

# *Anxa11* Cas9-KO Strategy

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# Overview

## Target Gene Name

- *Anxa11*

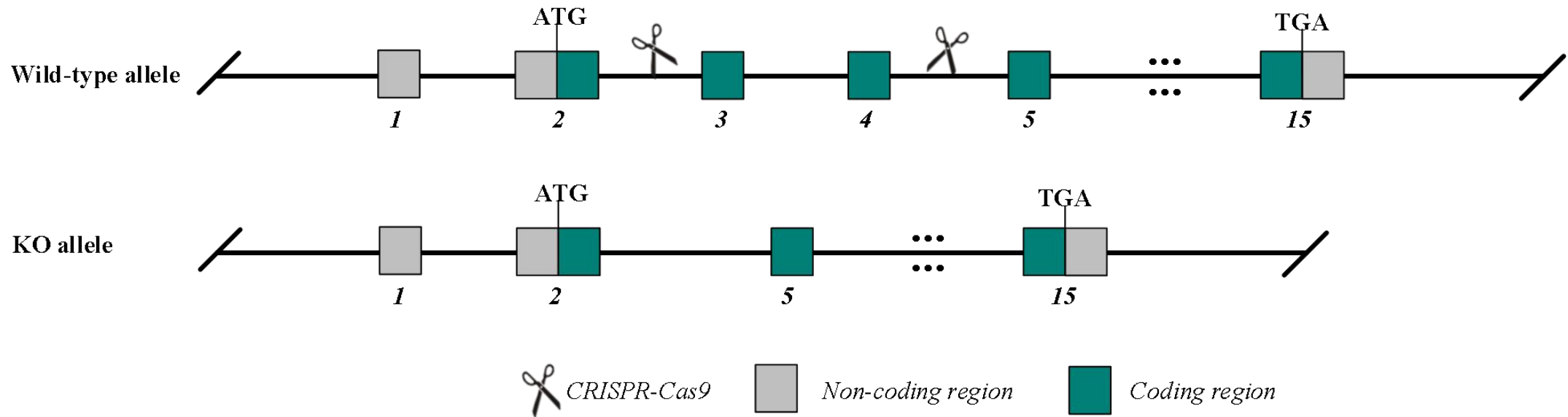
## Project Type

- Cas9-KO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Anxa11* gene.

# Technical Information

- The *Anxa11* gene has 4 transcripts. According to the structure of *Anxa11* gene, exon 3-4 of *Anxa11*-201 (ENSMUST00000022416.15) is recommended as the knockout region. The region contains 500 bp of coding sequence. Knockout the region will result in disruption of gene function.
- In this project, *Anxa11* gene will be modified by CRISPR-Cas9 technology. Briefly, gRNAs will be constructed in vitro. Cas9 and gRNAs were microinjected into the fertilized eggs of C57BL/6JGpt mice, to obtain positive F0 generation mice. The F0 positive mice will be bred with C57BL/6JGpt mice to obtain positive F1 mice. Pups from both F0 and F1 generations will be genotyped by PCR, followed by on-target sequencing analysis.

# Gene Information

Anxa11 annexin A11 [ *Mus musculus* (house mouse) ]

[Download Datasets](#)

Gene ID: 11744, updated on 12-Apr-2023

## Summary

<b>Official Symbol</b>	Anxa11 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	annexin A11 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:108481</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000021866</a> <a href="#">AllianceGenome:MGI:108481</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	Anx11; Gm2260; Gm2274; 100039484; 100039503; A830099O17Rik
<b>Summary</b>	Enables calcium ion binding activity; calcium-dependent phospholipid binding activity; and phosphatidylethanolamine binding activity. Predicted to be involved in cytokinetic process; phagocytosis; and response to calcium ion. Predicted to act upstream of or within cell division. Located in cytoplasm. Is expressed in several structures, including alimentary system; genitourinary system; nervous system; respiratory system; and sensory organ. Human ortholog(s) of this gene implicated in amyotrophic lateral sclerosis type 23. Orthologous to human ANXA11 (annexin A11). [provided by Alliance of Genome Resources, Apr 2022]
<b>Expression</b>	Broad expression in colon adult (RPKM 118.5), duodenum adult (RPKM 56.1) and 20 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>
<b>NEW</b>	Try the new <a href="#">Gene table</a>
	Try the new <a href="#">Transcript table</a>

