GemPharmatech™

Fga Cas9-CKO Strategy

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Design Date: 2022-12-14

Overview

Target Gene Name

- Fga

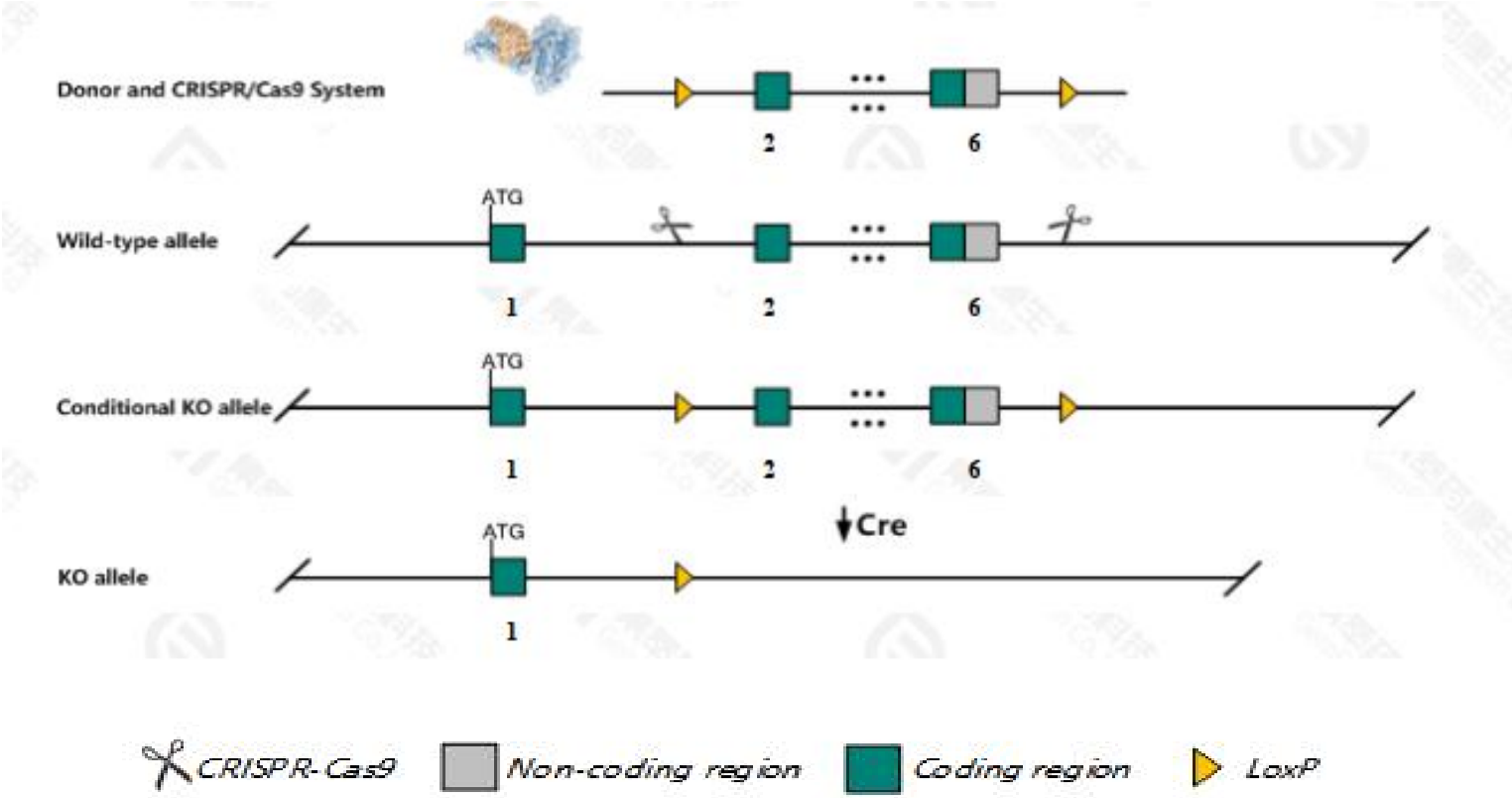
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Fga* gene.

