Sec23ip Cas9-KO Strategy

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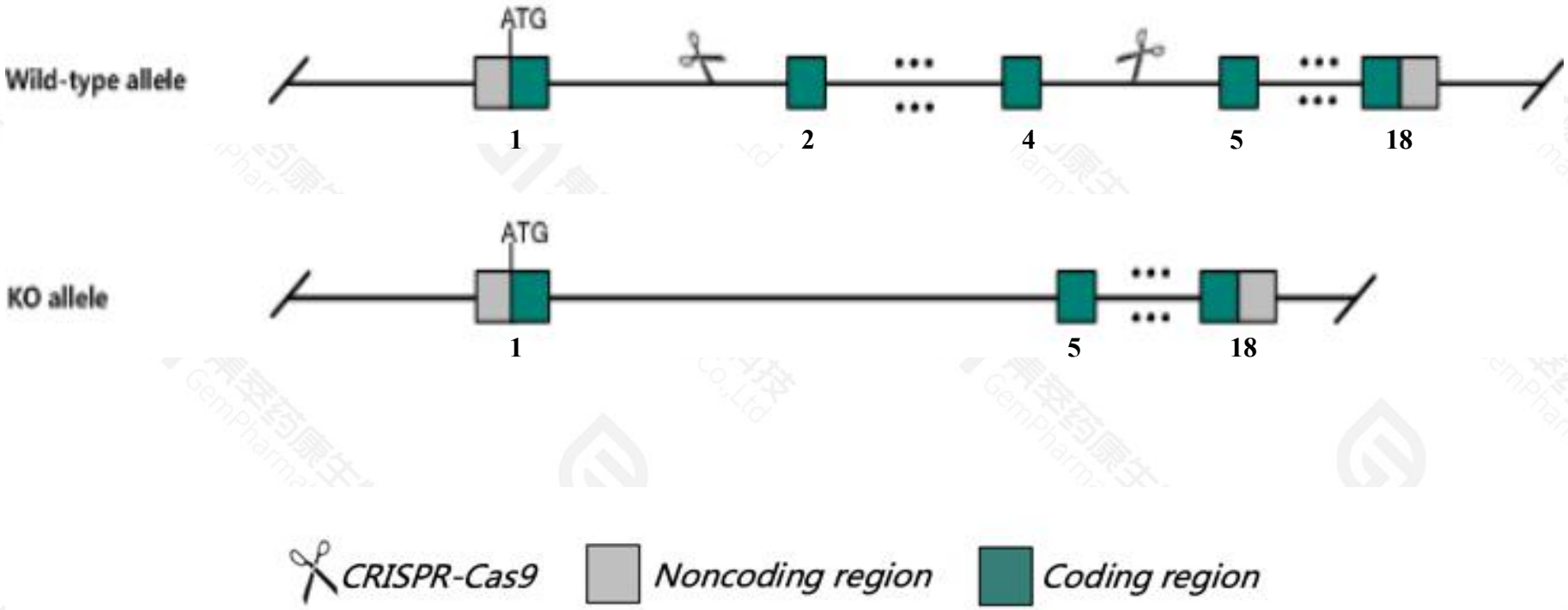
Project Overview

Project Name	***Sec23ip***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Sec23ip* gene. The schematic diagram is as follows:



Technical routes

➢ The *Sec23ip* gene has 4 transcripts. According to the structure of *Sec23ip* gene, exon2-exon4 of *Sec23ip-201*(ENSMUST00000042942.10) transcript is recommended as the knockout region.The region contains 932bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR-Cas9 technology to modify *Sec23ip* 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.

Notice

➢ According to the existing MGI data,male mice homozygous for a null allele display reduced fertility with globozoospermia and impaired fertilization.

