

$Snx2$ Cas9-CKO Strategy

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Project Overview

Project Name

$Snx2$

Project type

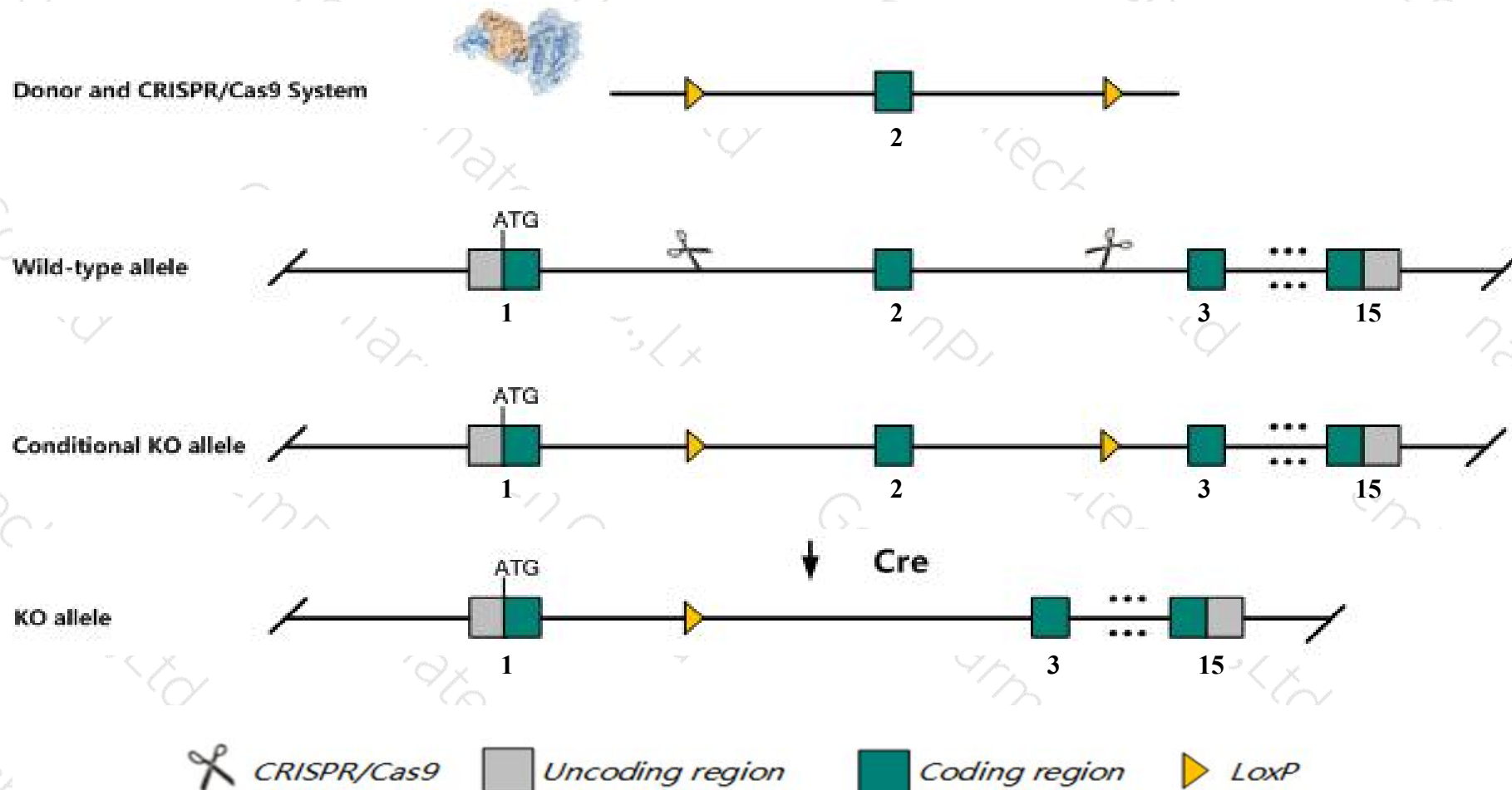
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Snx2* gene. The schematic diagram is as follows:



- The *Snx2* gene has 5 transcripts. According to the structure of *Snx2* gene, exon2 of *Snx2-201* (ENSMUST00000037850.6) transcript is recommended as the knockout region. The region contains 118bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Snx2* 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 mutant mice are viable and fertile and do not exhibit any apparent abnormalities.
- Transcript *Snx2*-203 may not be affected.
- The *Snx2* gene is located on the Chr18. 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)

Snx2 sorting nexin 2 [*Mus musculus* (house mouse)]

