Insrr Cas9-CKO Strategy

Designer: Daohua Xu
Reviewer: Huimin Su
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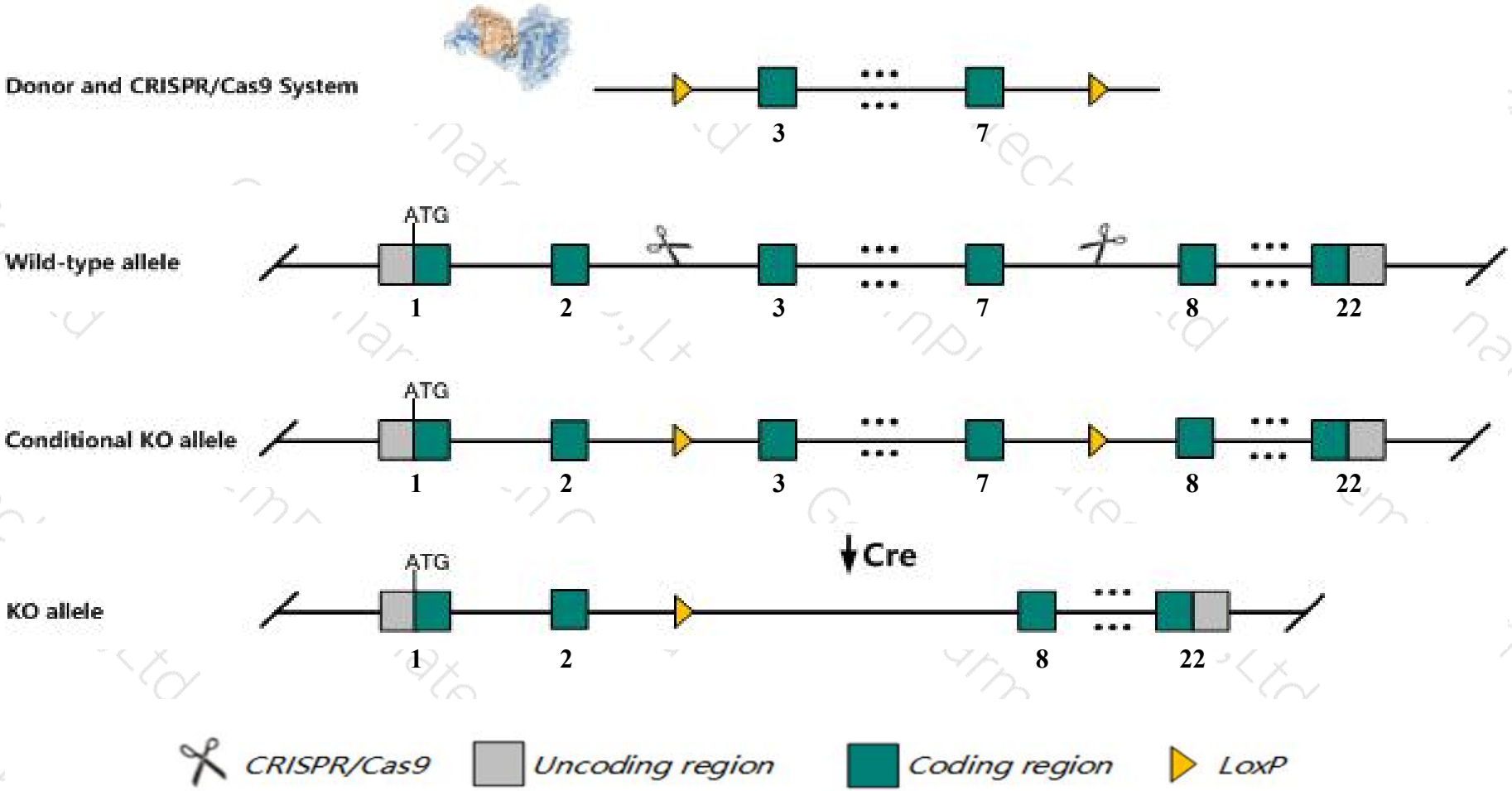
Project Overview

Project Name	***Insrr***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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



Technical routes

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- The *Insrr* gene has 4 transcripts. According to the structure of *Insrr* gene, exon3-exon7 of *Insrr-201* (ENSMUST00000029711.8) transcript is recommended as the knockout region.The region contains 934bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Insrr* 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

➢ According to the existing MGI data,Mice homozygous for a targeted null mutation exhibit no anomalies in pancreatic islet morphology, beta-cell mass or pancreatic secretory function. This mutation in combination with Insr mutant mice does not affect the diabetes predisposition of Insr mutant mice.

➢The KO region contains partial intron of the *Pear1* gene.Knockout the region may affect the function of *Pear1* gene.

