

Sec31a Cas9-CKO Strategy

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Project Overview

Project Name

Sec31a

Project type

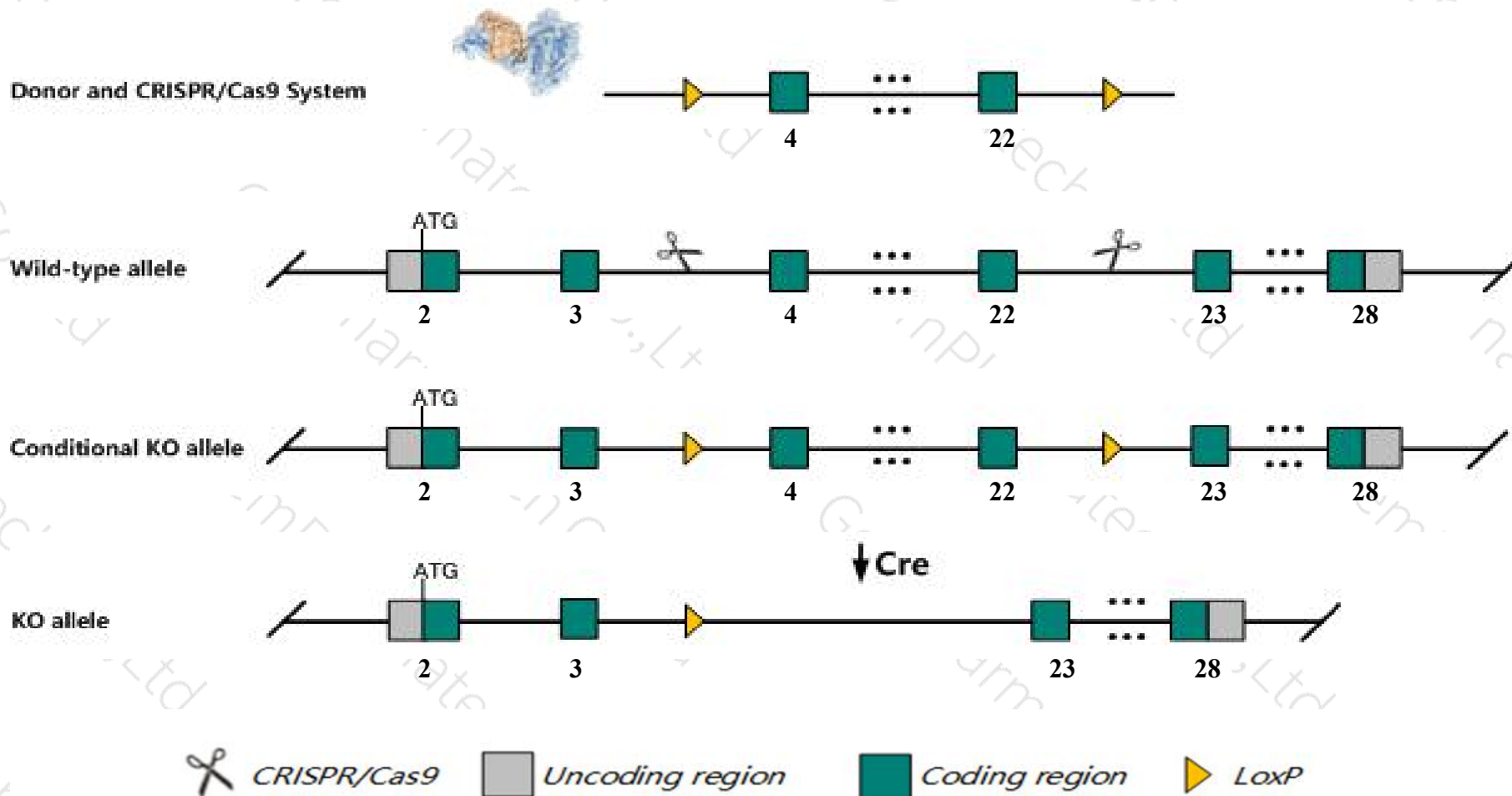
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sec31a* gene. The schematic diagram is as follows:



Technical routes

- The *Sec31a* gene has 12 transcripts. According to the structure of *Sec31a* gene, exon4-exon22 of *Sec31a-201* (ENSMUST00000094578.10) transcript is recommended as the knockout region. The region contains 2756bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sec31a* 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.

