

Anapc2 Cas9-CKO Strategy

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Project Overview

Project Name

Anapc2

Project type

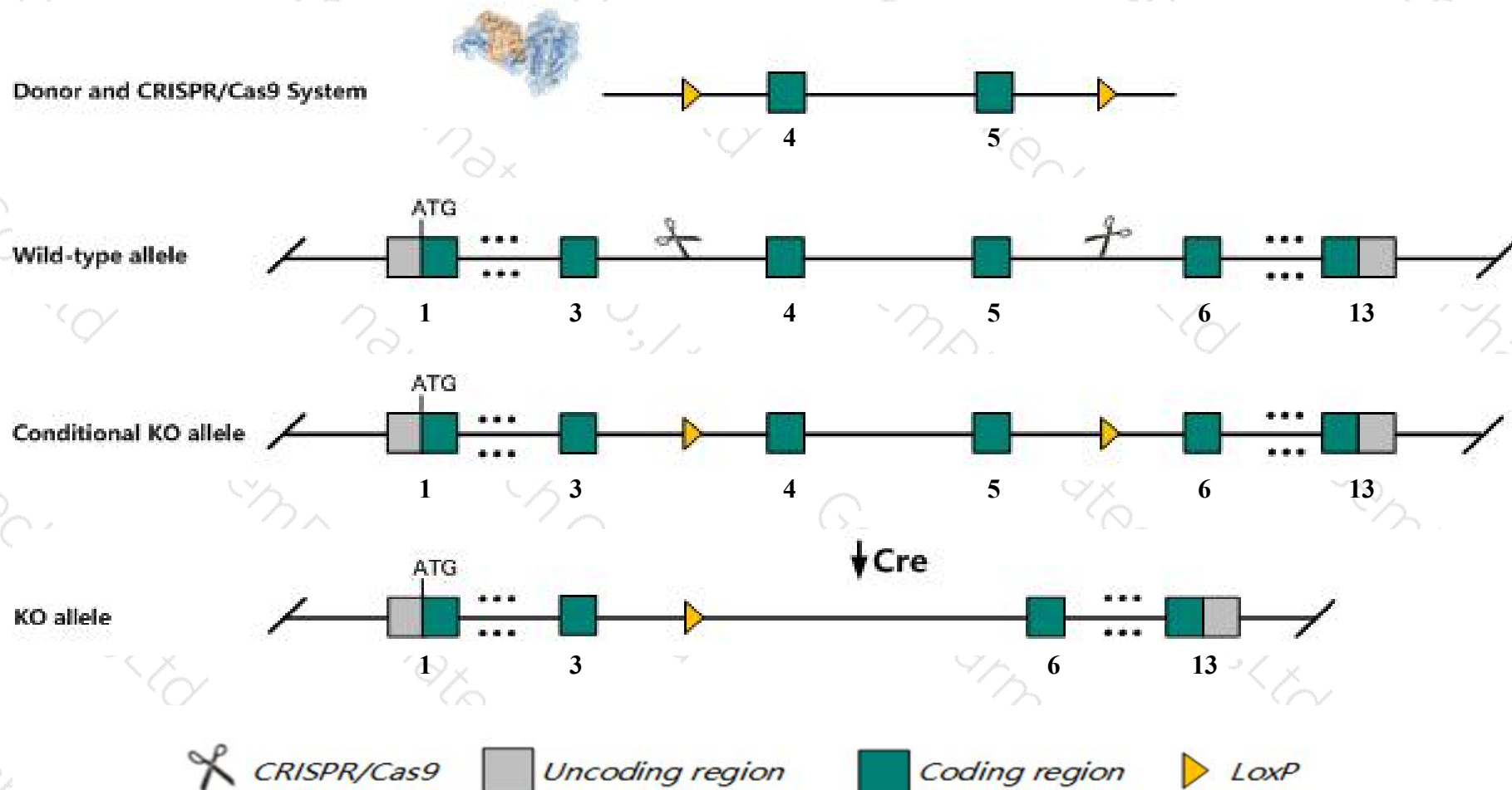
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Anapc2* gene. The schematic diagram is as follows:



- The *Anapc2* gene has 4 transcripts. According to the structure of *Anapc2* gene, exon4-exon5 of *Anapc2-201* (ENSMUST00000028341.10) transcript is recommended as the knockout region. The region contains 295bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Anapc2* 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, homozygous mutation of this gene results in embryonic lethality before e6.5. conditional ablation in the liver results in liver failure and premature death.
- Transcript *Anapc2*-202 may not be affected.
- The floxed region is near to the N-terminal of *Ssna1* gene, this strategy may influence the regulatory function of the N-terminal of *Ssna1* gene.
- The N-terminal of *Anapc2* gene will remain several amino acids, it may remain the partial function of *Anapc2* gene.
- The *Anapc2* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Anapc2 anaphase promoting complex subunit 2 [Mus musculus (house mouse)]

Gene ID: 99152, updated on 13-Mar-2020

Summary



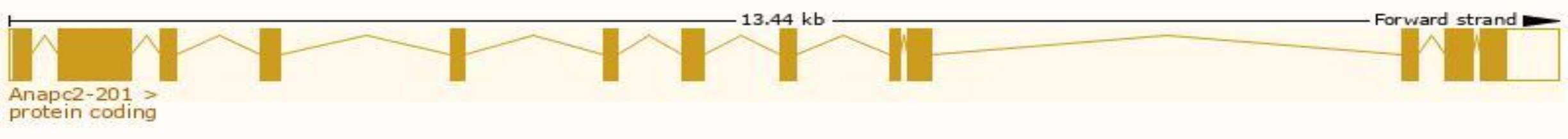
Official Symbol	Anapc2 provided by MGI
Official Full Name	anaphase promoting complex subunit 2 provided by MGI
Primary source	MGI:MGI:2139135
See related	Ensembl:ENSMUSG000000026965
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9230107K09Rik, AL024279, Apc2, Emi4, lmi4, mKIAA1406
Summary	This gene encodes a component of the anaphase promoting complex/cyclosome (APC/C), a cell cycle-regulated ubiquitin ligase that controls progression through mitosis and the G1 phase of the cell cycle by ubiquitinating its specific substrates, such as mitotic cyclins and anaphase inhibitor, for subsequent degradation by the proteasome. [provided by RefSeq, Oct 2009]
Expression	Ubiquitous expression in ovary adult (RPKM 38.6), limb E14.5 (RPKM 34.9) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

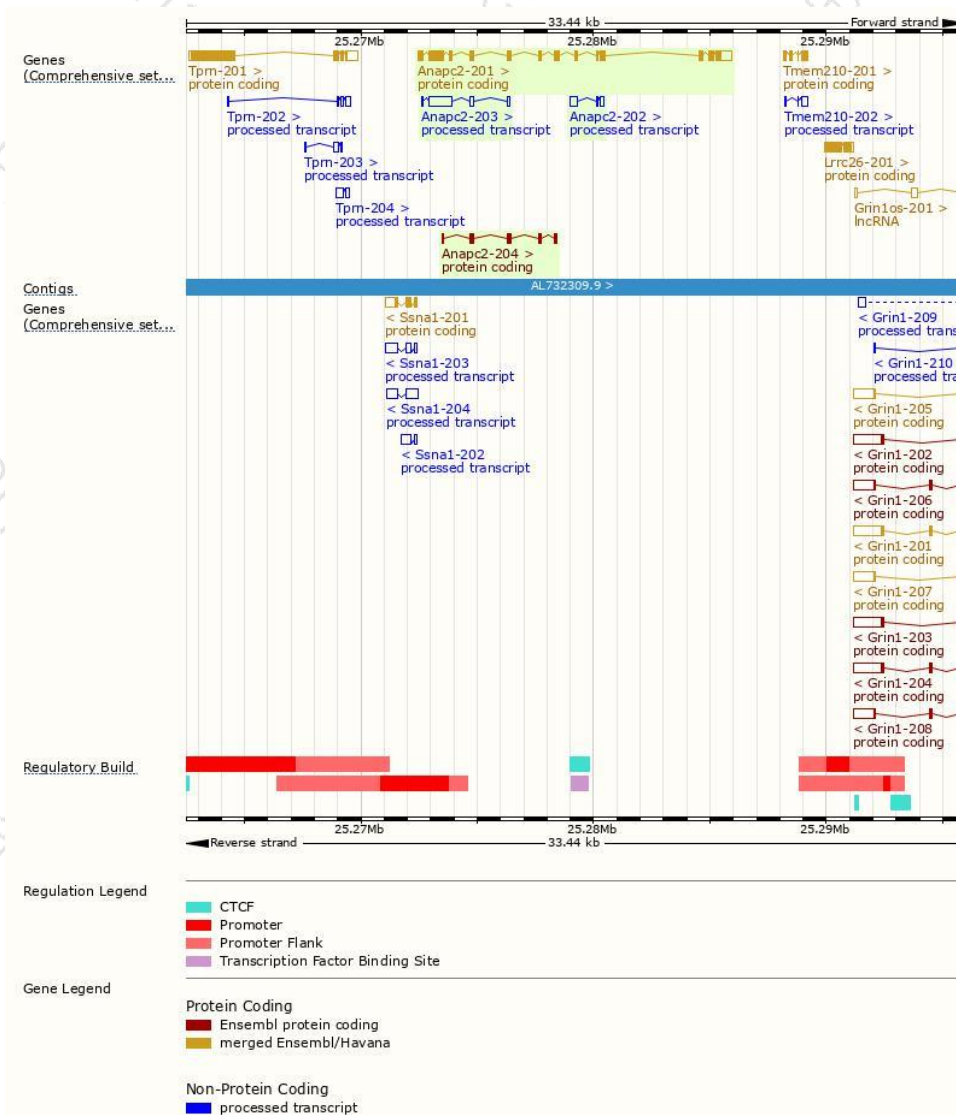
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Anapc2-201	ENSMUST00000028341.10	3004	837aa	Protein coding	CCDS15761	Q8BZQ7	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Anapc2-204	ENSMUST00000129300.1	555	185aa	Protein coding	-	A2A11	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Anapc2-203	ENSMUST00000129265.1	1332	No protein	Processed transcript	-	-	TSL:5
Anapc2-202	ENSMUST00000125885.1	572	No protein	Processed transcript	-	-	TSL:1

