

Insr Cas9-KO Strategy

Designer: Xiaojing Li
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Reviewer: JiaYu

Project Overview

Project Name

Insr

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Insr* gene has 5 transcripts. According to the structure of *Insr* gene, exon3 of *Insr-201* (ENSMUST00000091291.4) transcript is recommended as the knockout region. The region contains 322bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Insr* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Null mutants grow slowly and die by 7 days of age with ketoacidosis, high serum insulin and triglycerides, low glycogen stores and fatty livers. Tissue specific knockouts show milder lipid metabolism anomalies. Point mutation heterozygotes exhibit hyperglycemia, hyperinsulinemia and glucosuria.
- The *Insr* gene is located on the Chr8. 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)

Insr insulin receptor [*Mus musculus* (house mouse)]

Gene ID: 16337, updated on 27-Aug-2019

Summary

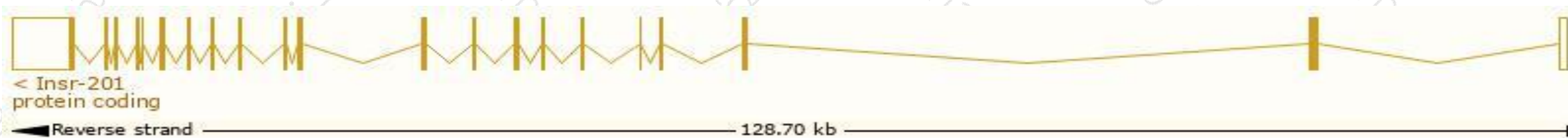
Official Symbol	Insr provided by MGI
Official Full Name	insulin receptor provided by MGI
Primary source	MGI:MGI:96575
See related	Ensembl:ENSMUSG00000005534
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	IR; IR-A; IR-B; CD220; 4932439J01Rik; D630014A15Rik
Summary	This gene encodes a member of the receptor tyrosine kinase family of transmembrane signaling proteins that play important roles in cell differentiation, growth and metabolism. The encoded preproprotein undergoes proteolytic processing to generate alpha and beta chains that form a disulfide-linked heterodimer which, in turn homodimerizes to form a mature, functional receptor. Mice lacking the encoded protein develop severe hyperglycemia and hyperketonemia, and die within a couple of days after birth as a result of diabetic ketoacidosis. [provided by RefSeq, Aug 2016]
Expression	Ubiquitous expression in heart adult (RPKM 8.5), adrenal adult (RPKM 7.8) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

