

***Anapc1* Cas9-KO Strategy**

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Reviewer: Yang Zeng

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Project Overview

Project Name

Anapc1

Project type

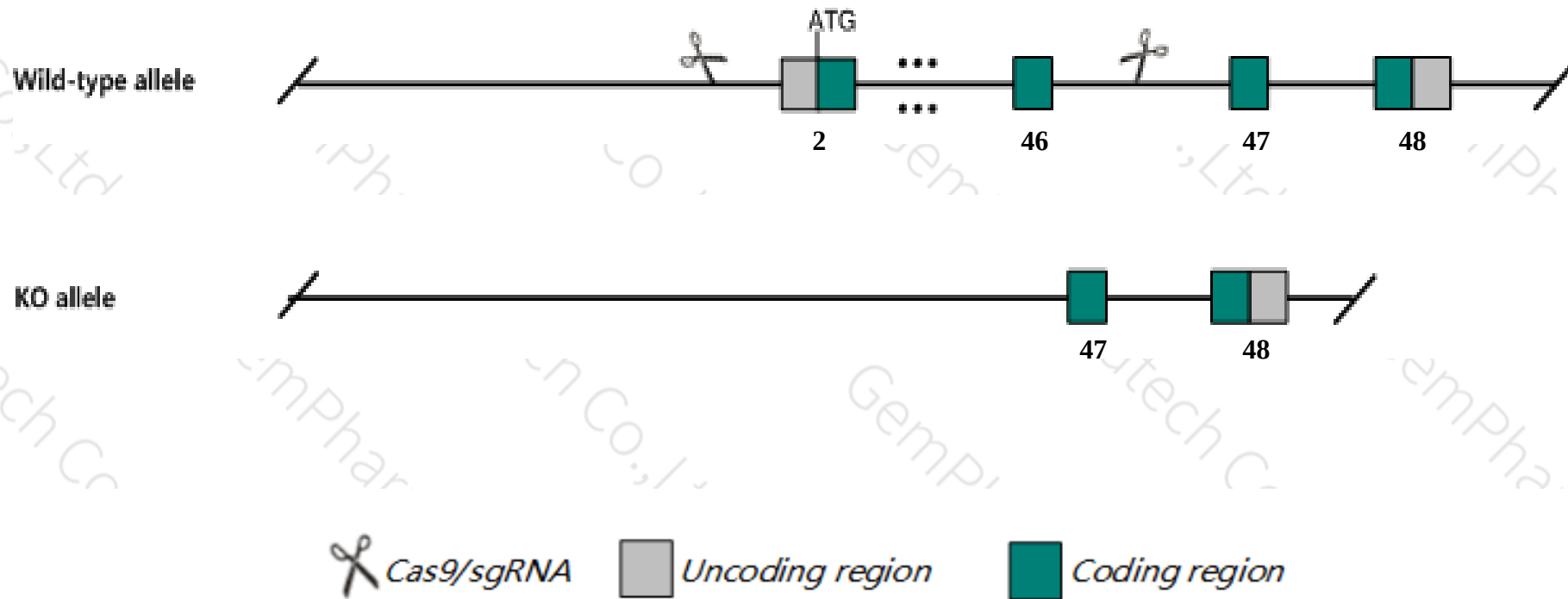
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Anapc1* gene. The schematic diagram is as follows:



- The *Anapc1* gene has 11 transcripts. According to the structure of *Anapc1* gene, exon2-exon46 of *Anapc1*-201(ENSMUST00000014499.9) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Anapc1* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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 *Anapc1* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Anapc1 anaphase promoting complex subunit 1 [Mus musculus (house mouse)]

Gene ID: 17222, updated on 13-Mar-2020

Summary

Official Symbol Anapc1 provided by [MGI](#)

Official Full Name anaphase promoting complex subunit 1 provided by [MGI](#)

Primary source [MGI:MGI:103097](#)

See related [Ensembl:ENSMUSG00000014355](#)

Gene type protein coding

RefSeq status VALIDATED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as 2610021O03Rik, AI047775, AI853536, AW547281, Apc1, Mcpr, tsg24

Expression Ubiquitous expression in CNS E11.5 (RPKM 13.6), limb E14.5 (RPKM 12.9) and 28 other tissues [See more](#)

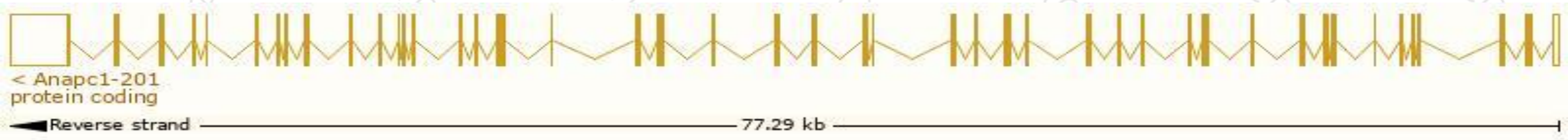
Orthologs [human](#) [all](#)

