

# *Anxa7* Cas9-KO Strategy

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# Project Overview



**Project Name**

*Anxa7*

**Project type**

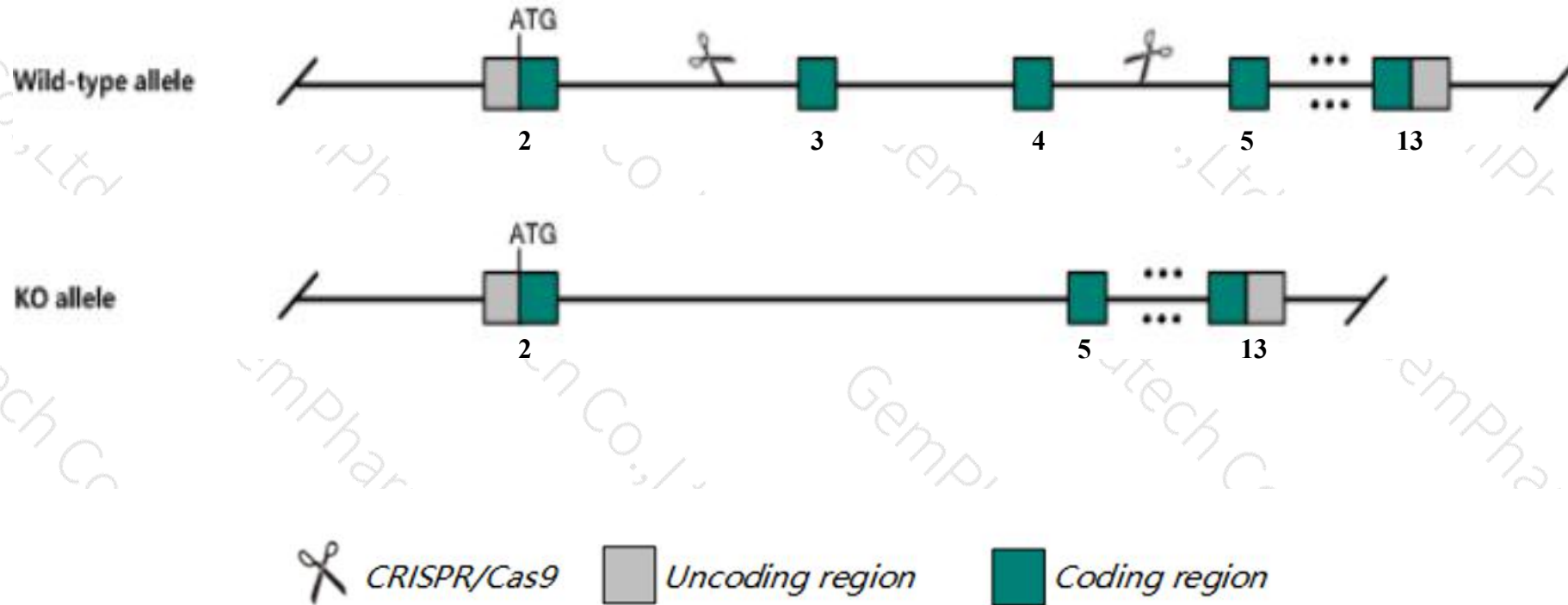
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Anxa7* gene. The schematic diagram is as follows:



- The *Anxa7* gene has 11 transcripts. According to the structure of *Anxa7* gene, exon3-exon4 of *Anxa7-201* (ENSMUST00000065504.16) transcript is recommended as the knockout region. The region contains 307bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Anxa7* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, homozygotes for a null allele are viable but exhibit altered  $Ca^{2+}$  signaling and/or homeostasis in cardiomyocytes and glia cells, and changes in erythrocyte shape, osmotic resistance, platelet number and aggregation velocity. homozygotes for another null allele die at  $\sim e10$  with cerebral hemorrhage.
- *Anxa7-210* transcript is incomplete, so the effect on it is unknown.
- The *Anxa7* gene is located on the Chr14. 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)