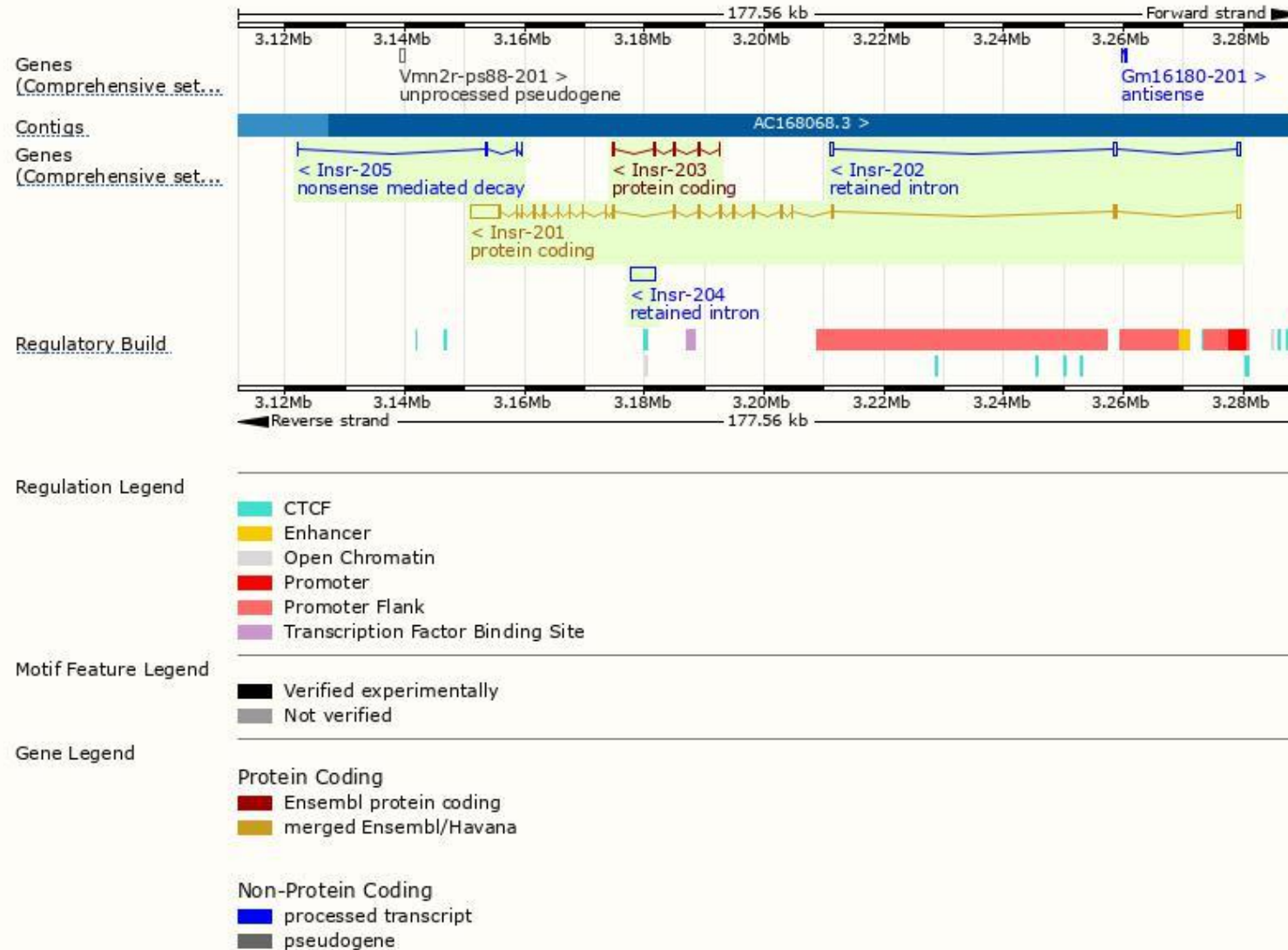
The gene has 5 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Insr-201	ENSMUST00000091291.4	9355	1372aa	Protein coding	CCDS22059	P15208	TSL:1 GENCODE basic APPRIS P1
Insr-203	ENSMUST00000207100.1	672	224aa	Protein coding	-	B8Q3N4	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:1
Insr-205	ENSMUST00000208839.1	551	90aa	Nonsense mediated decay	-	A0A140LI30	CDS 5' incomplete TSL:3
Insr-204	ENSMUST00000207295.1	4019	No protein	Retained intron	-	-	TSL:NA
Insr-202	ENSMUST00000139504.1	1675	No protein	Retained intron	-	-	TSL:1

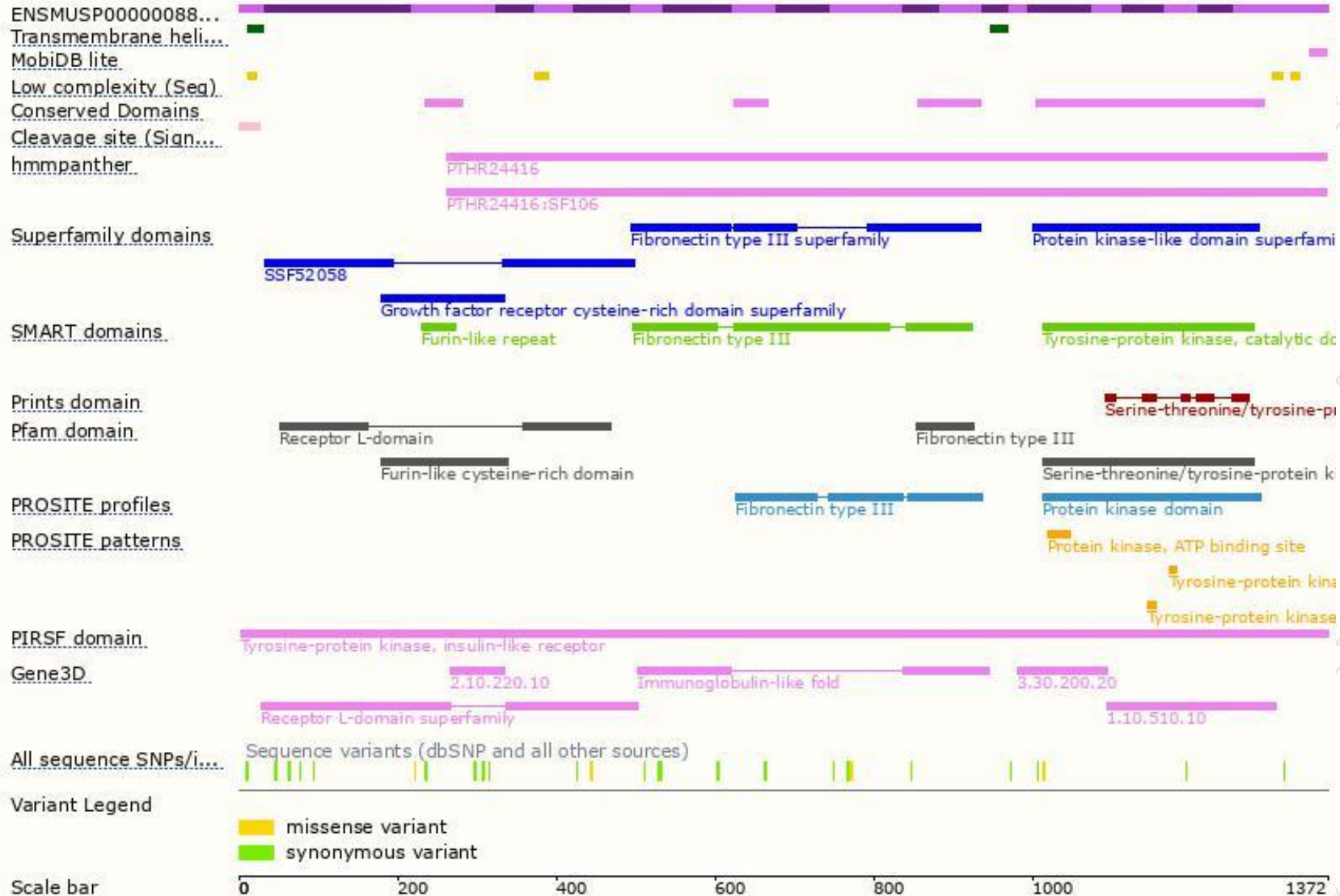
The strategy is based on the design of *Insr-201* transcript, The transcription is shown below



