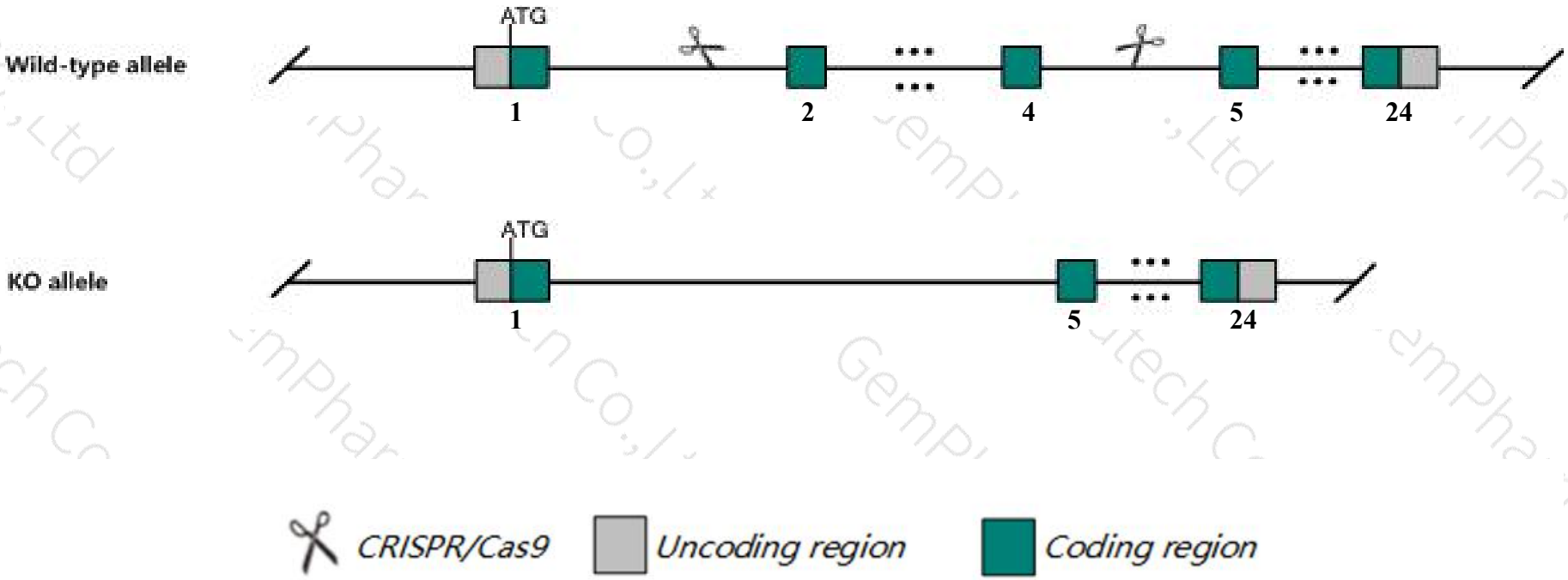
Project Overview

Project Name	***Adamts7***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Adamts7* gene. The schematic diagram is as follows:



Technical routes

➢ The *Adamts7* gene has 8 transcripts. According to the structure of *Adamts7* gene, exon2-exon4 of *Adamts7-201* (ENSMUST00000113059.7) transcript is recommended as the knockout region.The region contains 701bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Adamts7* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- According to the existing MGI data,Homozygotes for a null allele show increased lung function parameters, reduced endothelial cell migration and proliferation, increased re-endothelialization and ameliorated neointima formation after carotid artery injury, and increased oval cell activation and biliary fibrosis after liver injury.