Transcript information（Ensembl）

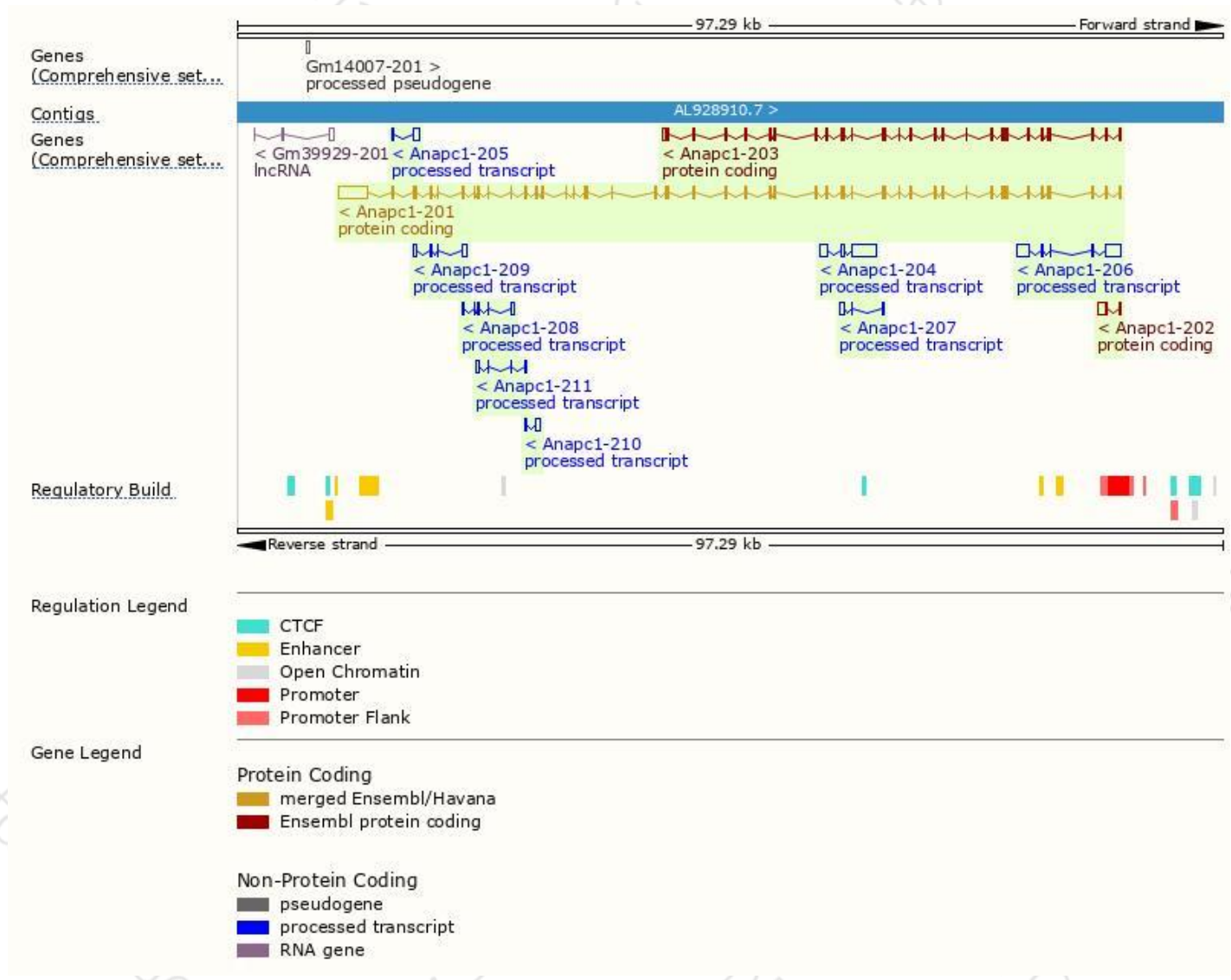
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Anapc1-201	ENSMUST0000014499.9	8942	1944aa	Protein coding	CCDS16715	P53995	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
Anapc1-203	ENSMUST00000110333.1	4214	1213aa	Protein coding	-	A2ATQ5	TSL:1 GENCODE basic
Anapc1-202	ENSMUST00000110332.1	1214	80aa	Protein coding	-	Q6PG65	TSL:1 GENCODE basic
Anapc1-204	ENSMUST00000123503.1	3261	No protein	Processed transcript	-	-	TSL:1
Anapc1-206	ENSMUST00000134485.1	3007	No protein	Processed transcript	-	-	TSL:1
Anapc1-209	ENSMUST00000151171.1	836	No protein	Processed transcript	-	-	TSL:2
Anapc1-208	ENSMUST00000145906.7	742	No protein	Processed transcript	-	-	TSL:2
Anapc1-205	ENSMUST00000124418.1	691	No protein	Processed transcript	-	-	TSL:2
Anapc1-210	ENSMUST00000154320.1	667	No protein	Processed transcript	-	-	TSL:3
Anapc1-207	ENSMUST00000143007.1	627	No protein	Processed transcript	-	-	TSL:3
Anapc1-211	ENSMUST00000154995.1	564	No protein	Processed transcript	-	-	TSL:3

