

***Snapc2* Cas9-KO Strategy**

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Project Overview

Project Name

Snapc2

Project type

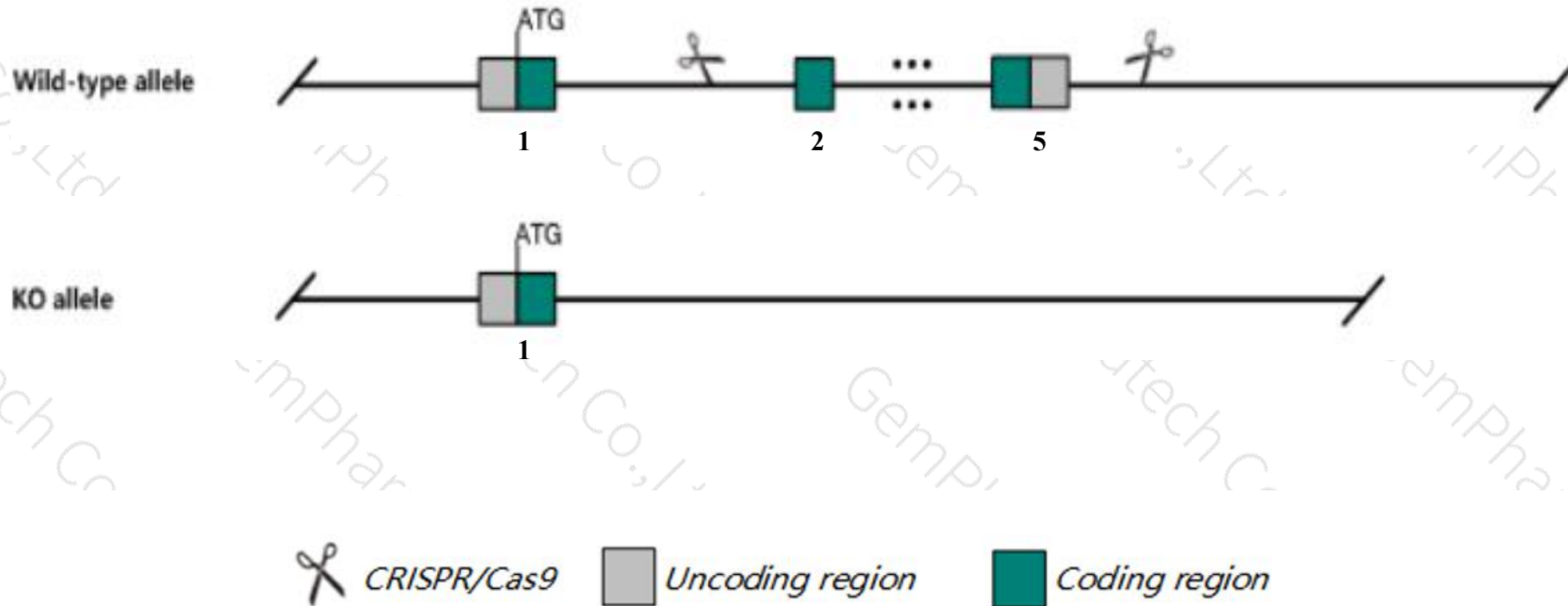
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Snapc2* gene. The schematic diagram is as follows:



Technical routes

- The *Snapc2* gene has 4 transcripts. According to the structure of *Snapc2* gene, exon2-exon5 of *Snapc2*-201(ENSMUST00000011981.4) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Snapc2* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for a knock-out allele show complete embryonic lethality before implantation associated with abnormal morula morphology, increased cell death, and failure of blastocyst formation.
- The *Snapc2* gene is located on the Chr8. 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)

Snapc2 small nuclear RNA activating complex, polypeptide 2 [Mus musculus (house mouse)]

Gene ID: 102209, updated on 13-Mar-2020

Summary



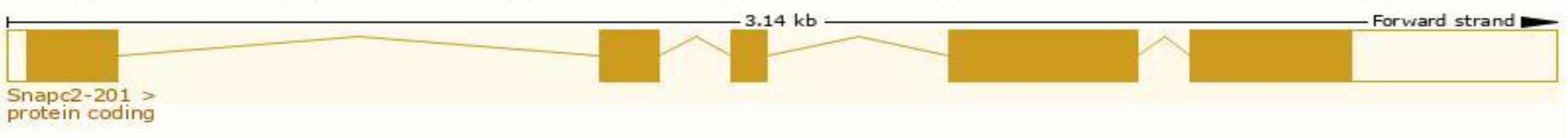
Official Symbol	Snapc2 provided by MGI
Official Full Name	small nuclear RNA activating complex, polypeptide 2 provided by MGI
Primary source	MGI:MGI:1914861
See related	Ensembl:ENSMUSG00000011837
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	0610007H10Rik, AU015675
Expression	Ubiquitous expression in ovary adult (RPKM 32.8), adrenal adult (RPKM 22.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