Technical Information

- The *Fga* gene has 2 transcripts. According to the structure of *Fga* gene, exon2-exon6 of *Fga-202*(ENSMUST00000166581.4) transcript is recommended as the knockout region.The region contains most of the coding sequence.Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Fga* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

Gene Information

Fga fibrinogen alpha chain [Mus musculus (house mouse)]

Gene ID: 14161, updated on 13-Mar-2020

Summary

Official Symbol	Fga provided by MGI
Official Full Name	fibrinogen alpha chain provided by MGI
Primary source	MGI:MGI:1316726
See related	Ensembl:ENSMUSG00000028001
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	Fib
Summary	This gene encodes a subunit of the coagulation factor fibrinogen, which is a component of the blood clot. The encoded protein is proteolytically processed by thrombin during the conversion of fibrinogen to fibrin. Mice lacking the encoded protein display bleeding in the peritoneal cavity, skin and soft tissues around joints immediately after birth, and are predisposed to spontaneous fatal abdominal hemorrhage as they grow. Pregnant mice lacking the encoded protein succumb to uterine bleeding during gestation. Alternative splicing results in multiple transcript variants encoding different isoforms that may undergo similar proteolytic processing. [provided by RefSeq, Nov 2015]
Expression	Biased expression in liver E18 (RPKM 1349.0), liver adult (RPKM 247.4) and 3 other tissues See more
Orthologs	human all

Source: https://www.ncbi.nlm.nih.gov/

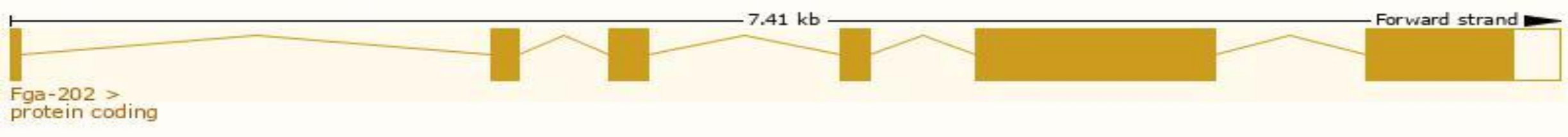
Transcript Information

The gene has 2 transcripts,all transcripts are shown below:

Show/hide columns (1 hidden) Filter

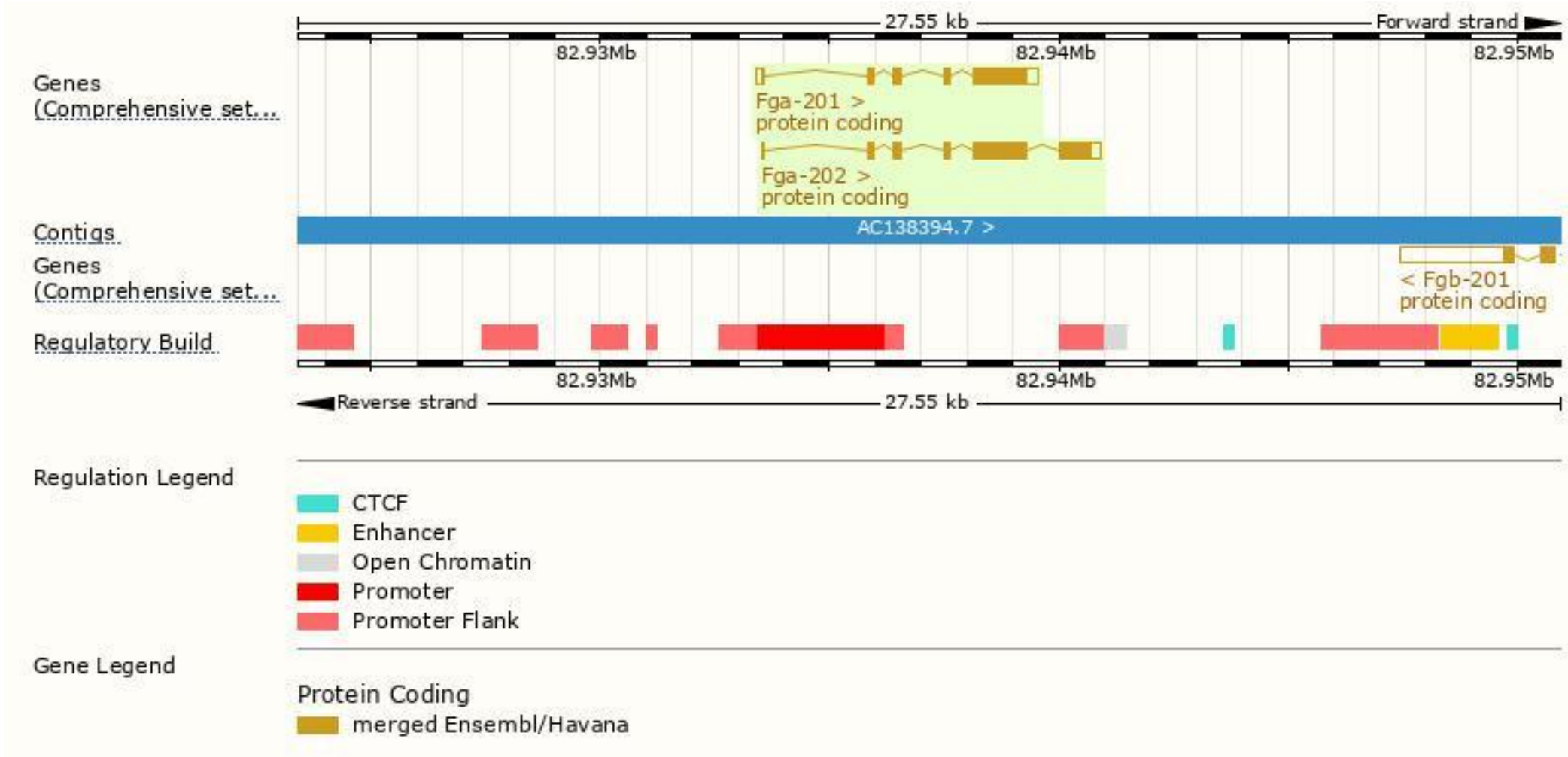
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000166581.4	Fga-202	2587	789aa	Protein coding	CCDS50939	E9PV24-1	Ensembl Canonical GENCODE basic APPRIS P1 TSL:5
ENSMUST00000029630.15	Fga-201	2083	557aa	Protein coding	CCDS17431	E9PV24-2	GENCODE basic TSL:1