## Anxa7 annexin A7 [ *Mus musculus* (house mouse) ]

Gene ID: 11750, updated on 3-May-2020

### Summary

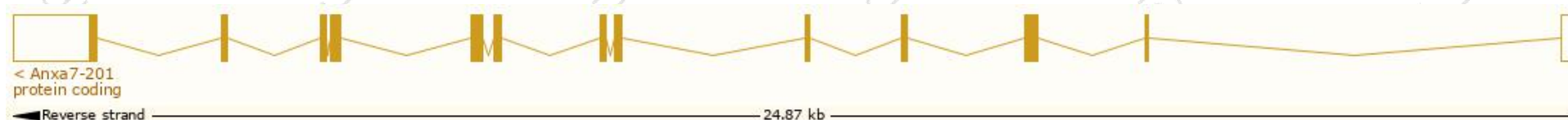
Official Symbol	Anxa7 provided by <a href="#">MGI</a>
Official Full Name	annexin A7 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:88031</a>
See related	<a href="#">Ensembl:ENSMUSG00000021814</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Anx7; synexin; AI265384; AI316497
Expression	Ubiquitous expression in placenta adult (RPKM 48.4), bladder adult (RPKM 40.7) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

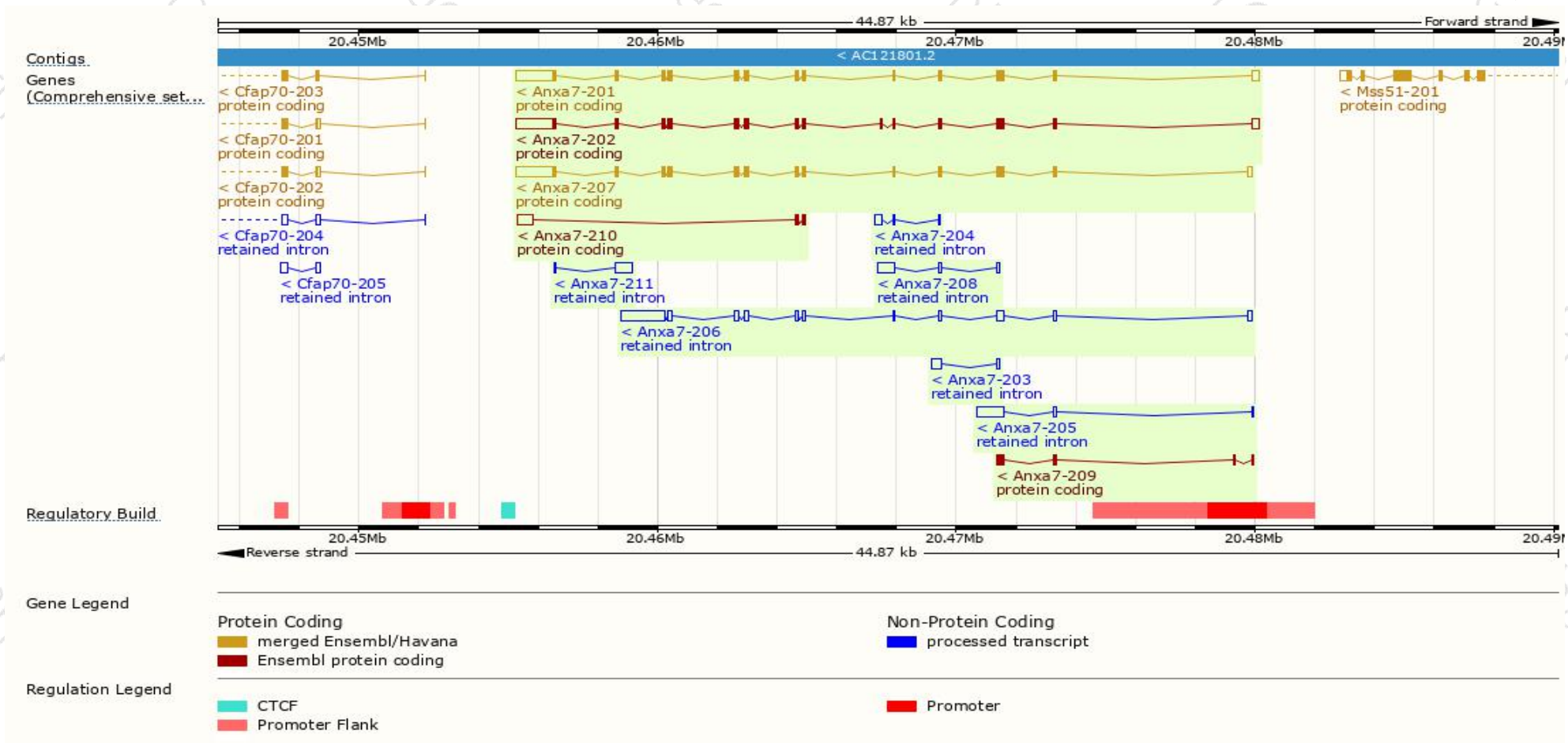
The gene has 11 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Anxa7-201	<a href="#">ENSMUST00000065504.16</a>	2851	<a href="#">463aa</a>	Protein coding	<a href="#">CCDS26845</a>	<a href="#">Q07076</a>	TSL:1 GENCODE basic APPRIS P2
Anxa7-207	<a href="#">ENSMUST00000224975.1</a>	2727	<a href="#">463aa</a>	Protein coding	<a href="#">CCDS26845</a>	<a href="#">Q07076</a>	GENCODE basic APPRIS P2