- The effect on transcript *Sec31a*-202&205&208&211&212 is unknown.
- Transcript *Sec31a*-203&204&207 may not be affected.
- The *Sec31a* gene is located on the Chr5. 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)



Sec31a Sec31 homolog A (S. cerevisiae) [Mus musculus (house mouse)]

Gene ID: 69162, updated on 25-Feb-2020

Summary

- Official Symbol** Sec31a provided by [MGI](#)
- Official Full Name** Sec31 homolog A (S. cerevisiae) provided by [MGI](#)
- Primary source** [MGI:MGI:1916412](#)
- See related** [Ensembl:ENSMUSG00000035325](#)
- 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** ABP125; ABP130; HSPC275; Sec31I1; AU042160; 1810024J13Rik
- Expression** Ubiquitous expression in duodenum adult (RPKM 58.7), small intestine adult (RPKM 54.6) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 5; 5 E4 [See Sec31a in Genome Data Viewer](#)

Exon count: 32

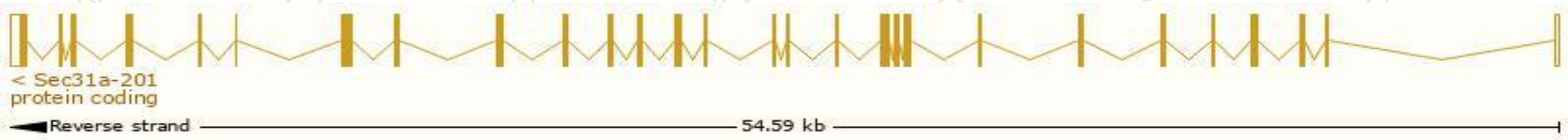
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	5	NC_000071.6 (100361649..100416273, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	5	NC_000071.5 (100790668..100845253, complement)

Transcript information (Ensembl)

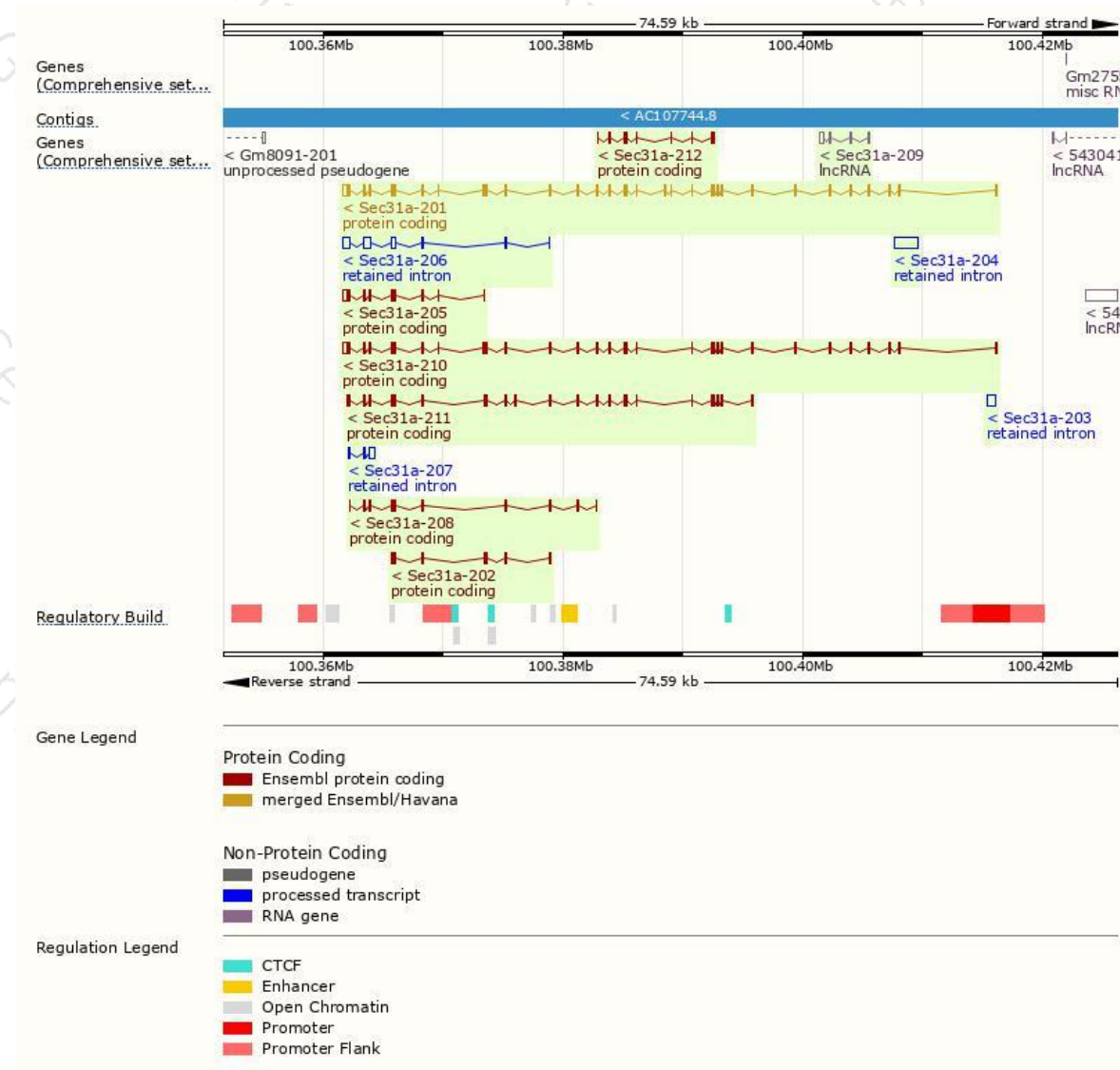
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sec31a-201	ENSMUST00000094578.10	4228	1230aa	Protein coding	CCDS51573	Q3UPL0	TSL:5 GENCODE basic APPRIS P2
Sec31a-210	ENSMUST00000182886.7	4047	1191aa	Protein coding	-	Q3UPL0	TSL:5 GENCODE basic APPRIS ALT2
Sec31a-211	ENSMUST00000182988.7	2846	934aa	Protein coding	-	S4R2A9	CDS 5' incomplete TSL:5
Sec31a-205	ENSMUST00000182433.7	1195	264aa	Protein coding	-	S4R1T5	CDS 5' incomplete TSL:1
Sec31a-208	ENSMUST00000182812.7	1093	364aa	Protein coding	-	S4R256	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
Sec31a-202	ENSMUST00000182002.1	887	296aa	Protein coding	-	S4R1Y8	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:2
Sec31a-212	ENSMUST00000183247.1	744	248aa	Protein coding	-	S4R192	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Sec31a-204	ENSMUST00000182171.1	1931	No protein	Retained intron	-	-	TSL:NA
Sec31a-206	ENSMUST00000182569.1	1686	No protein	Retained intron	-	-	TSL:1
Sec31a-203	ENSMUST00000182144.1	756	No protein	Retained intron	-	-	TSL:NA
Sec31a-207	ENSMUST00000182664.1	600	No protein	Retained intron	-	-	TSL:1
Sec31a-209	ENSMUST00000182850.1	683	No protein	lncRNA	-	-	TSL:3

