

***Sec13* Cas9-CKO Strategy**

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Project Overview

Project Name

Sec13

Project type

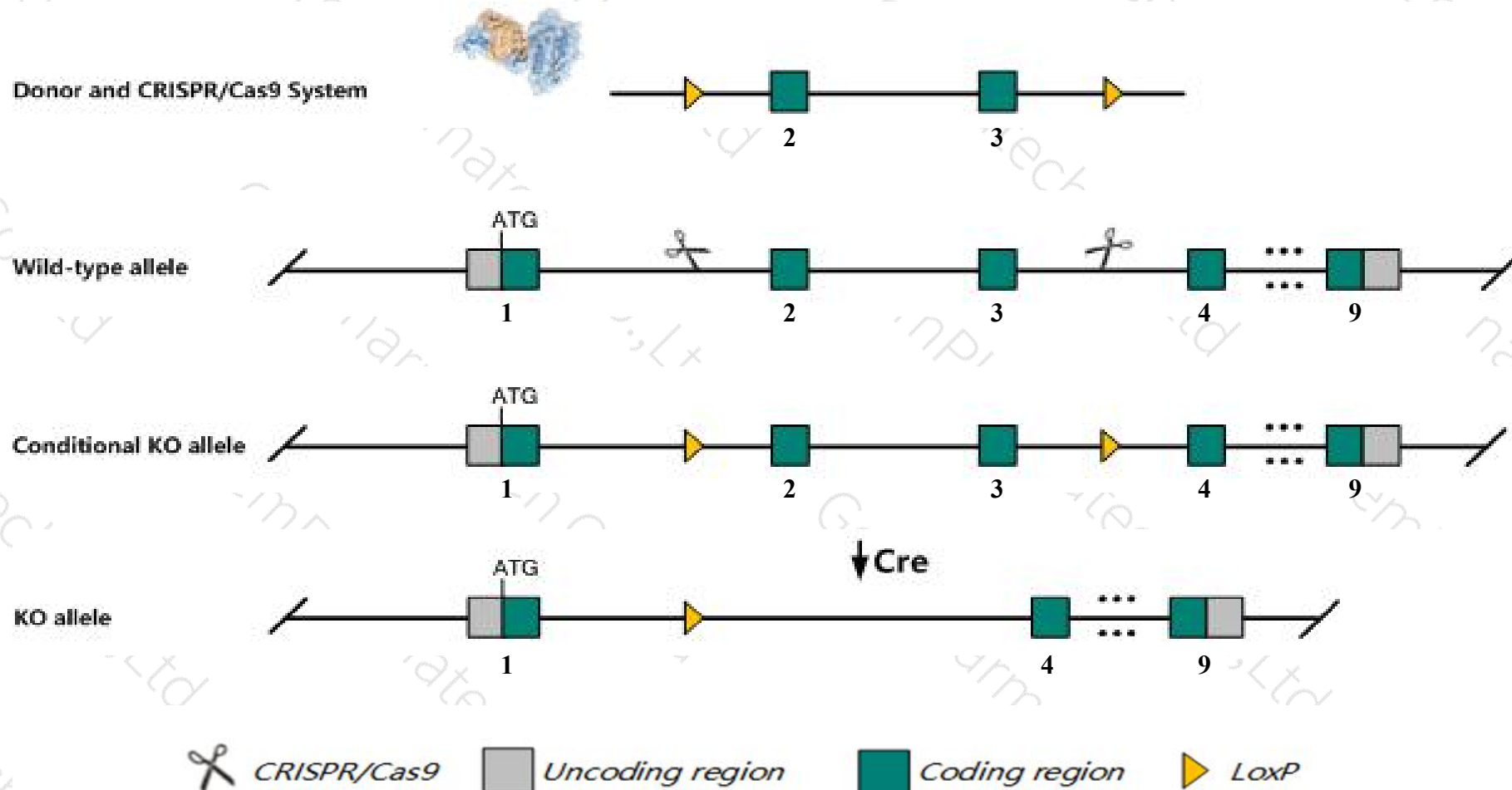
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sec13* gene. The schematic diagram is as follows:



Technical routes

- The *Sec13* gene has 4 transcripts. According to the structure of *Sec13* gene, exon2-exon3 of *Sec13-201* (ENSMUST00000032440.5) transcript is recommended as the knockout region. The region contains 161bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sec13* 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.

Notice

- Transcript *Sec13*-202&203&204 may not be affected.
- The *Sec13* gene is located on the Chr6. 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)

Sec13 SEC13 homolog, nuclear pore and COPII coat complex component [*Mus musculus* (house mouse)]

Gene ID: 110379, updated on 27-Aug-2019

Summary

- Official Symbol** Sec13 provided by MGI
- Official Full Name** SEC13 homolog, nuclear pore and COPII coat complex component provided by MGI
- Primary source** [MGI:MGI:99832](#)
- See related** [Ensembl:ENSMUSG000000030298](#)
- 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** Sec13r; Sec13l1; 1110003H02Rik
- Expression** Ubiquitous expression in large intestine adult (RPKM 114.3), limb E14.5 (RPKM 92.9) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 6 E3; 6 52.84 cM

See Sec13 in [Genome Data Viewer](#)