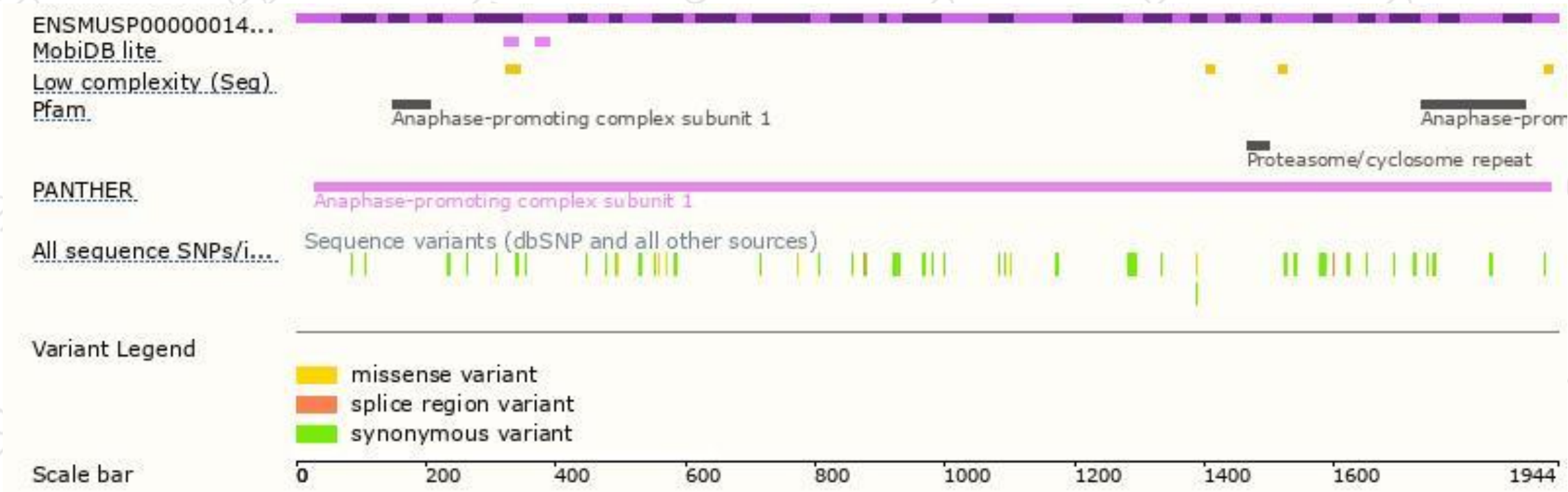
The strategy is based on the design of *Anapc1-201* transcript,the transcription is shown below:



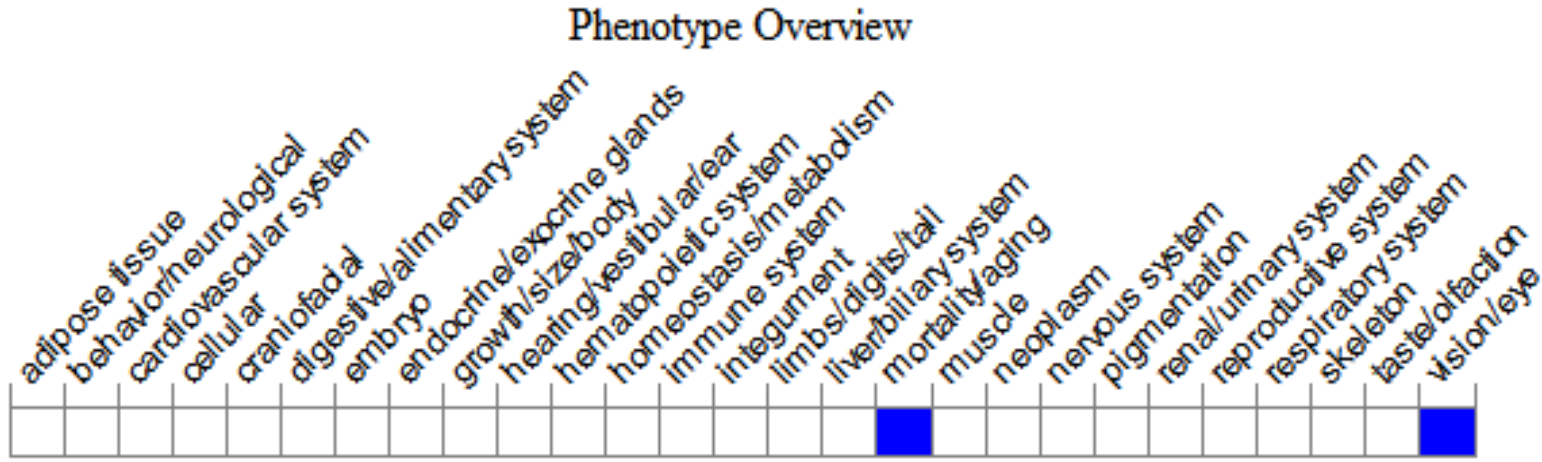
Genomic location distribution



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/>).

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

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