## Genomic context

**Location:** 14 A3; 14 15.06 cM

See Anxa11 in [Genome Data Viewer](#)

**Exon count:** 16

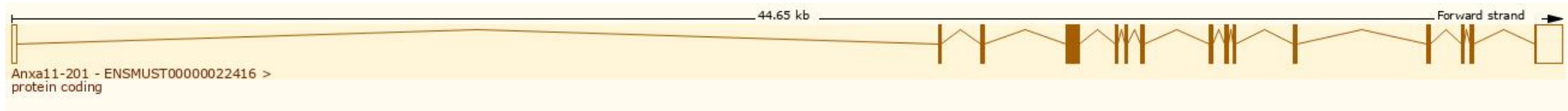
<https://www.ncbi.nlm.nih.gov/gene/11744>

# Transcript Information

The gene has 4 transcripts, as shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
<a href="#">ENSMUST00000022416.15</a>	Anxa11-201	2394	<a href="#">503aa</a>	Protein coding	<a href="#">CCDS26875</a>	<a href="#">P97384</a>	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
<a href="#">ENSMUST00000112364.8</a>	Anxa11-202	1625	<a href="#">447aa</a>	Protein coding		<a href="#">D3Z7U0</a>	GENCODE basic TSL:1
<a href="#">ENSMUST00000124704.8</a>	Anxa11-203	2643	No protein	Retained intron		-	TSL:2
<a href="#">ENSMUST00000133547.2</a>	Anxa11-204	2733	No protein	Retained intron		-	TSL:2

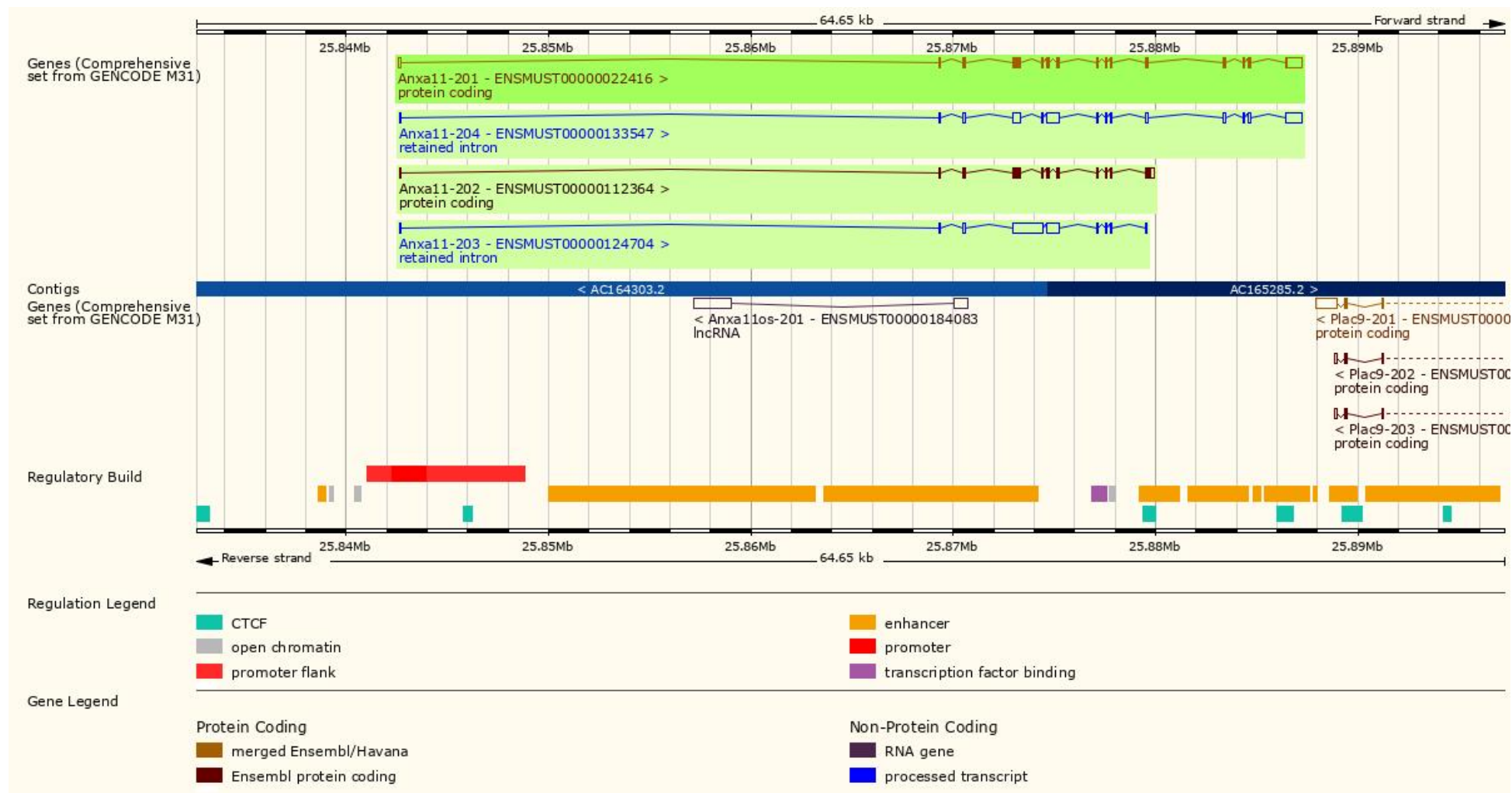
The strategy is based on *Anxa11-201* transcript, as shown below:



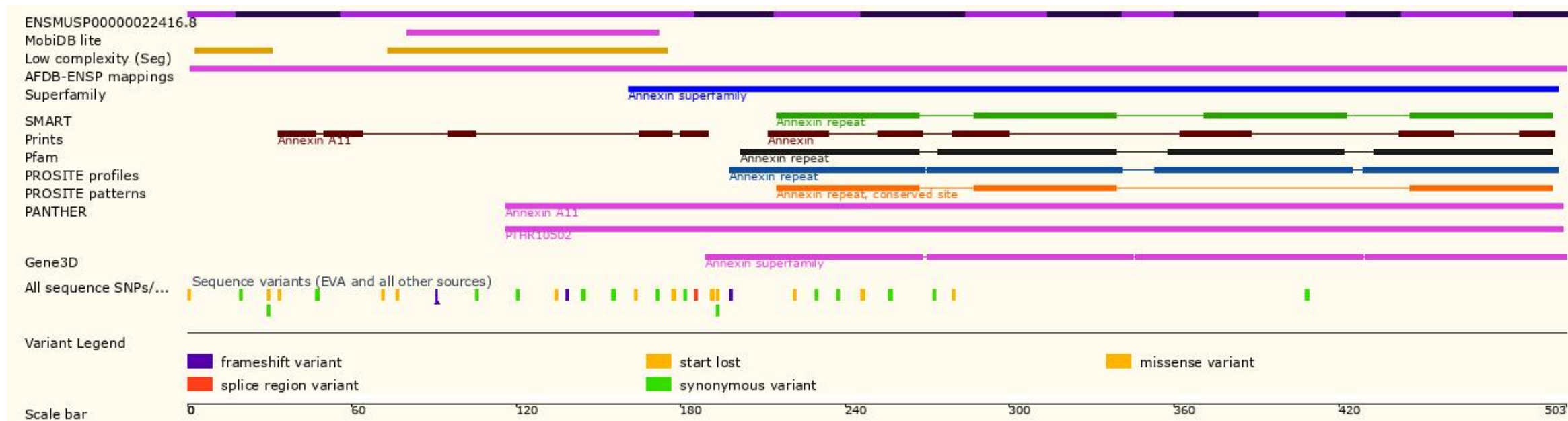
Source: <http://asia.ensembl.org/>



# Genomic Information



# Protein Information





# Important Information

- The knockout region overlaps with *Anxialios* gene, which may affect the function of this gene.
- Mouse *Anxa11* gene is located on Chr 14. Please take the chromosomal location in consideration when breeding this mutant strain with other genetic engineered strains. Shall this mutant strain be crossed with another strain to obtain double homozygous mutant offspring, be mindful about linkage effect when the other mutation is also on Chr 14.
- This strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.