

Anxa2 Cas9-CKO Strategy

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Project Overview

Project Name

Anxa2

Project type

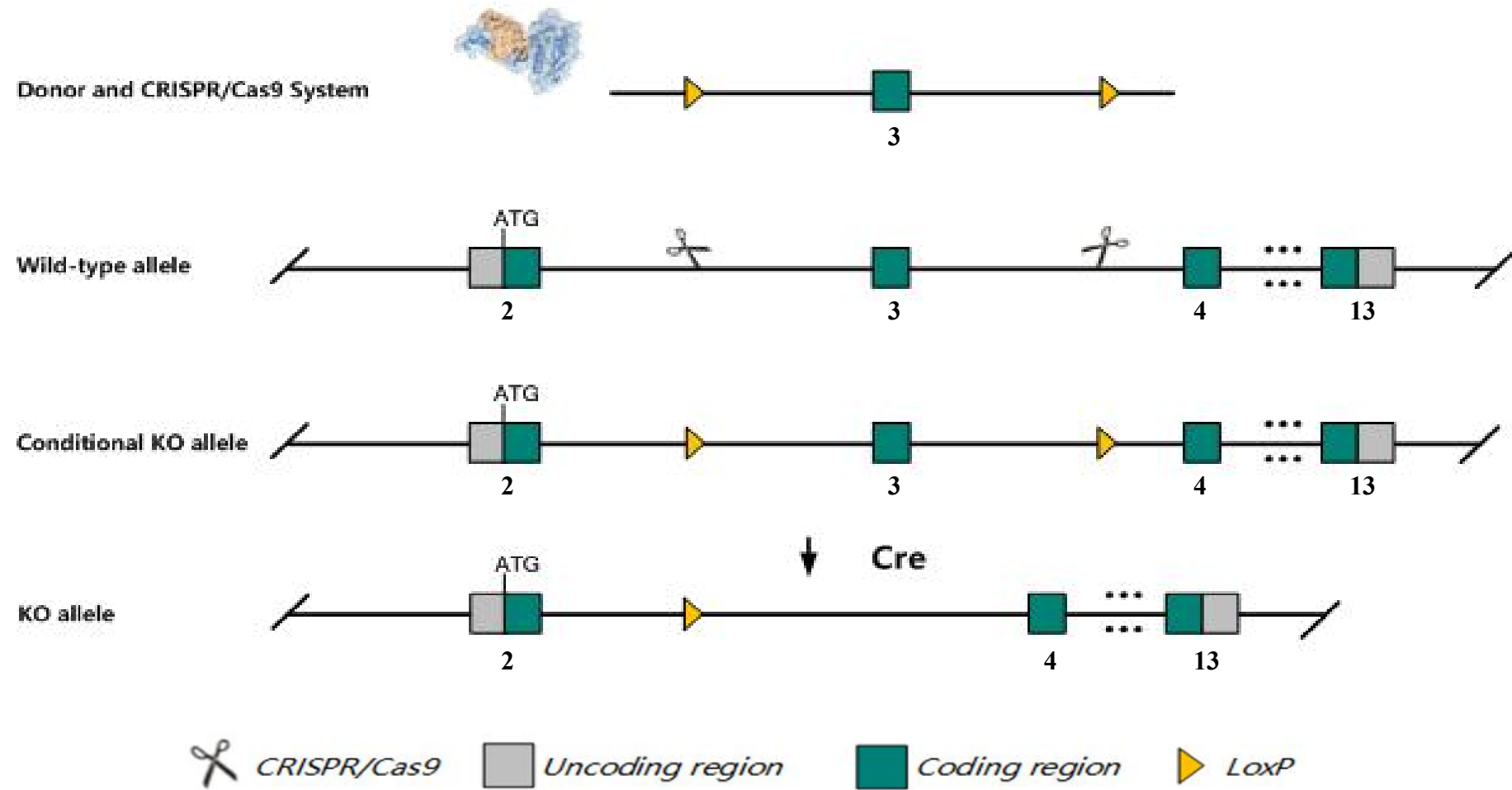
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Anxa2* gene. The schematic diagram is as follows:



The *Anxa2* gene has 6 transcripts. According to the structure of *Anxa2* gene, exon3 of *Anxa2-201* (ENSMUST00000034756.14) transcript is recommended as the knockout region. The region contains 100bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Anxa2* 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.