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



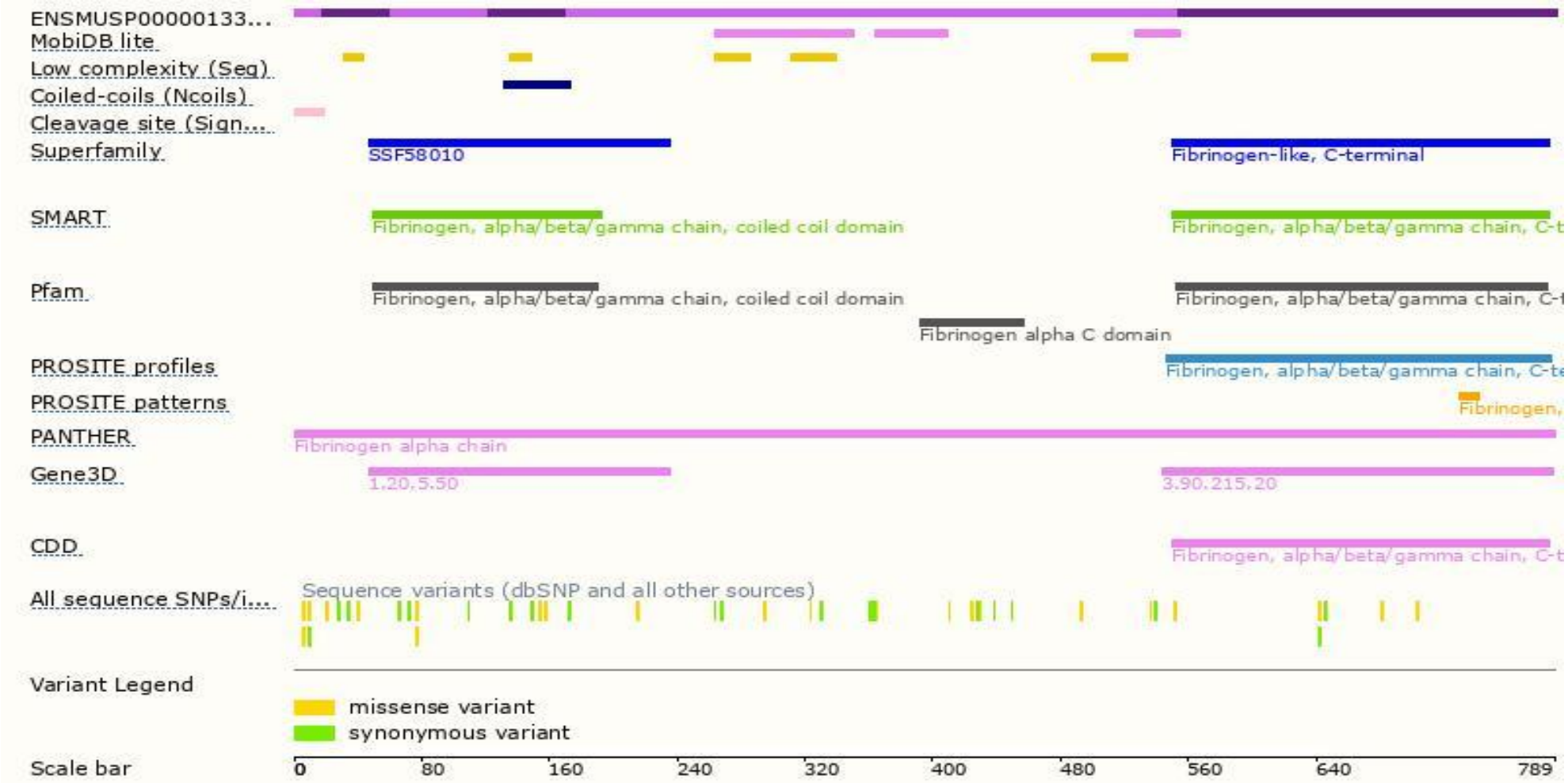
Source: https://www.ensembl.org

Genomic Information



Source: : https://www.ensembl.org

Protein Information



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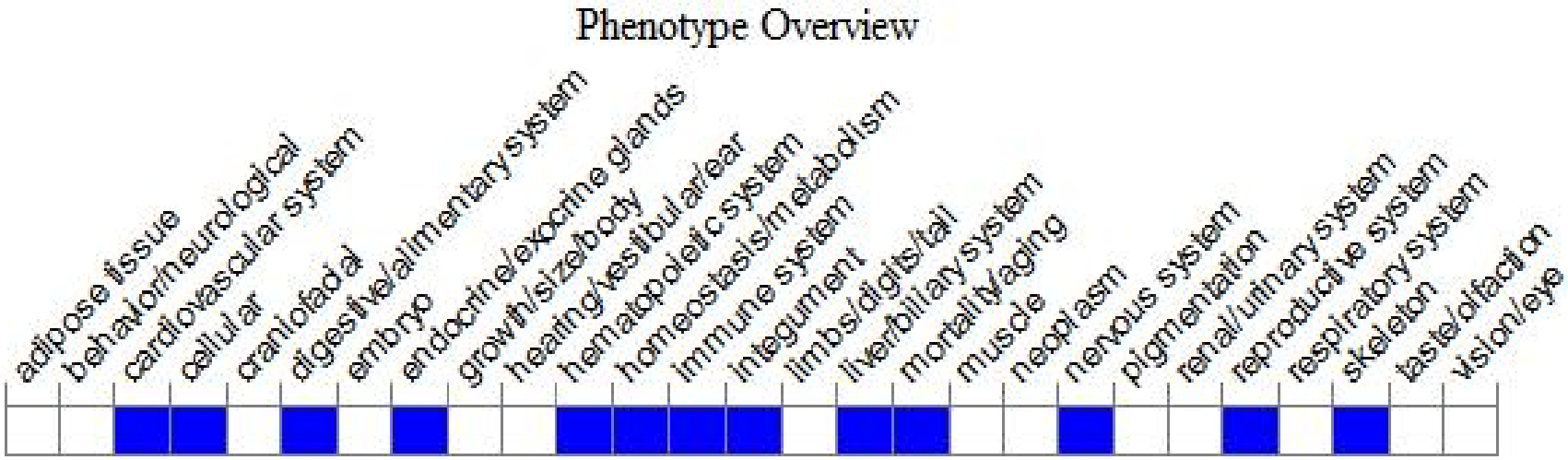
Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)

- Mice homozygous for disruptions of this gene have blood that is unable to clot. On some genetic backgrounds this can lead to fatal hemorrhaging.



Source: https://www.informatics.jax.org

Important Information

➢According to the existing MGI data,mice homozygous for disruptions of this gene have blood that is unable to clot. On some genetic backgrounds this can lead to fatal hemorrhaging.

➢ The Fga gene is located on the Chr 3. 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.