The strategy is based on the design of *Anapc2-201* transcript,the transcription is shown below



Genomic location distribution

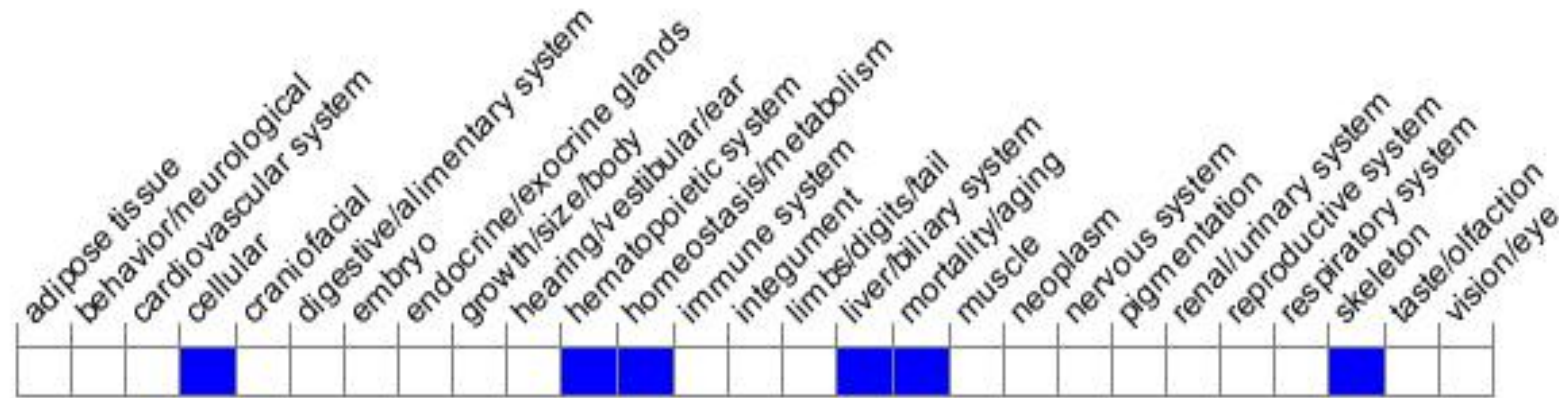


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



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, homozygous mutation of this gene results in embryonic lethality before E6.5.

Conditional ablation in the liver results in liver failure and premature death.

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

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