According to the existing MGI data, Mice homozygous for disruptions in this gene are viable and fertile but suffer from growth deficits, impaired angiogenesis, and increased susceptibility to thrombosis.

The *Anxa2* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information

NCBI

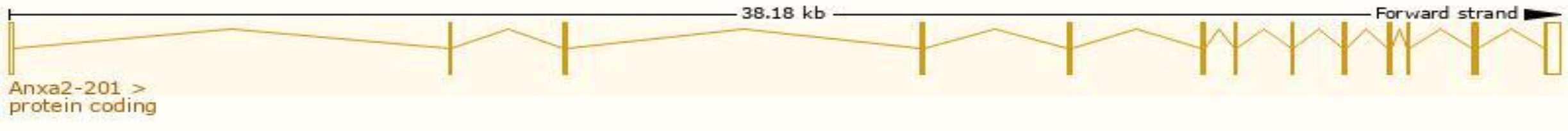


Transcript information Ensembl

The gene has 6 transcripts,all transcripts are shown below:

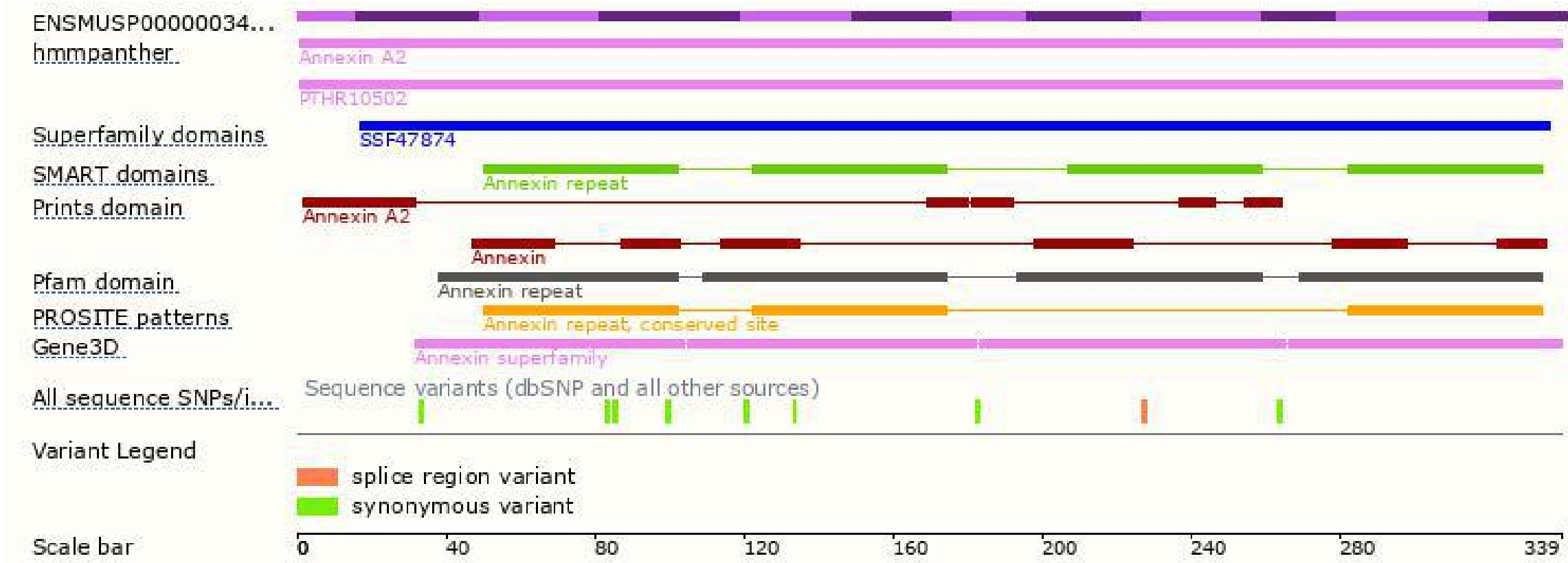
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Anxa2-201	ENSMUST00000034756.14	1447	339aa	Protein coding	CCDS23316	P07356 Q542G9	TSL:1 GENCODE basic APPRIS P1
Anxa2-204	ENSMUST00000136282.2	827	272aa	Protein coding	-	B0V2N5	CDS 5' incomplete TSL:3
Anxa2-202	ENSMUST00000123470.7	678	196aa	Protein coding	-	B0V2N7	CDS 3' incomplete TSL:5
Anxa2-203	ENSMUST00000134907.7	641	176aa	Protein coding	-	B0V2N8	CDS 3' incomplete TSL:5
Anxa2-205	ENSMUST00000143878.1	2280	No protein	Retained intron	-	-	TSL:1
Anxa2-206	ENSMUST00000154591.1	920	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Anxa2-201* transcript,The transcription is shown below