➢ The *Sec23ip* gene is located on the Chr7. 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）

集萃药康 GemPharmatech

Sec23ip Sec23 interacting protein [Mus musculus (house mouse)]

Gene ID: 207352, updated on 13-Mar-2020

Summary

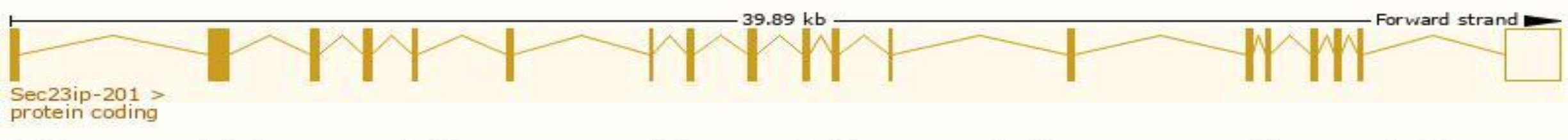
Official Symbol	Sec23ip provided by MGI
Official Full Name	Sec23 interacting protein provided byMGI
Primary source	MGI:MGI:2450915
See related	Ensembl:ENSMUSG00000055319
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	D7Ertd373e, p125
Expression	Ubiquitous expression in testis adult (RPKM 24.2), thymus adult (RPKM 11.5) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

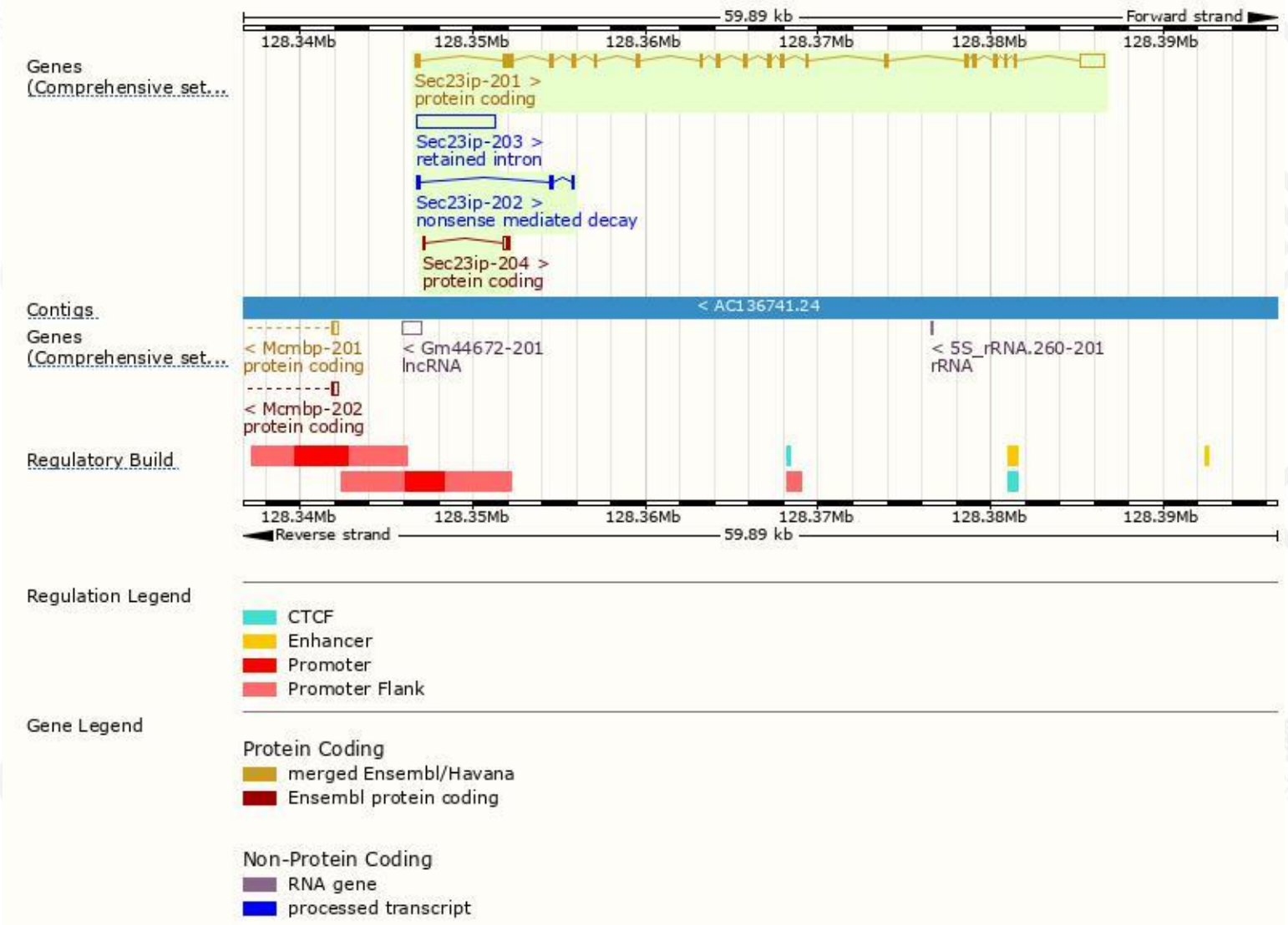
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sec23ip-201	ENSMUST00000042942.9	4505	998aa	Protein coding	CCDS21900	G3X928	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Sec23ip-204	ENSMUST00000206986.1	399	56aa	Protein coding	-	A0A0U1RPB3	CDS 3' incomplete TSL:2
Sec23ip-202	ENSMUST00000205856.1	444	97aa	Nonsense mediated decay	-	A0A0U1RP39	CDS 5' incomplete TSL:3
Sec23ip-203	ENSMUST00000206504.1	4604	No protein	Retained intron	-	-	TSL:NA