Anxa7-202	<a href="#">ENSMUST00000100844.5</a>	2904	<a href="#">485aa</a>	Protein coding	-	<a href="#">A0A2C9F2D2</a>	TSL:1 GENCODE basic APPRIS ALT2
Anxa7-210	<a href="#">ENSMUST00000225941.1</a>	739	<a href="#">72aa</a>	Protein coding	-	<a href="#">A0A286YCW4</a>	CDS 5' incomplete
Anxa7-209	<a href="#">ENSMUST00000225132.1</a>	364	<a href="#">86aa</a>	Protein coding	-	<a href="#">A0A286YCS5</a>	CDS 3' incomplete
Anxa7-206	<a href="#">ENSMUST00000224410.1</a>	2653	No protein	Retained intron	-	-	-
Anxa7-205	<a href="#">ENSMUST00000224344.1</a>	988	No protein	Retained intron	-	-	-
Anxa7-208	<a href="#">ENSMUST00000225118.1</a>	761	No protein	Retained intron	-	-	-
Anxa7-211	<a href="#">ENSMUST00000226001.1</a>	673	No protein	Retained intron	-	-	-
Anxa7-203	<a href="#">ENSMUST00000223681.1</a>	420	No protein	Retained intron	-	-	-
Anxa7-204	<a href="#">ENSMUST00000223960.1</a>	387	No protein	Retained intron	-	-	-