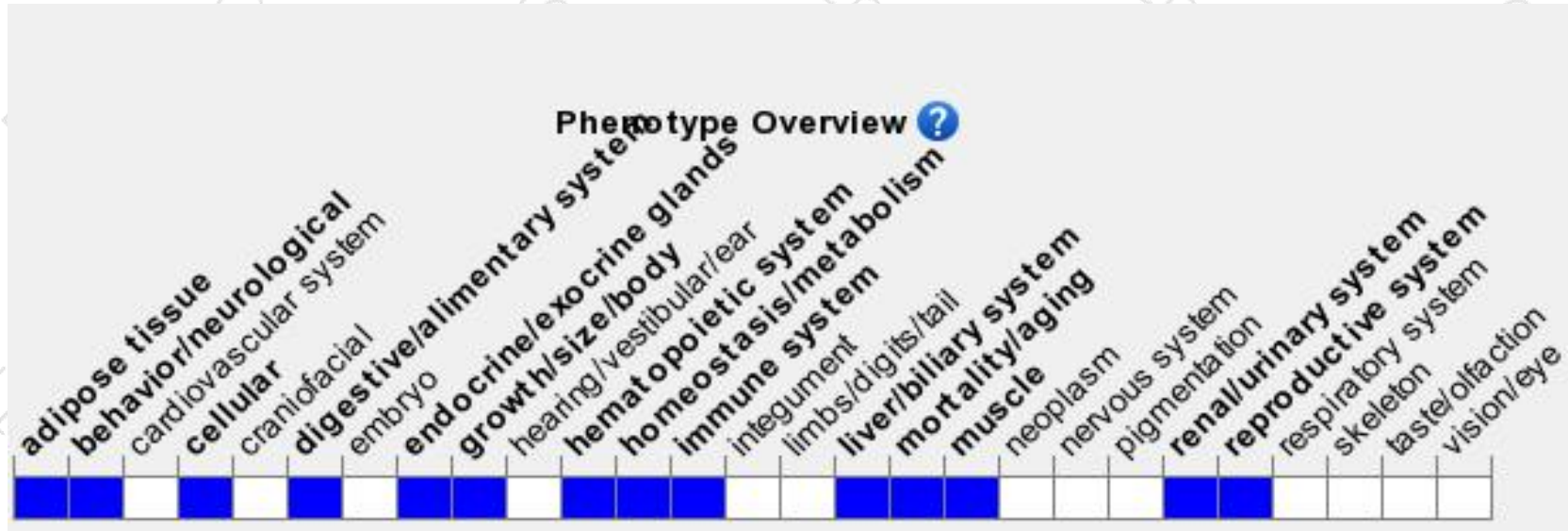
Genomic location distribution



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/>).

According to the existing MGI data, Null mutants grow slowly and die by 7 days of age with ketoacidosis, high serum insulin and triglycerides, low glycogen stores and fatty livers. Tissue specific knockouts show milder lipid metabolism anomalies. Point mutation heterozygotes exhibit hyperglycemia, hyperinsulinemia and glucosuria.

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

Tel: 400-9660890