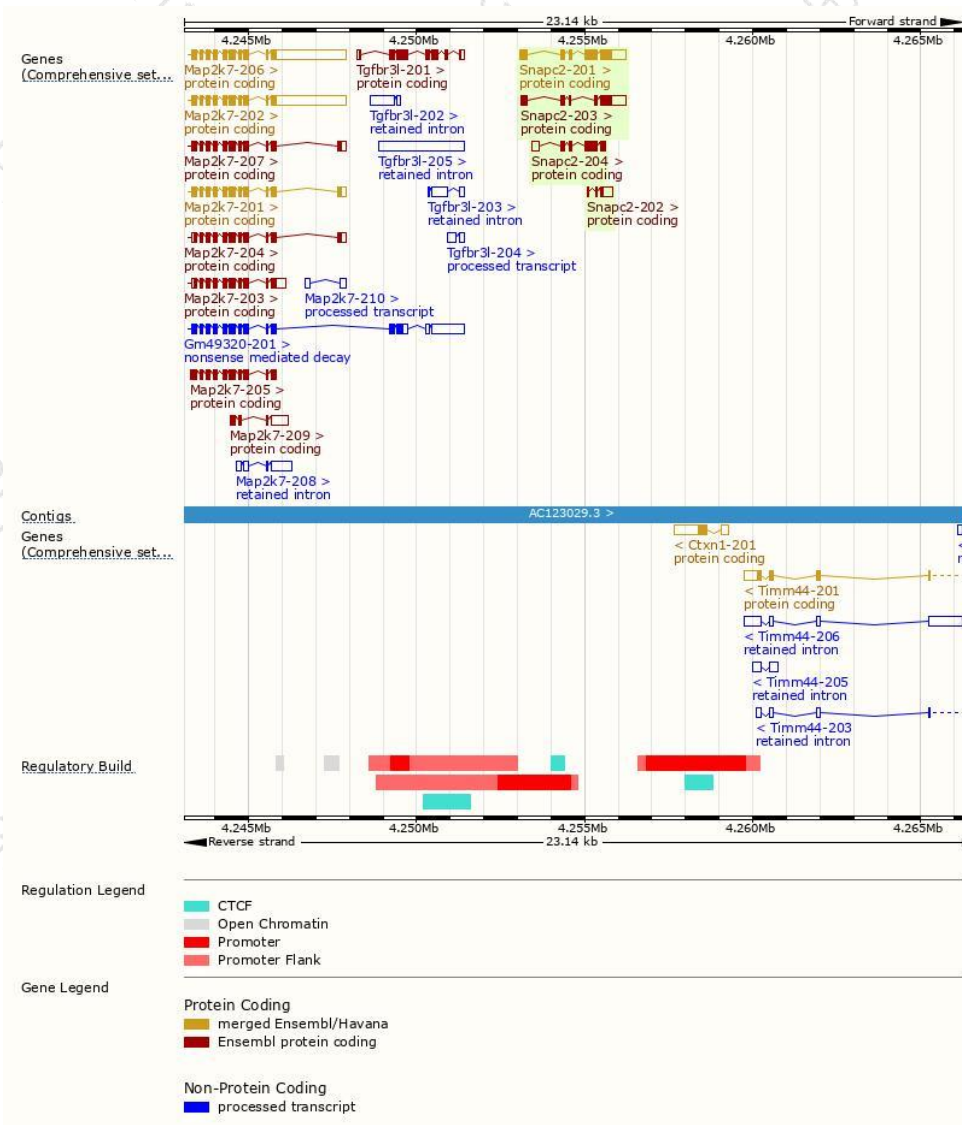
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Snapc2-201	ENSMUST00000011981.4	1536	359aa	Protein coding	CCDS22081	Q91XA5	TSL:1 GENCODE basic APPRIS P1
Snapc2-203	ENSMUST00000208316.1	1190	249aa	Protein coding	-	A0A140LID1	TSL:1 GENCODE basic
Snapc2-204	ENSMUST00000208459.1	956	222aa	Protein coding	-	A0A140LHV3	CDS 3' incomplete TSL:3
Snapc2-202	ENSMUST00000208110.1	428	55aa	Protein coding	-	A0A140LHE1	CDS 5' incomplete TSL:3

