

Insrr Cas9-KO Strategy

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Project Overview

Project Name

Insrr

Project type

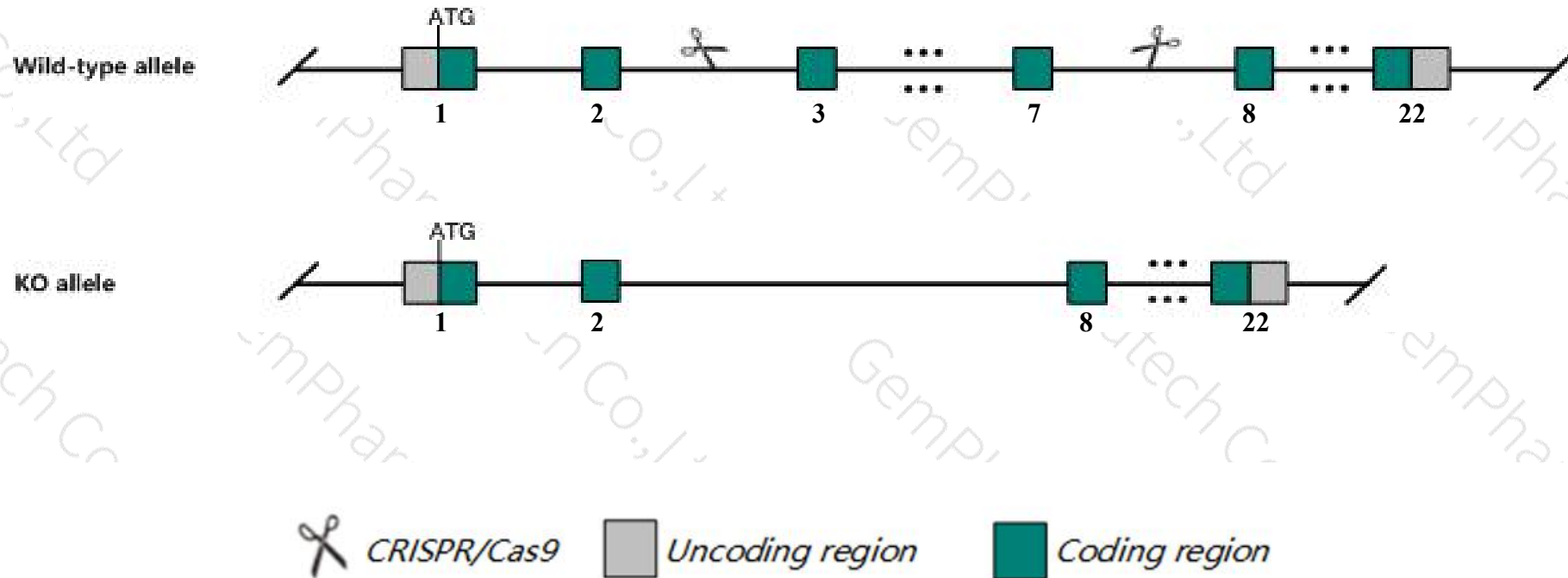
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- 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 v

- 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 *Insr* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

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

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

Summary



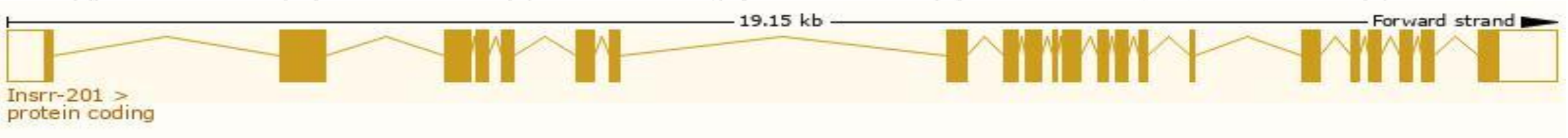
Official Symbol	Insrr provided by MGI
Official Full Name	insulin receptor-related receptor provided by MGI
Primary source	MGI:MGI:1346037
See related	Ensembl:ENSMUSG000000005640
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; 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)