Exon count: 9

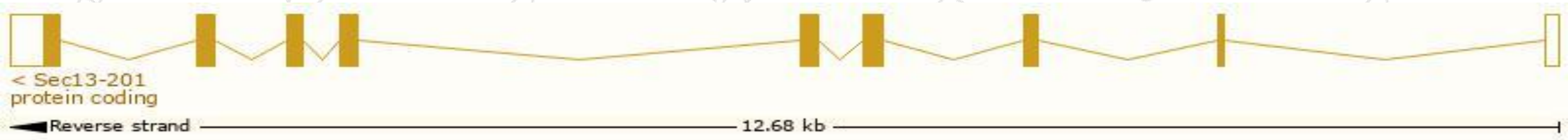
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	6	NC_000072.6 (113728052..113740681, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	6	NC_000072.5 (113678046..113690675, complement)

Transcript information (Ensembl)

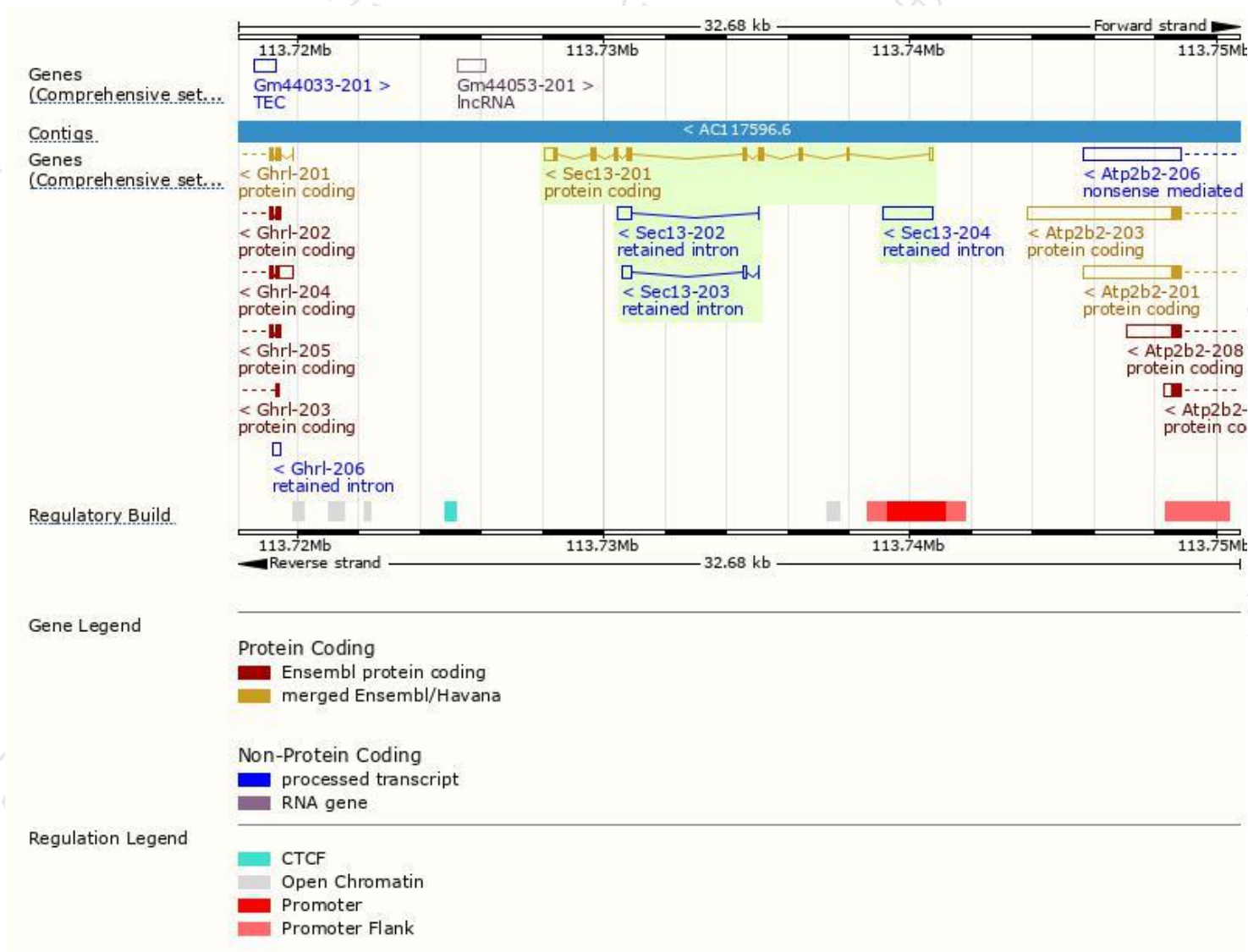
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sec13-201	ENSMUST00000032440.5	1353	322aa	Protein coding	CCDS39596	Q9D1M0	TSL:1 GENCODE basic APPRIS P1
Sec13-204	ENSMUST00000205135.1	1599	No protein	Retained intron	-	-	TSL:NA
Sec13-202	ENSMUST00000138204.7	492	No protein	Retained intron	-	-	TSL:5
Sec13-203	ENSMUST00000145979.1	460	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Sec13-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain

ENSMUSP00000032...

Superfamily

WD40-repeat-containing domain superfamily

SMART

WD40 repeat

Pfam

WD40 repeat

PROSITE profiles

WD40 repeat

WD40-repeat-containing domain

PANTHER

Sec13/Seh1 family

Protein Sec13

Gene3D

WD40/YVTN repeat-like-containing domain superfamily

All sequence SNPs/i...

Sequence variants (dbSNP and all other sources)

Variant Legend

- missense variant
- splice region variant
- synonymous variant

Scale bar

0 40 80 120 160 200 240 280 322

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

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