

$Snx1$ Cas9-KO Strategy

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Project Overview

Project Name

$Snx1$

Project type

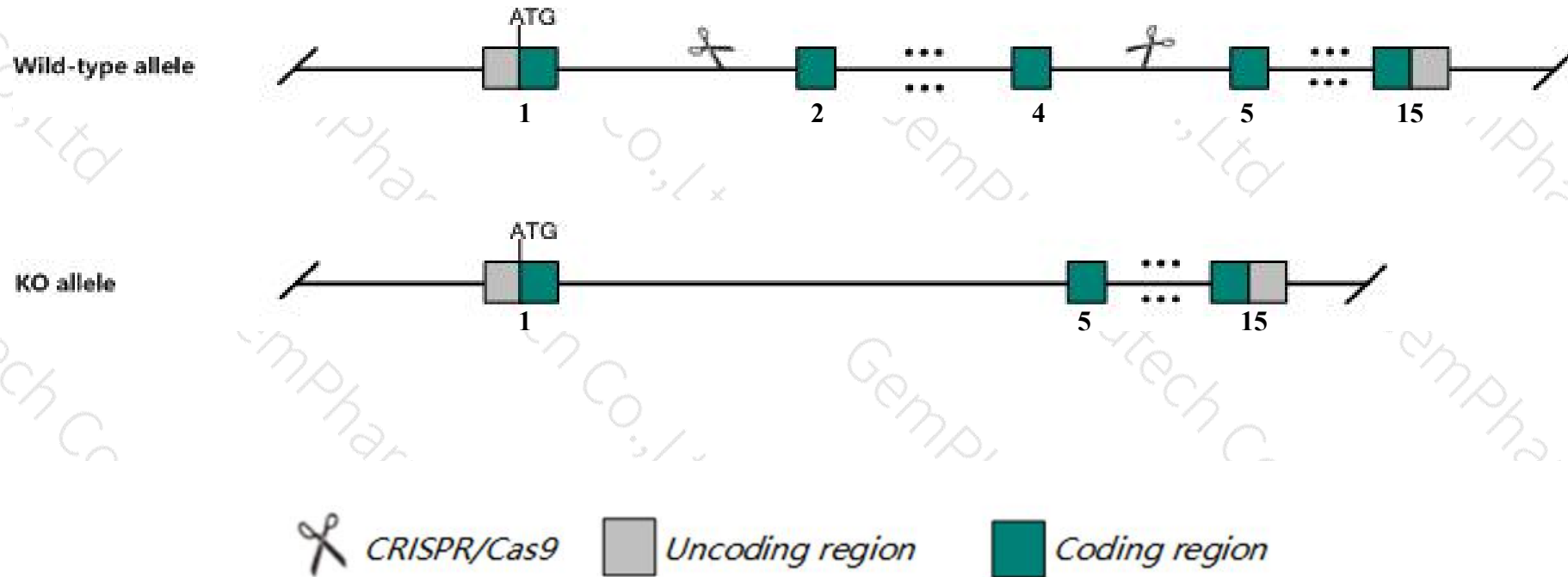
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Snx1* gene. The schematic diagram is as follows:



- The *Snx1* gene has 7 transcripts. According to the structure of *Snx1* gene, exon2-exon4 of *Snx1-201* (ENSMUST00000034946.14) transcript is recommended as the knockout region. The region contains 304bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Snx1* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygous mutant mice are viable and fertile and do not exhibit any apparent abnormalities.
- Transcript *Snx1*-202&204&205 may not be affected.
- The *Snx1* gene is located on the Chr9. 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)

Snx1 sorting nexin 1 [*Mus musculus* (house mouse)]

Gene ID: 56440, updated on 21-Oct-2019

Summary

- Official Symbol** Snx1 provided by [MGI](#)
- Official Full Name** sorting nexin 1 provided by [MGI](#)
- Primary source** [MGI:MGI:1928395](#)
- See related** [Ensembl:ENSMUSG000000032382](#)
- 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
- Expression** Ubiquitous expression in placenta adult (RPKM 53.7), genital fat pad adult (RPKM 44.0) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 9; 9 C See Snx1 in [Genome Data Viewer](#)

Exon count: 15

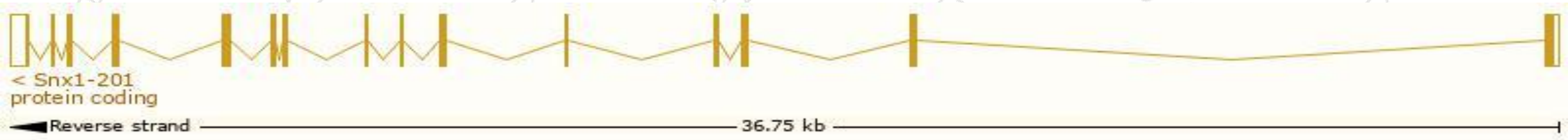
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	9	NC_000075.6 (66088127..66124886, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	9	NC_000075.5 (65935934..65972693, complement)