➢ The *Insrr* gene is located on the Chr3. 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）

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Insrr insulin receptor-related receptor [Mus musculus (house mouse)]

Gene ID: 23920, updated on 24-Feb-2019

Summary

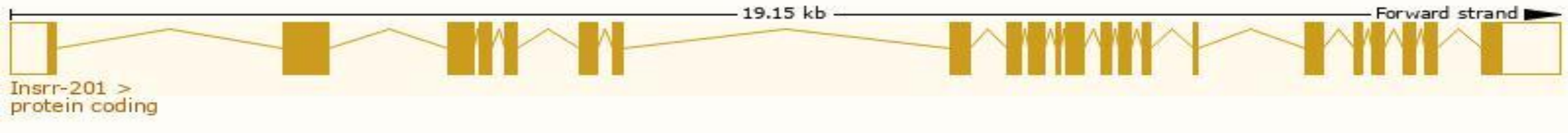
Official Symbol	Insrr provided by MGI
Official Full Name	insulin receptor-related receptor provided by MGI
Primary source	MGI:MGI:1346037
See related	Ensembl:ENSMUSG00000005640
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Irr
Expression	Biased expression in kidney adult (RPKM 10.4), colon adult (RPKM 3.5) and 9 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

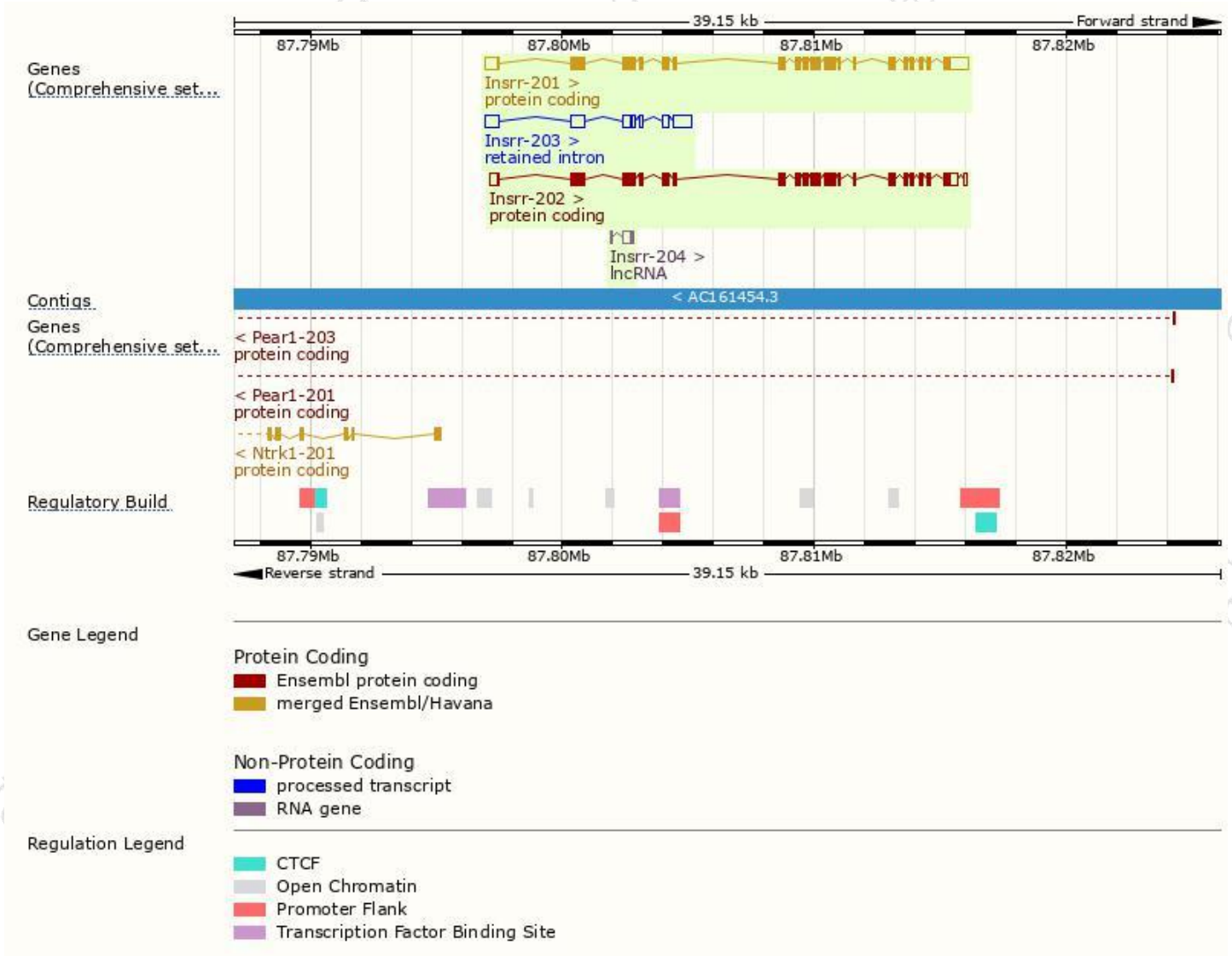
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Insrr-201	ENSMUST00000029711.8	5102	1300aa	Protein coding	CCDS17454	Q9WTL4	TSL:1 GENCODE basic APPRIS P1
Insrr-202	ENSMUST00000107582.2	4694	1300aa	Protein coding	CCDS17454	Q9WTL4	TSL:5 GENCODE basic APPRIS P1
Insrr-203	ENSMUST00000166771.7	2610	No protein	Retained intron	-	-	TSL:2
Insrr-204	ENSMUST00000166866.1	376	No protein	lncRNA	-	-	TSL:5

