Adamts13 Cas9-KO Strategy

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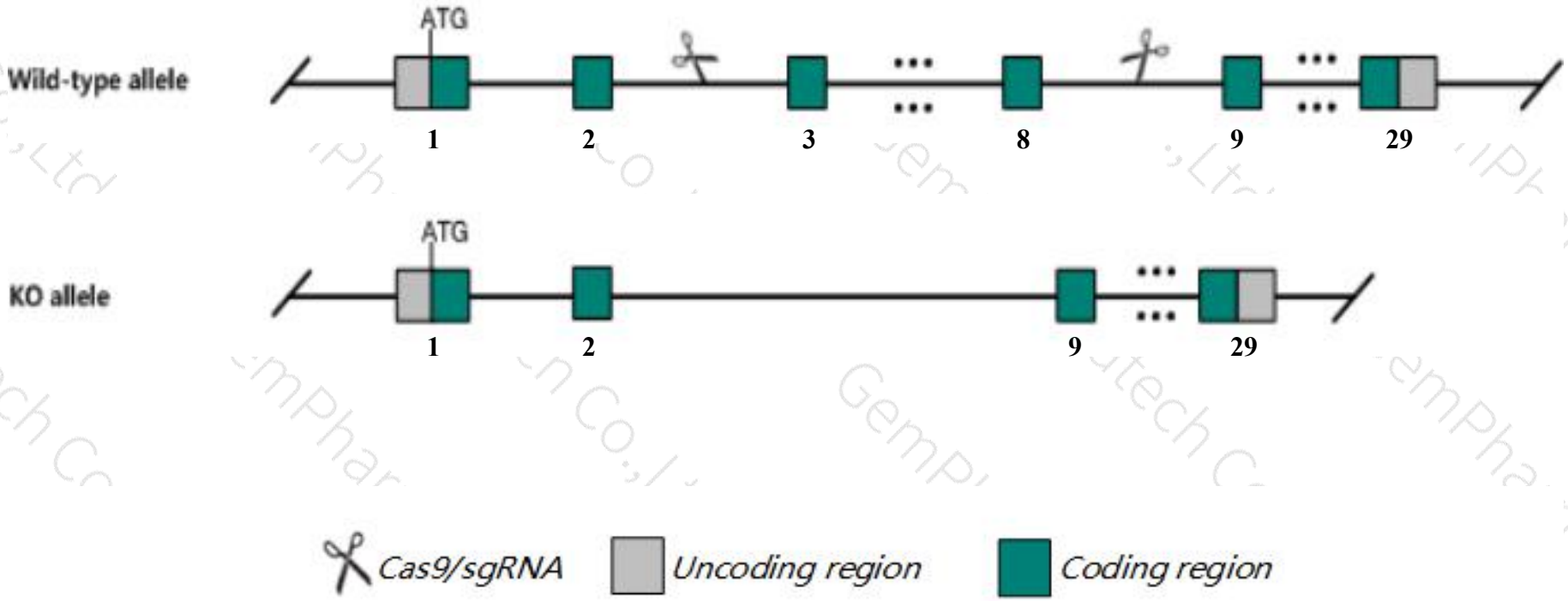
Design Date: 2020-10-30

Project Overview

Project Name	***Adamts13***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Adamts13* gene. The schematic diagram is as follows:



Technical routes

➢ The *Adamts13* gene has 3 transcripts. According to the structure of *Adamts13* gene, exon3-exon8 of *Adamts13-202*(ENSMUST00000102891.3) transcript is recommended as the knockout region.The region contains 815bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Adamts13* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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.

Notice

➢ According to the existing MGI data,homozygous mutation of this gene results in thrombocytopenia, decreased survival, and increased susceptibility to developing thrombotic thrombocytopenic purpura after shiga toxin injection. On a different background, mutants are viable and fertile.