The strategy is based on the design of *Sec23ip-201* transcript,the transcription is shown below:

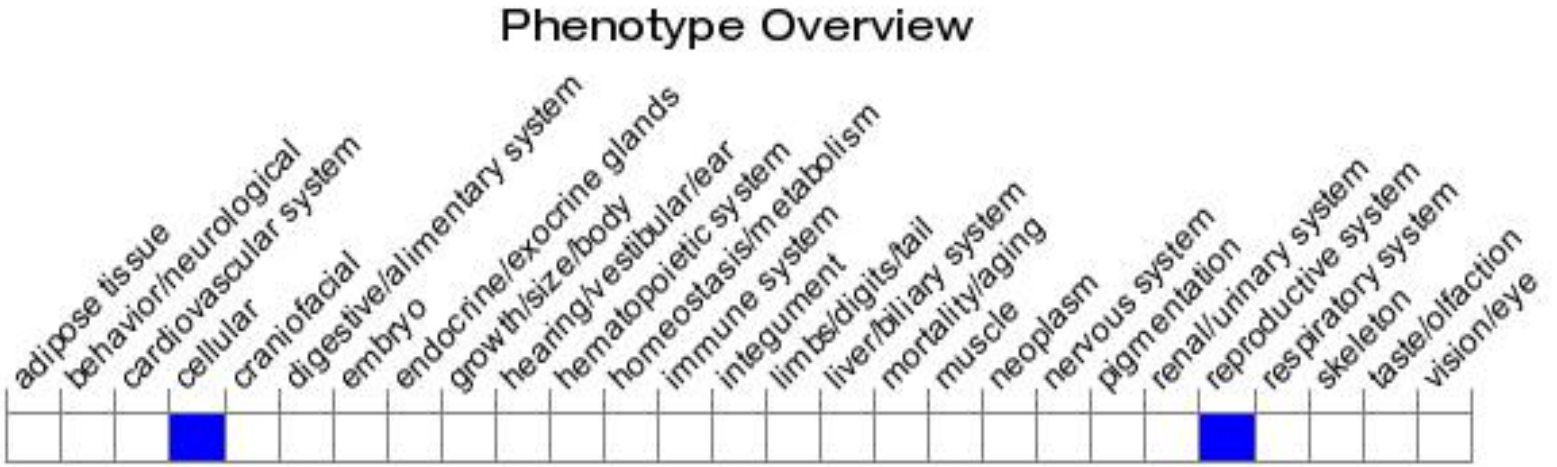


Genomic location distribution



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/).

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