Transcript information (Ensembl)

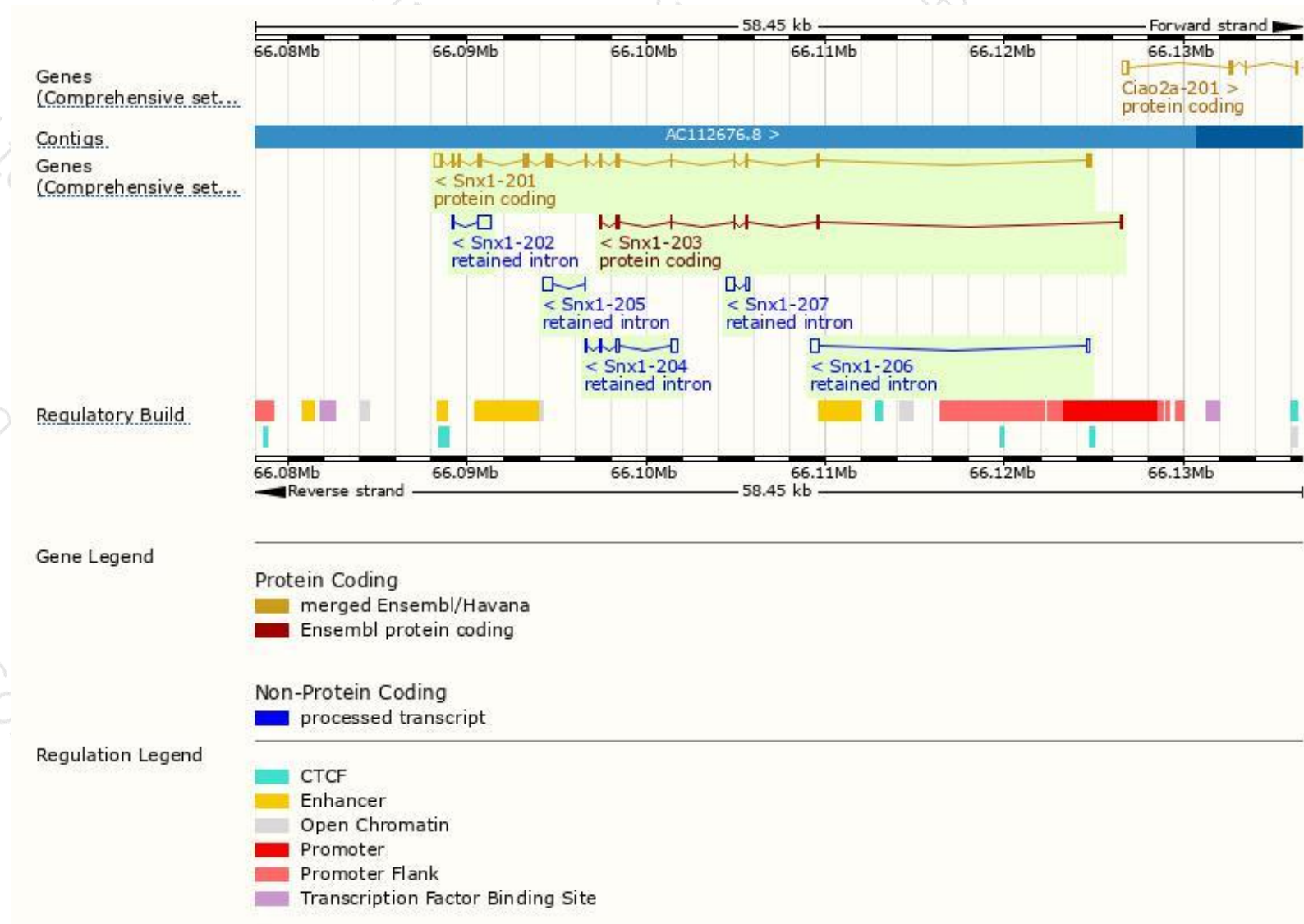
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Snx1-201	ENSMUST00000034946.14	2073	521aa	Protein coding	CCDS52839	Q6NZD2	TSL:1 GENCODE basic APPRIS P1
Snx1-203	ENSMUST00000137542.1	707	192aa	Protein coding	-	D3YWH1	CDS 3' incomplete TSL:5
Snx1-202	ENSMUST00000132841.1	827	No protein	Retained intron	-	-	TSL:3
Snx1-206	ENSMUST00000145449.1	678	No protein	Retained intron	-	-	TSL:2
Snx1-207	ENSMUST00000146893.1	666	No protein	Retained intron	-	-	TSL:3
Snx1-204	ENSMUST00000139872.1	654	No protein	Retained intron	-	-	TSL:5
Snx1-205	ENSMUST00000143148.1	583	No protein	Retained intron	-	-	TSL:3