➢ The *Adamts13* gene is located on the Chr2. 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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Adamts13 a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 13 [*Mus musculus* (house mouse)]

Gene ID: 279028, updated on 25-Sep-2020

Summary

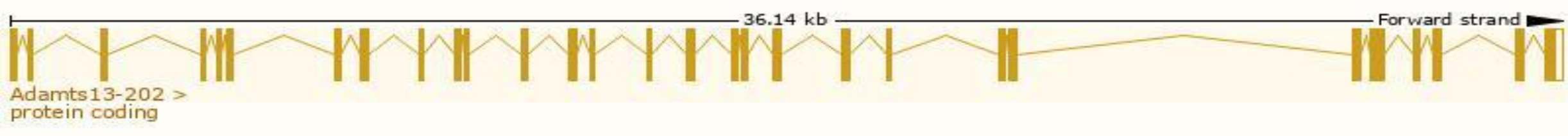
Official Symbol	Adamts13 provided by MGI
Official Full Name	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 13 provided by MGI
Primary source	MGI:MGI:2685556
See related	Ensembl:ENSMUSG00000014852
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Gm710; vWF-CP; ADAM-TS13; ADAMTS-13
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. In certain mouse strains (C57BL/6, for example) an intracisternal A-type particle (IAP) retrotransposon sequence is located in the intron 23 that causes an alternate splicing event resulting in a shorter transcript variants encoding shorter isoforms. The encoded preproprotein undergoes proteolytic processing to generate an active enzyme that cleaves von Willebrand factor (VWF) in circulating blood. [provided by RefSeq, Jul 2016]
Expression	Biased expression in liver adult (RPKM 2.2), liver E18 (RPKM 1.0) and 14 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

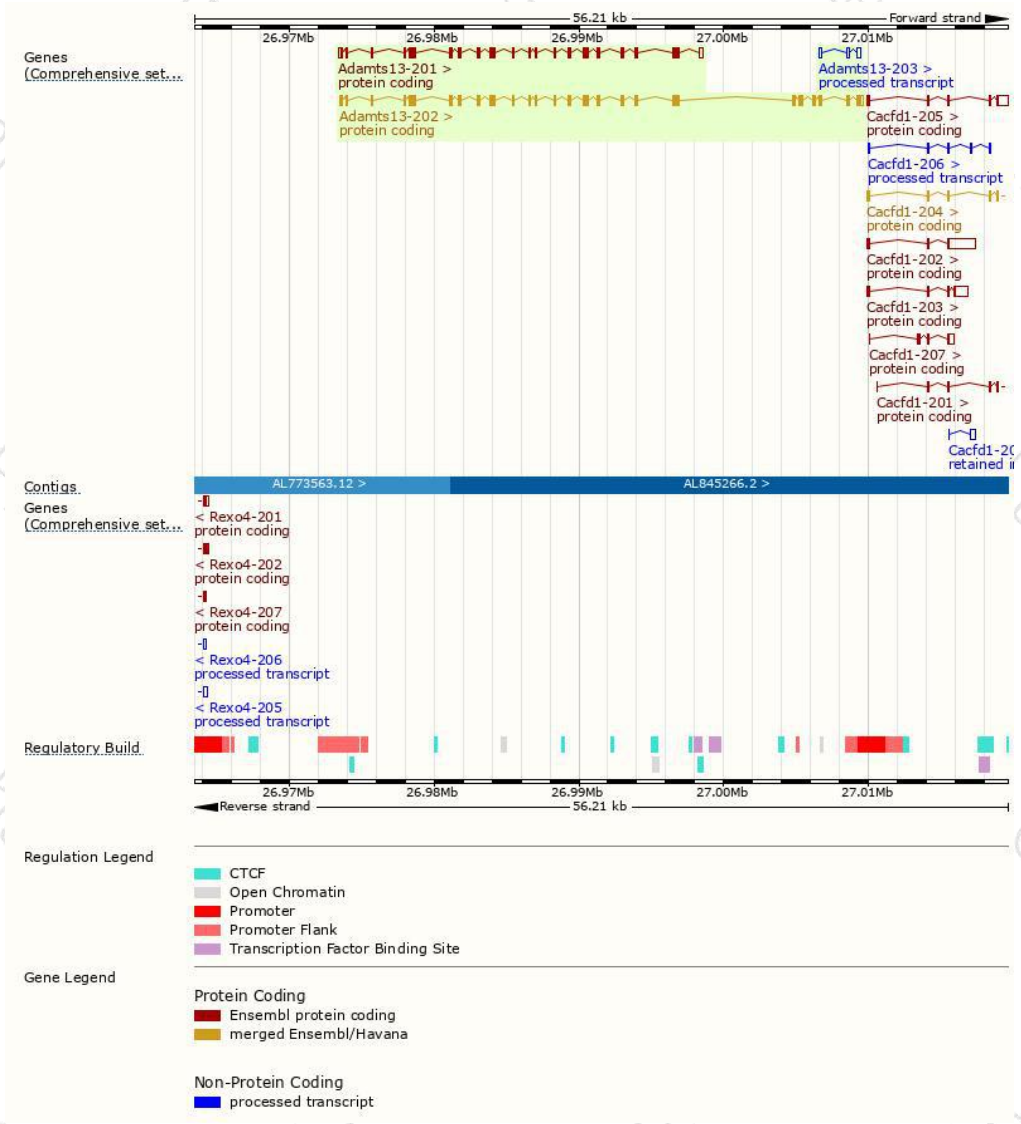
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Adamts13-202	ENSMUST00000102891.3	4506	1426aa	Protein coding	CCDS15820	Q769J6	TSL:1 GENCODE basic APPRIS P1
Adamts13-201	ENSMUST00000014996.13	3474	1037aa	Protein coding	CCDS71010	A2ALB3	TSL:1 GENCODE basic
Adamts13-203	ENSMUST00000147216.1	603	No protein	Processed transcript	-	-	TSL:3