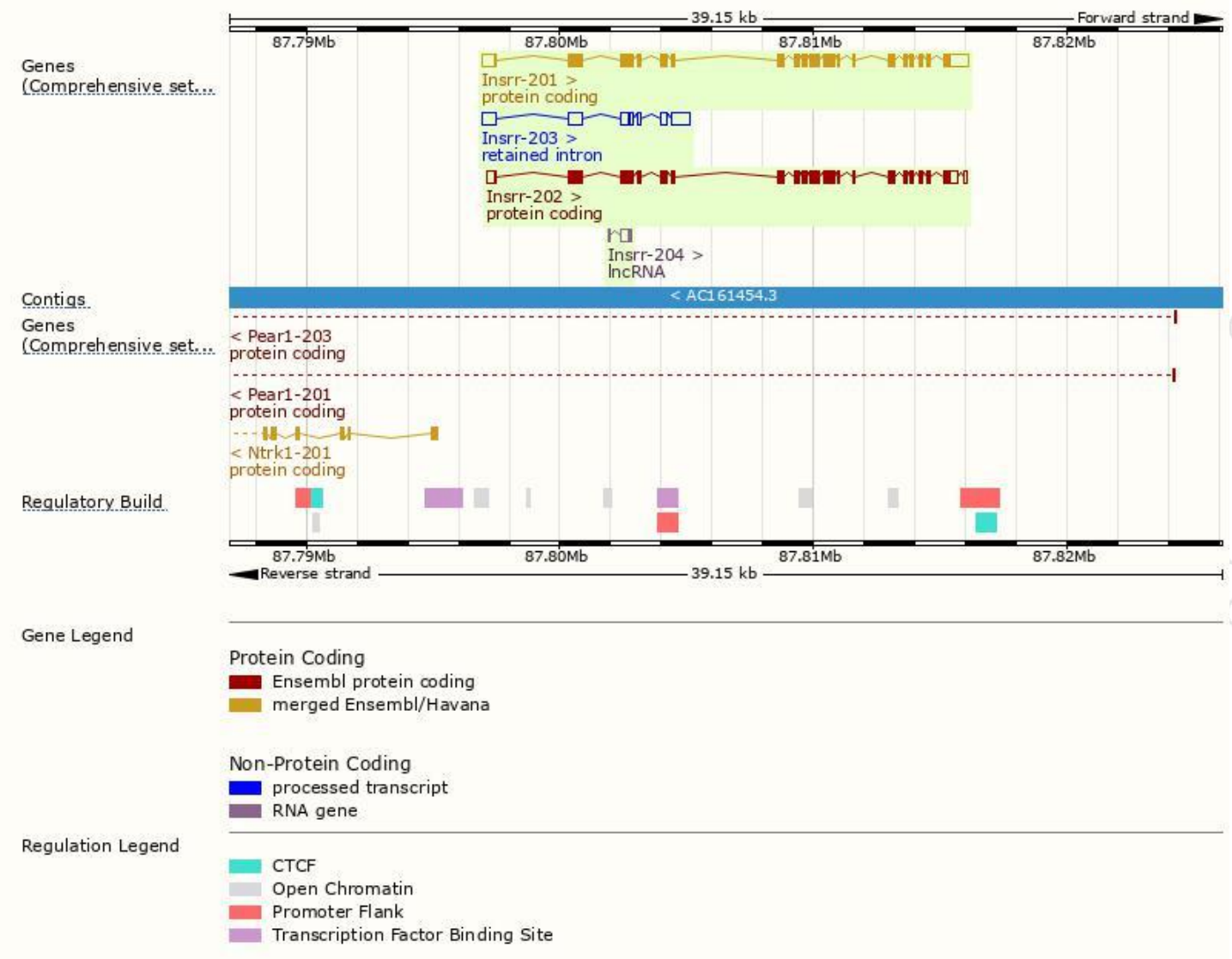
The gene has 4 transcripts,all transcripts are shown below:

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

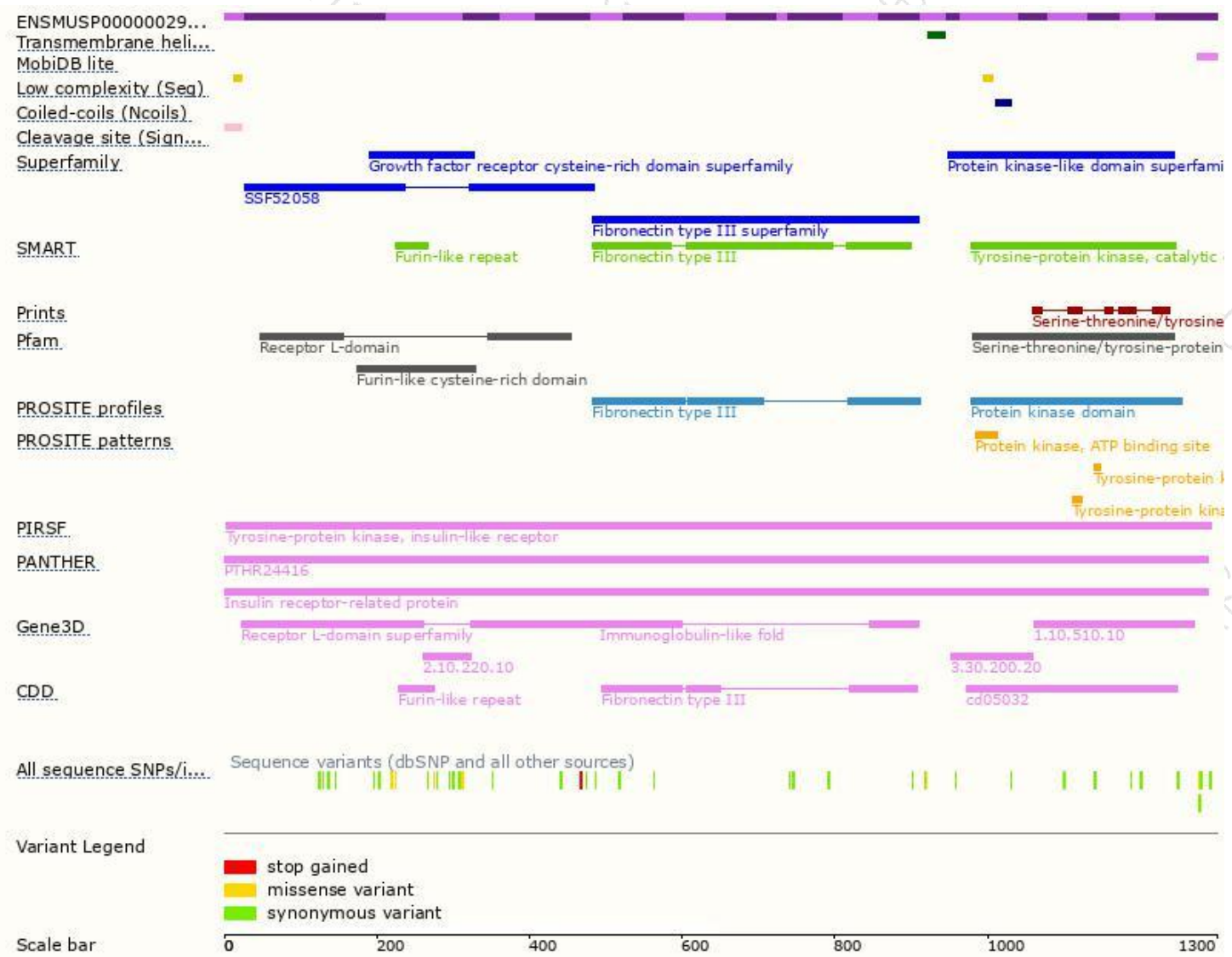
The strategy is based on the design of *Insrr-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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