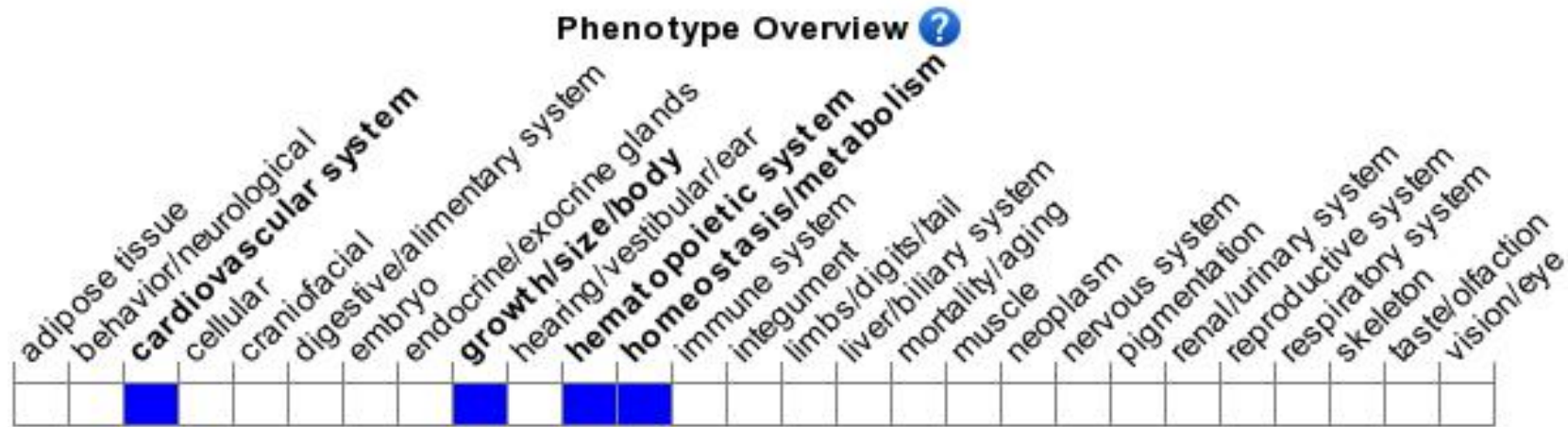


Genomic location distribution

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, Mice homozygous for disruptions in this gene are viable and fertile but suffer from growth deficits, impaired angiogenesis, and increased susceptibility to thrombosis.

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