Gene ID: 67804, updated on 27-Feb-2020

Summary

- Official Symbol** Snx2 provided by [MGI](#)
- Official Full Name** sorting nexin 2 provided by [MGI](#)
- Primary source** [MGI:MGI:1915054](#)
- See related** [Ensembl:ENSMUSG00000034484](#)
- 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** 0610030A03Rik
- Expression** Ubiquitous expression in placenta adult (RPKM 55.9), bladder adult (RPKM 30.8) and 26 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 18; 18 D1

See Snx2 in [Genome Data Viewer](#)

Exon count: 16

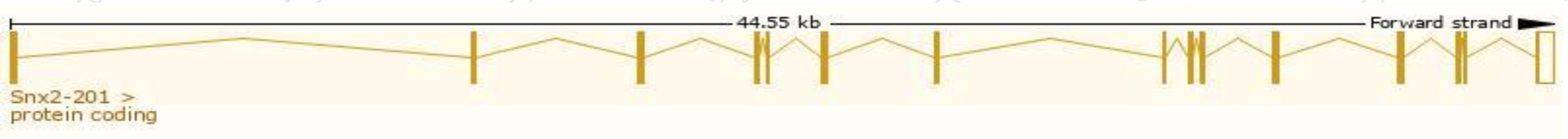
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	18	NC_000084.6 (53176292..53220866)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	18	NC_000084.5 (53336019..53380514)

Transcript information (Ensembl)

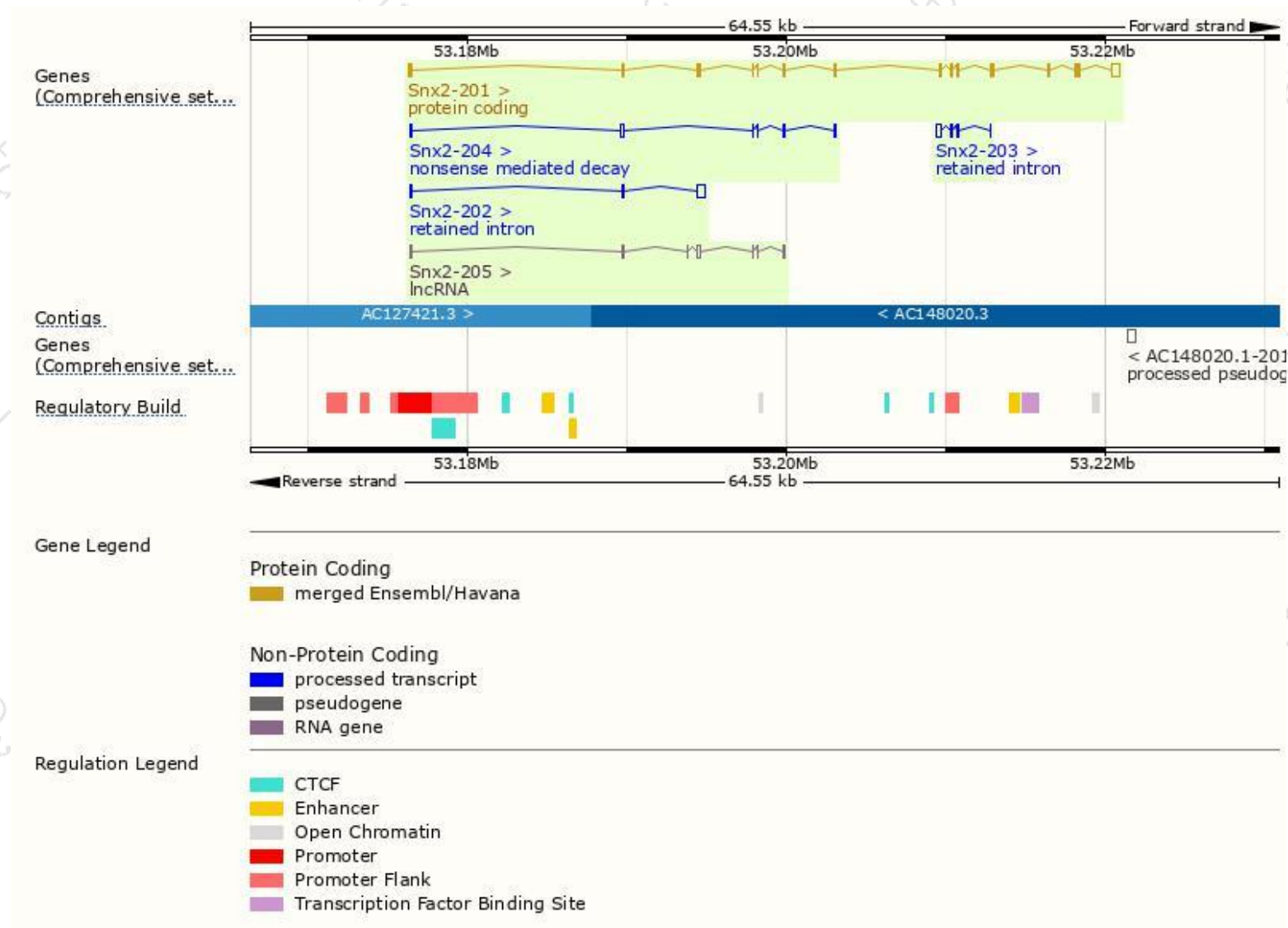
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Snx2-201	ENSMUST00000037850.6	2067	519aa	Protein coding	CCDS37821	Q9CWK8	TSL:1 GENCODE basic APPRIS P1
Snx2-204	ENSMUST00000236911.1	616	40aa	Nonsense mediated decay	-	-	
Snx2-202	ENSMUST00000235943.1	735	No protein	Retained intron	-	-	
Snx2-203	ENSMUST00000236111.1	576	No protein	Retained intron	-	-	
Snx2-205	ENSMUST00000237238.1	661	No protein	lncRNA	-	-	