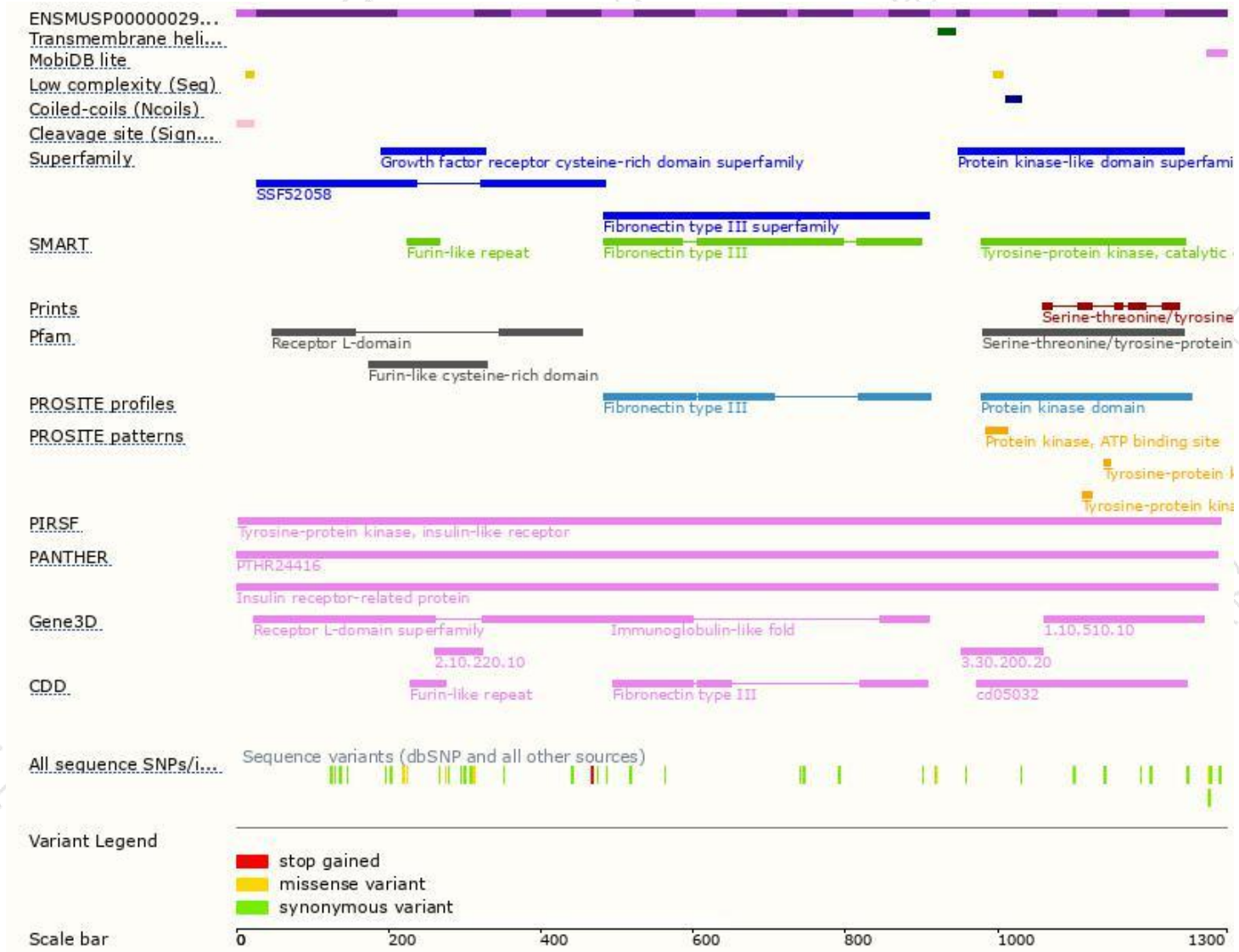
The strategy is based on the design of *Insrr-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

Tel: 400-9660890

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