- The *Adamts7* gene is located on the Chr9. 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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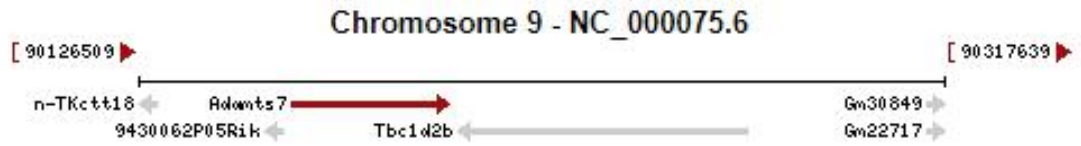
Adamts7 a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 7 [*Mus musculus* (house mouse)]

Gene ID: 108153, updated on 30-Nov-2019

Summary

Official Symbol	Adamts7 provided by MGI
Official Full Name	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 7 provided by MGI
Primary source	MGI:MGI:1347346
See related	Ensembl:ENSMUSG00000032363
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	ADAM-TS7; ADAMTS7B
Summary	This gene encodes a member of "a disintegrin and metalloproteinase with thrombospondin motifs" (ADAMTS) family of multi-domain matrix-associated metalloendopeptidases that have diverse roles in tissue morphogenesis and pathophysiological remodeling, in inflammation and in vascular biology. The encoded preproprotein undergoes proteolytic processing to generate an active, zinc-dependent enzyme that degrades cartilage oligomeric matrix protein. The deficiency of the encoded protein decreases atherosclerosis in genetically hyperlipidemic mice and in response to vascular injury. Alternative splicing results in multiple transcript variants encoding different isoforms, some of which may undergo similar processing. [provided by RefSeq, May 2016]
Expression	Broad expression in limb E14.5 (RPKM 11.2), subcutaneous fat pad adult (RPKM 9.1) and 21 other tissues See more
Orthologs	human all