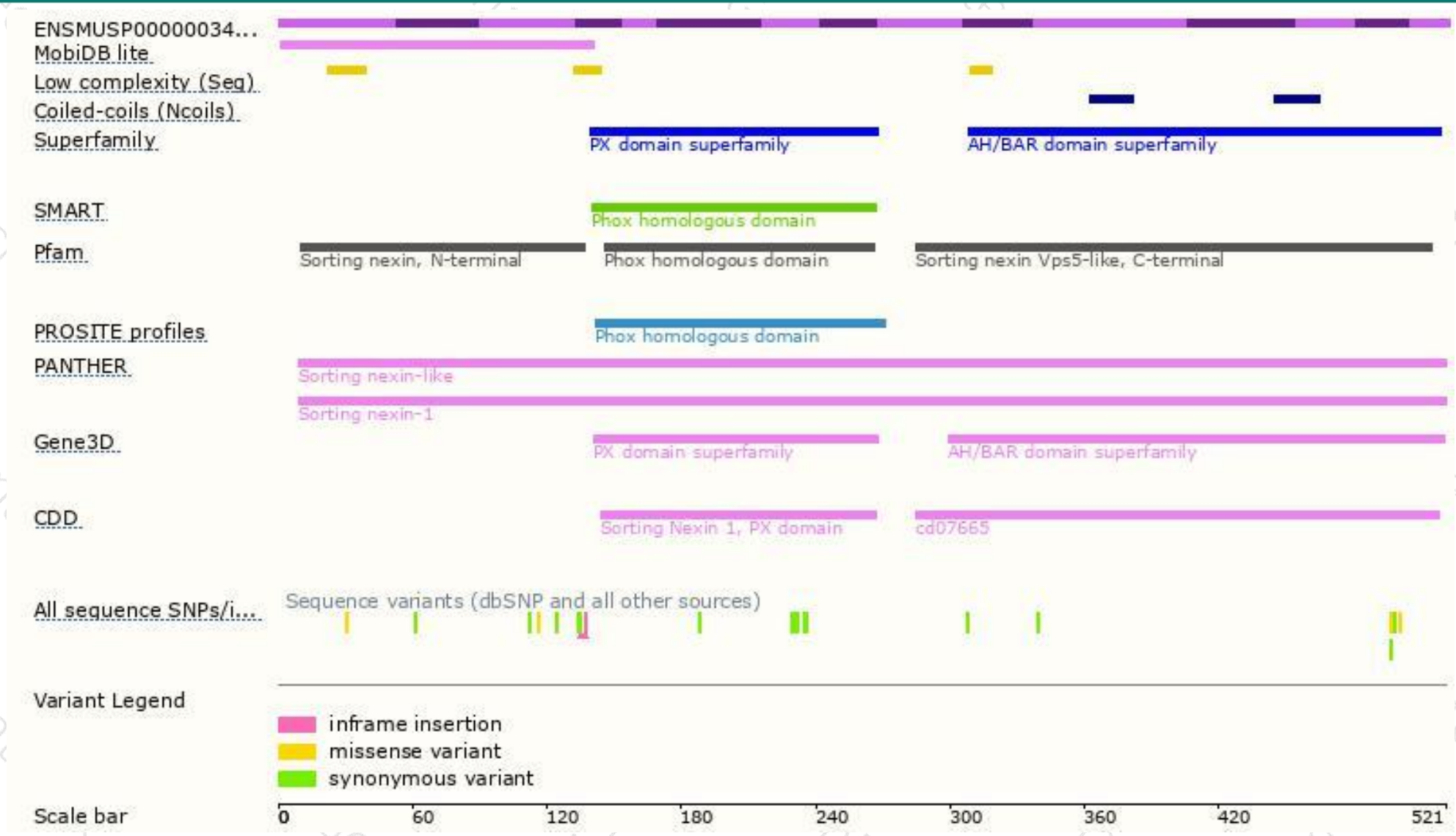
The strategy is based on the design of *Snx1-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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