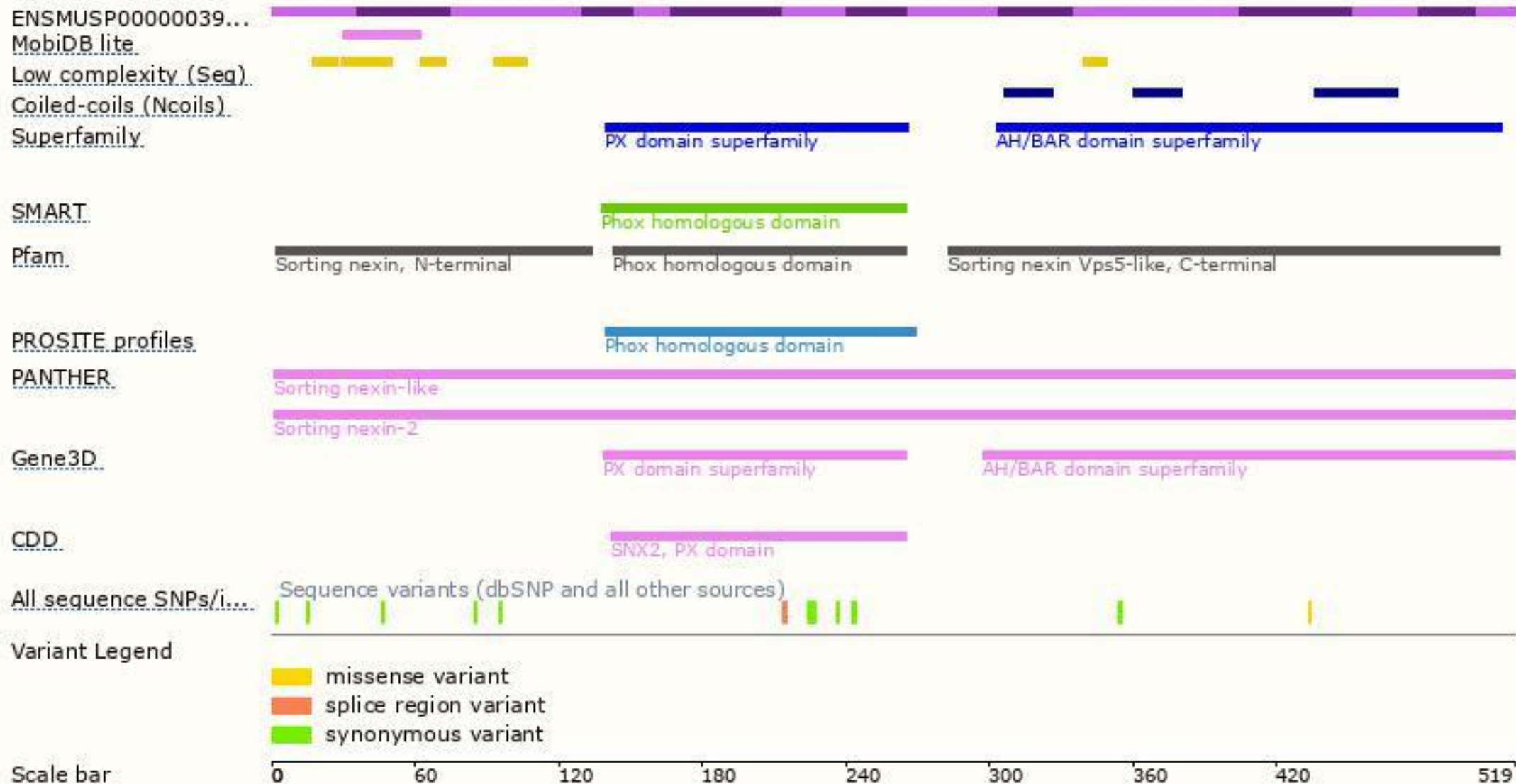
The strategy is based on the design of *Snx2-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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