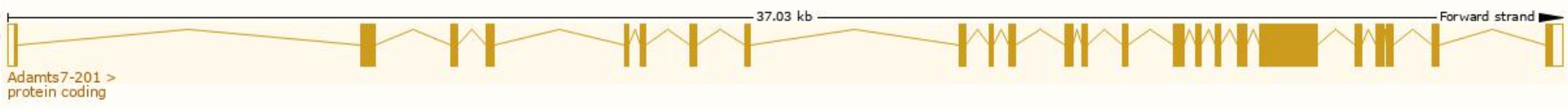


Transcript information（Ensembl）

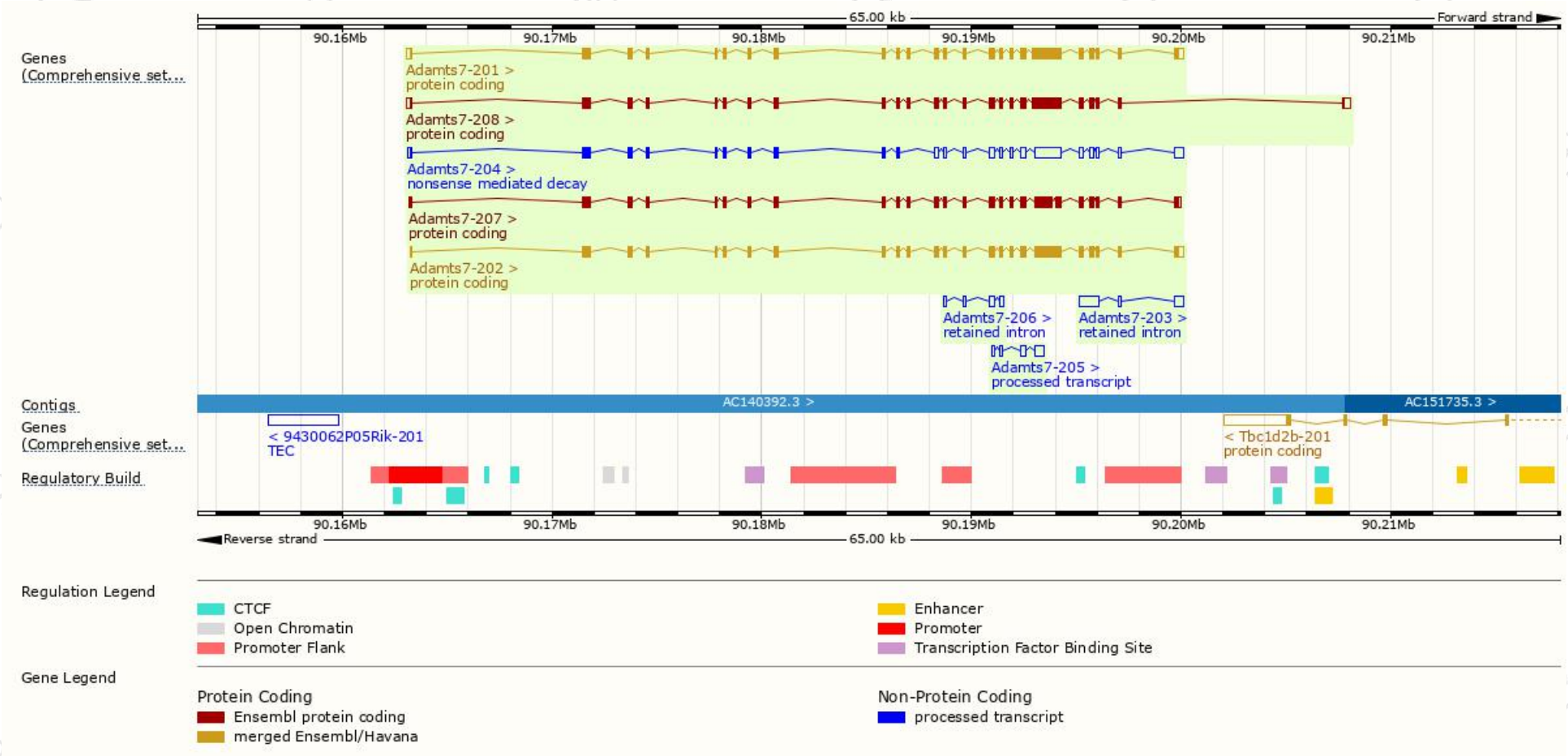
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Adamts7-201	ENSMUST00000113059.7	5379	1657aa	Protein coding	CCDS85708	Q68SA9	TSL:5 GENCODE basic APPRIS ALT2
Adamts7-202	ENSMUST00000113060.2	5098	1615aa	Protein coding	CCDS40724	Q68SA9	TSL:1 GENCODE basic APPRIS P3
Adamts7-207	ENSMUST00000147250.7	4833	1556aa	Protein coding	CCDS81050	F6UD05	TSL:1 GENCODE basic APPRIS ALT2
Adamts7-208	ENSMUST00000167122.7	5338	1633aa	Protein coding	-	E9PX36	TSL:5 GENCODE basic APPRIS ALT2
Adamts7-204	ENSMUST00000134996.7	5052	506aa	Nonsense mediated decay	-	D6RI90	TSL:1
Adamts7-205	ENSMUST00000138227.1	922	No protein	Processed transcript	-	-	TSL:3
Adamts7-203	ENSMUST00000124441.1	1497	No protein	Retained intron	-	-	TSL:1
Adamts7-206	ENSMUST00000144943.1	706	No protein	Retained intron	-	-	TSL:3