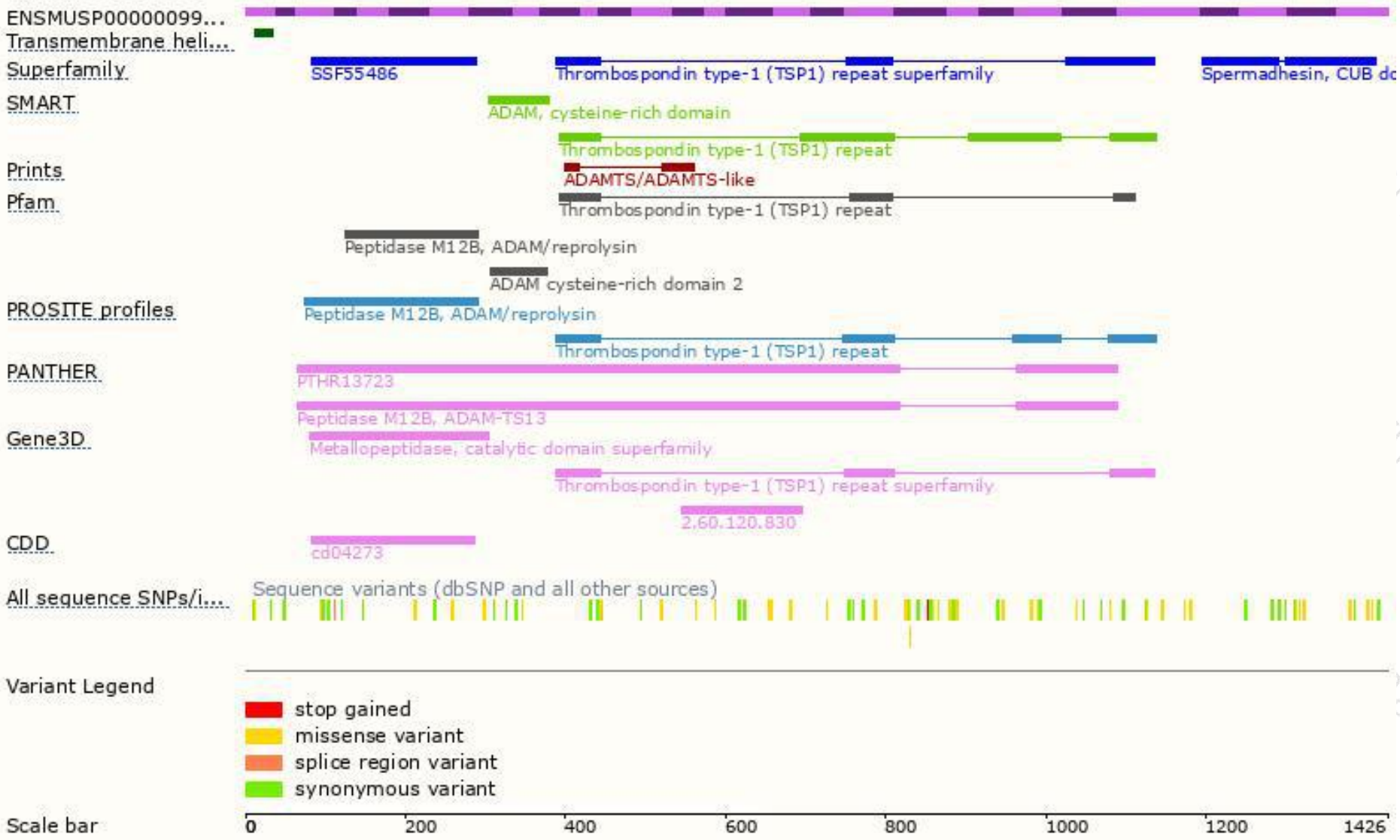
The strategy is based on the design of *Adamts13-202* transcript,the transcription is shown below:



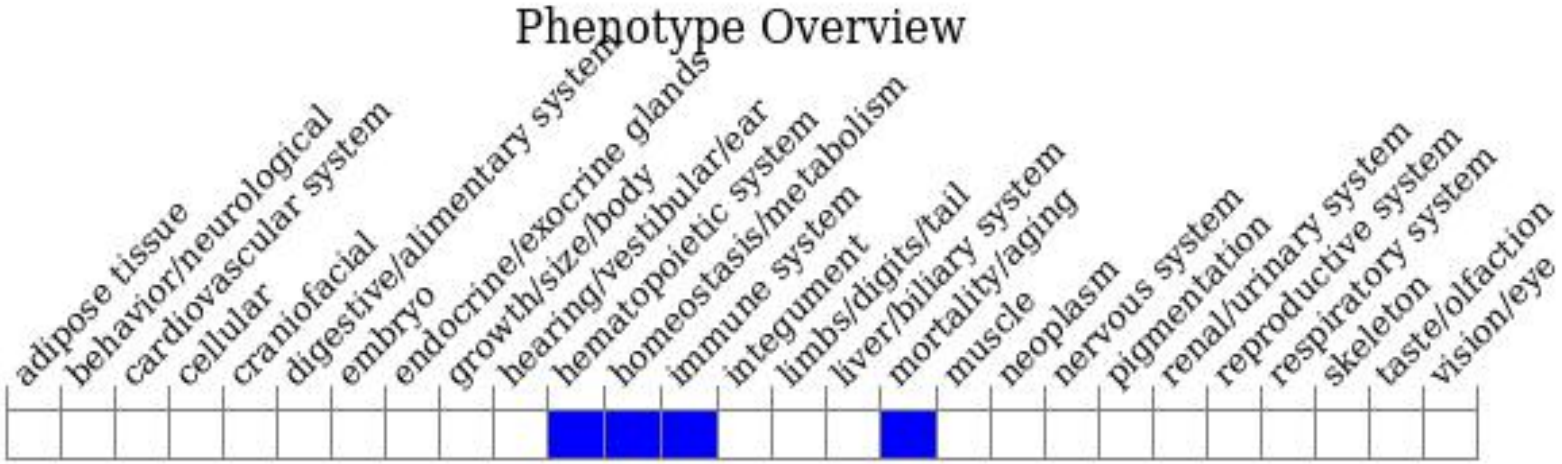
Genomic location distribution



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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