The strategy is based on the design of *Anxa7-201* transcript, the transcription is shown below

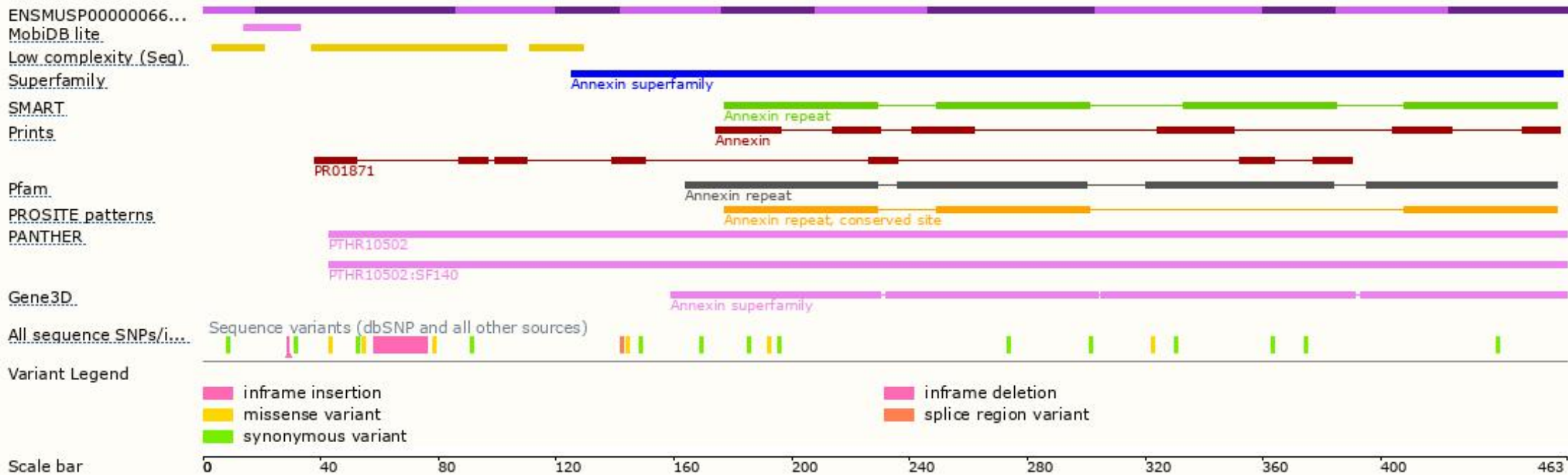


# Genomic location distribution

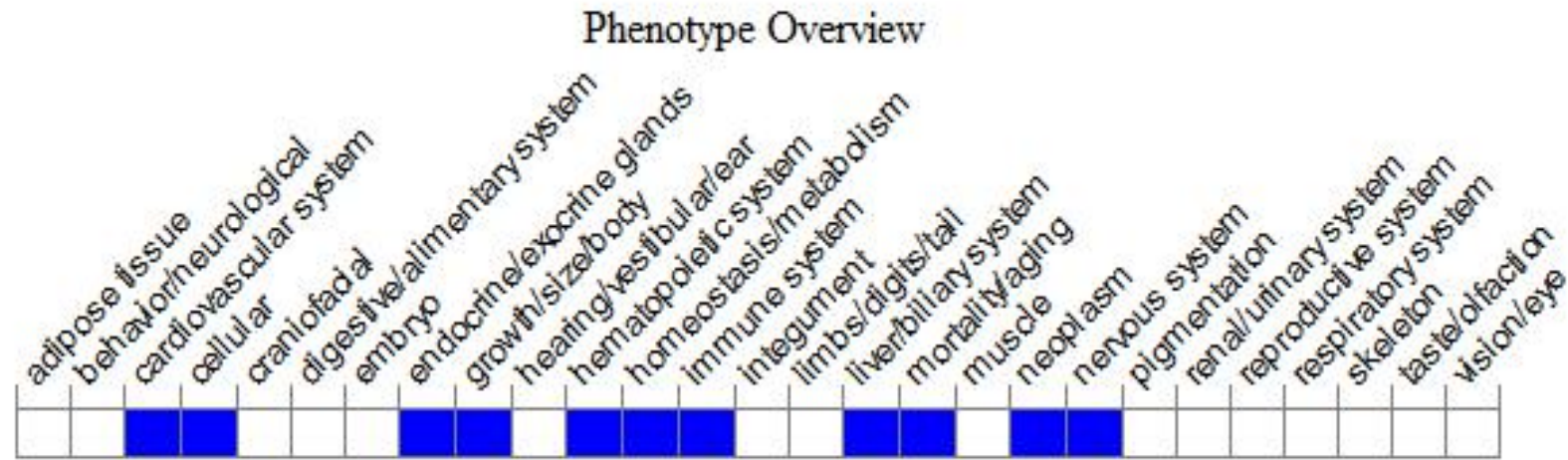




# Protein domain



# 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 are viable but exhibit altered Ca<sup>2+</sup> signaling and/or homeostasis in cardiomyocytes and glia cells, and changes in erythrocyte shape, osmotic resistance, platelet number and aggregation velocity. Homozygotes for another null allele die at ~E10 with cerebral hemorrhage.

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

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