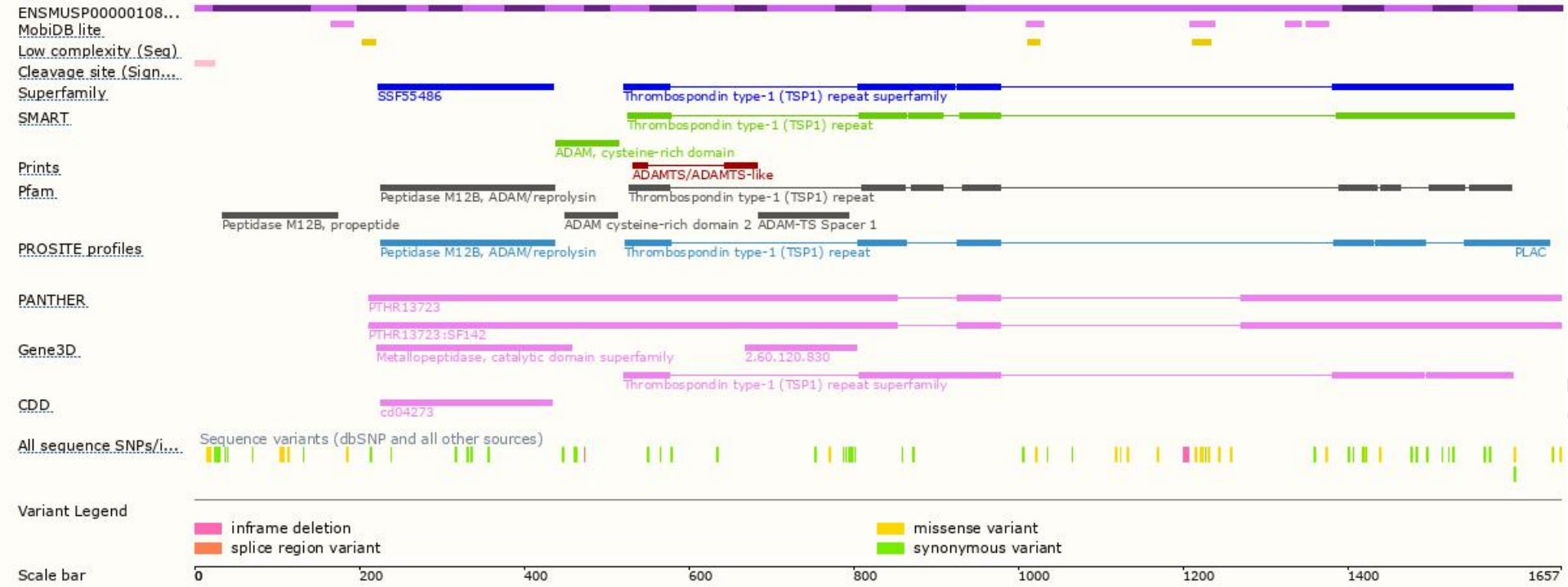
The strategy is based on the design of *Adamts7-201* transcript,The transcription is shown below



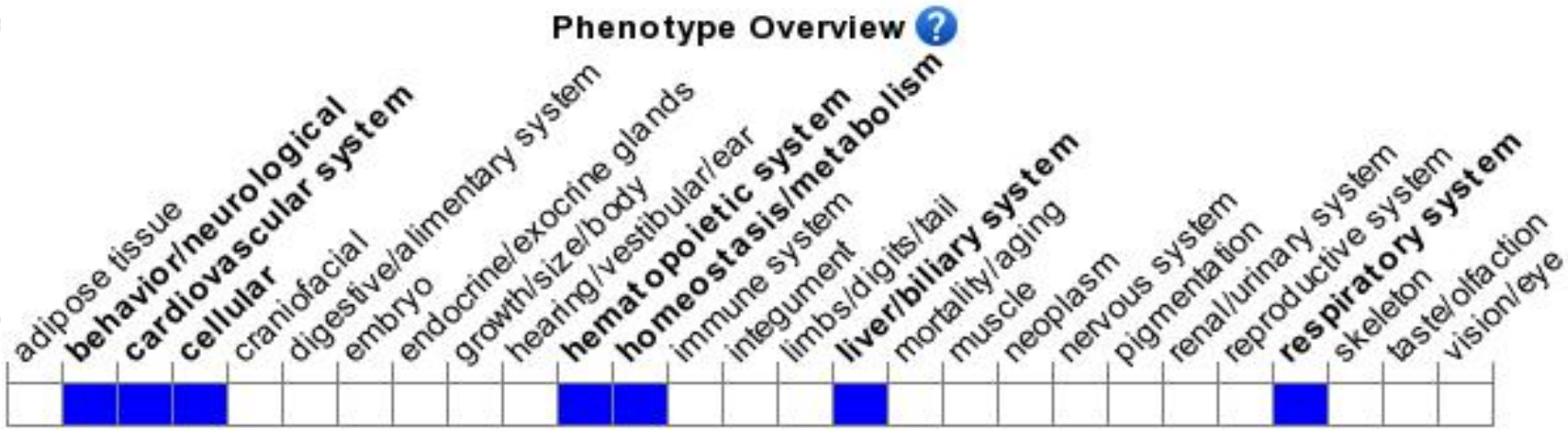
Genomic location distribution



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,Homozygotes for a null allele show increased lung function parameters, reduced endothelial cell migration and proliferation, increased re-endothelialization and ameliorated neointima formation after carotid artery injury, and increased oval cell activation and biliary fibrosis after liver injury.

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

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