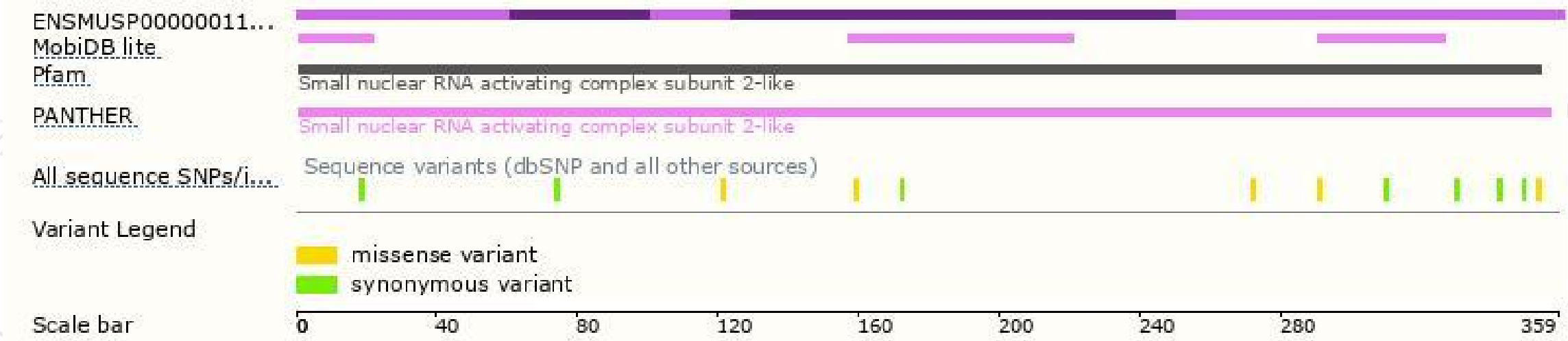
The strategy is based on the design of *Snapc2-201* transcript,the transcription is shown below:



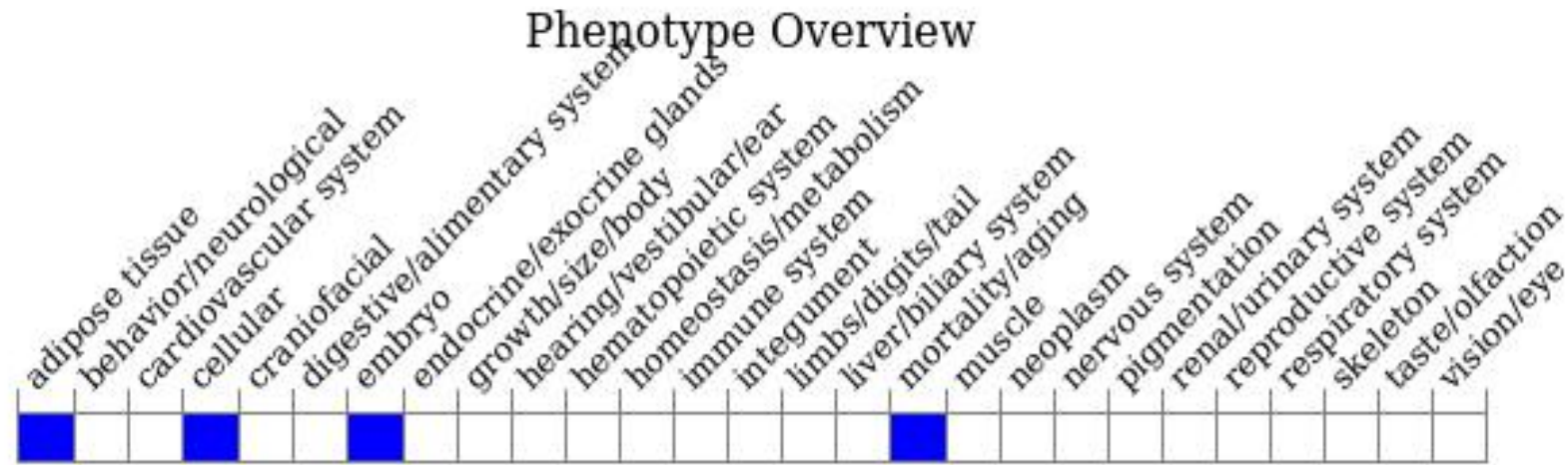
Genomic location distribution



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 a knock-out allele show complete embryonic lethality before implantation associated with abnormal morula morphology, increased cell death, and failure of blastocyst formation.

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

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