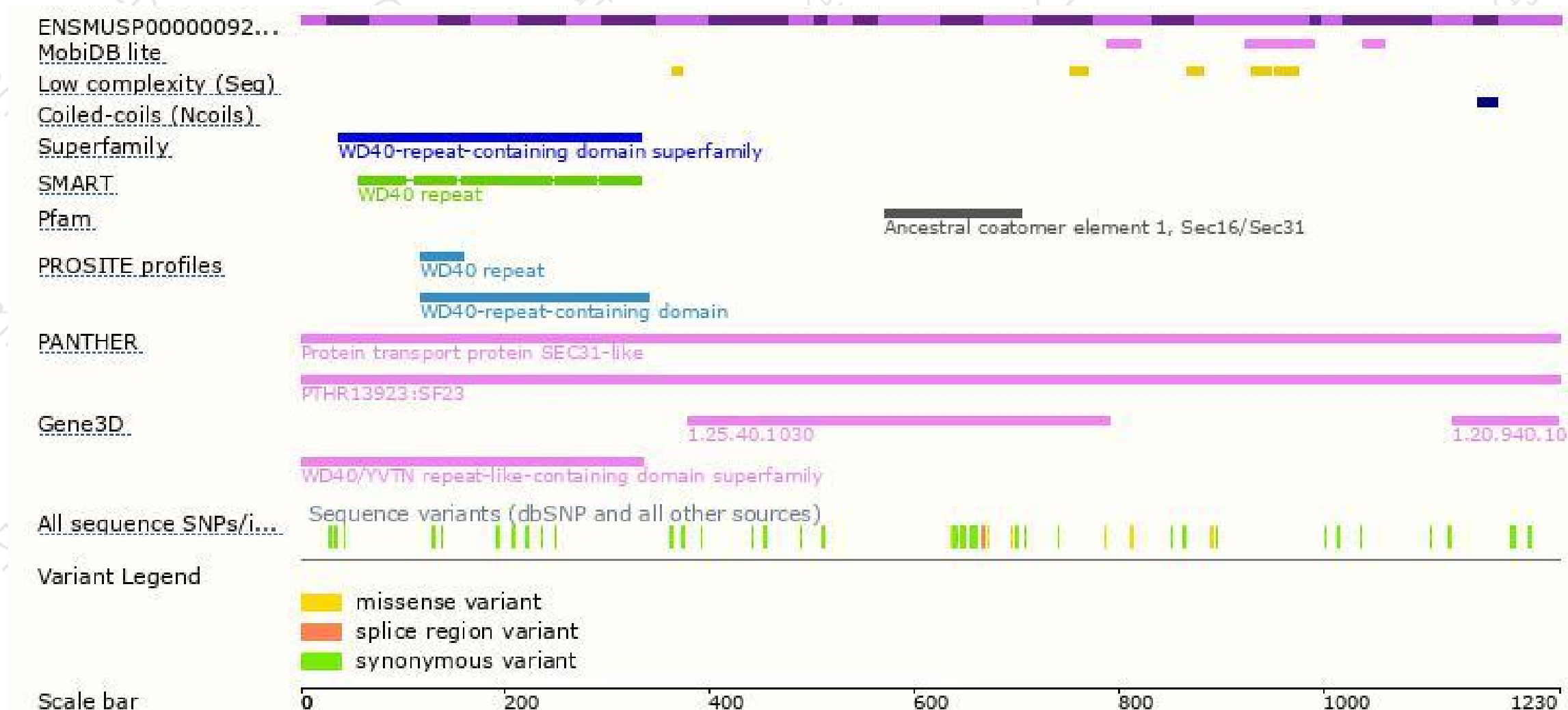
The strategy is based on the design of *Sec31a-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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