

Ssr1 Cas9-KO Strategy

Designer: Yanhua Shen

Project Overview

Project Name

Ssr1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ssr1* gene. The schematic diagram is as follows:



- The *Ssr1* gene has 4 transcripts. According to the structure of *Ssr1* gene, exon2 of *Ssr1-201* (ENSMUST00000021864.7) transcript is recommended as the knockout region. The region contains 113bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ssr1* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygous mutation of this gene results in neonatal lethality, subcutaneous edema, and cardiac defects, including absence of septation of the proximal part of the outflow tract, double outlet right ventricle, persistent truncus arteriosus, and abnormal development of the endocardial cushion.
- The *Ssr1* gene is located on the Chr13. 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)

Ssr1 signal sequence receptor, alpha [Mus musculus (house mouse)]

Gene ID: 107513, updated on 31-Jan-2019

Summary



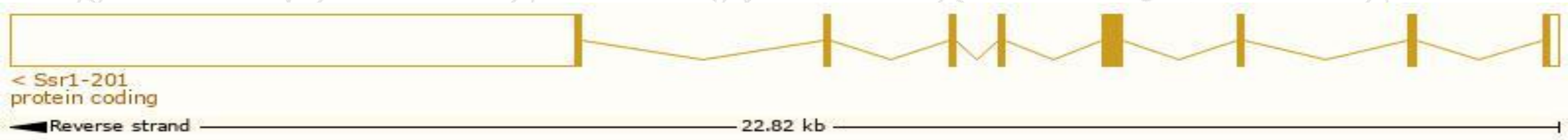
Official Symbol	Ssr1 provided by MGI
Official Full Name	signal sequence receptor, alpha provided by MGI
Primary source	MGI:MGI:105082
See related	Ensembl:ENSMUSG000000021427
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2510001K09Rik, 6330400D04, AI159733, AI452176, SSR, TRAPA
Expression	Ubiquitous expression in placenta adult (RPKM 16.8), CNS E11.5 (RPKM 10.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

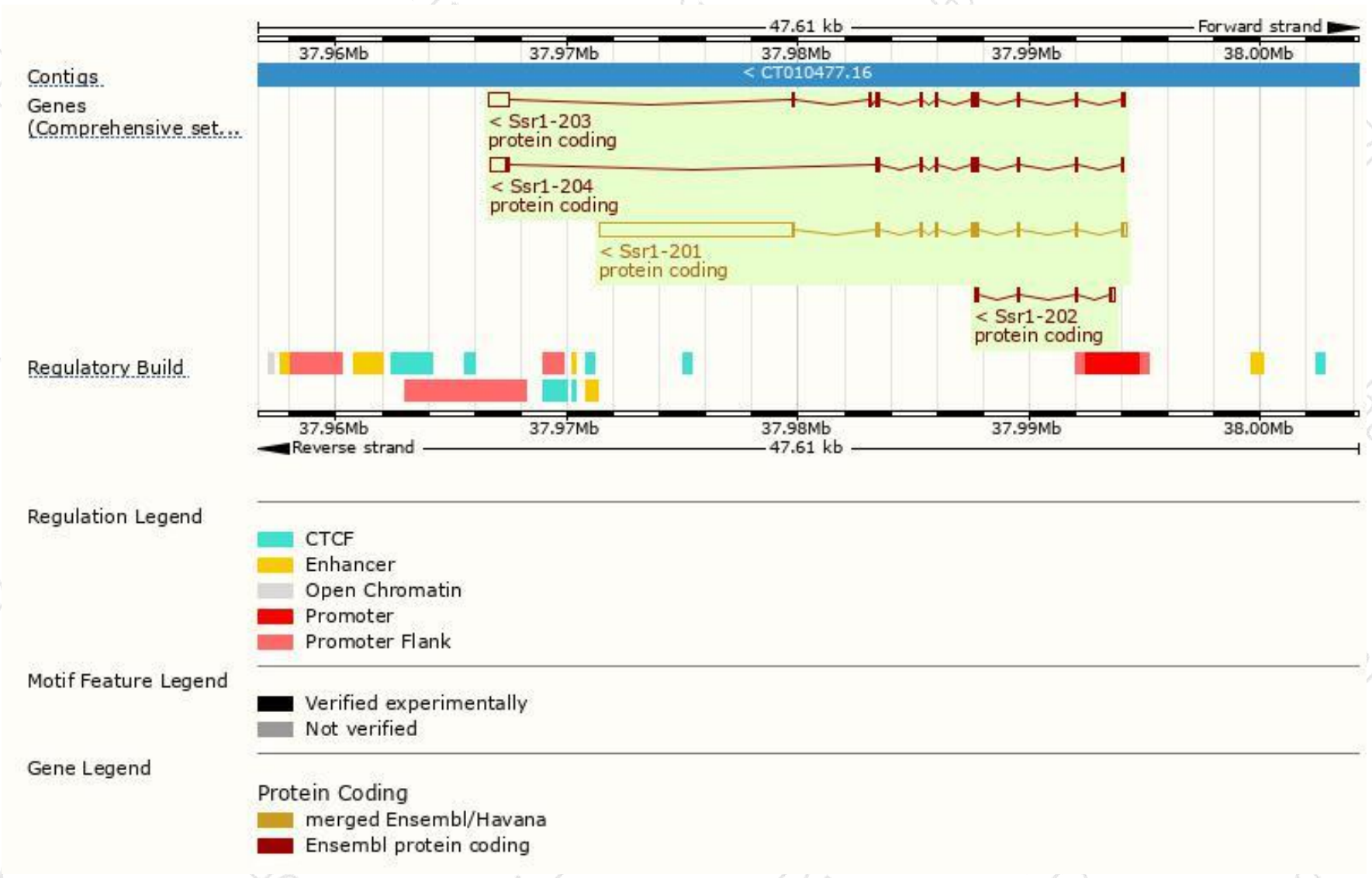
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ssr1-201	ENSMUST00000021864.7	9333	286aa	Protein coding	CCDS26459	Q9CY50	TSL:1 GENCODE basic APPRIS P1
Ssr1-203	ENSMUST00000225246.1	1825	298aa	Protein coding	-	A0A286YCT4	GENCODE basic
Ssr1-204	ENSMUST00000225319.1	1610	318aa	Protein coding	-	A0A286YCG8	GENCODE basic
Ssr1-202	ENSMUST00000224399.1	523	115aa	Protein coding	-	A0A286YDB7	CDS 3' incomplete

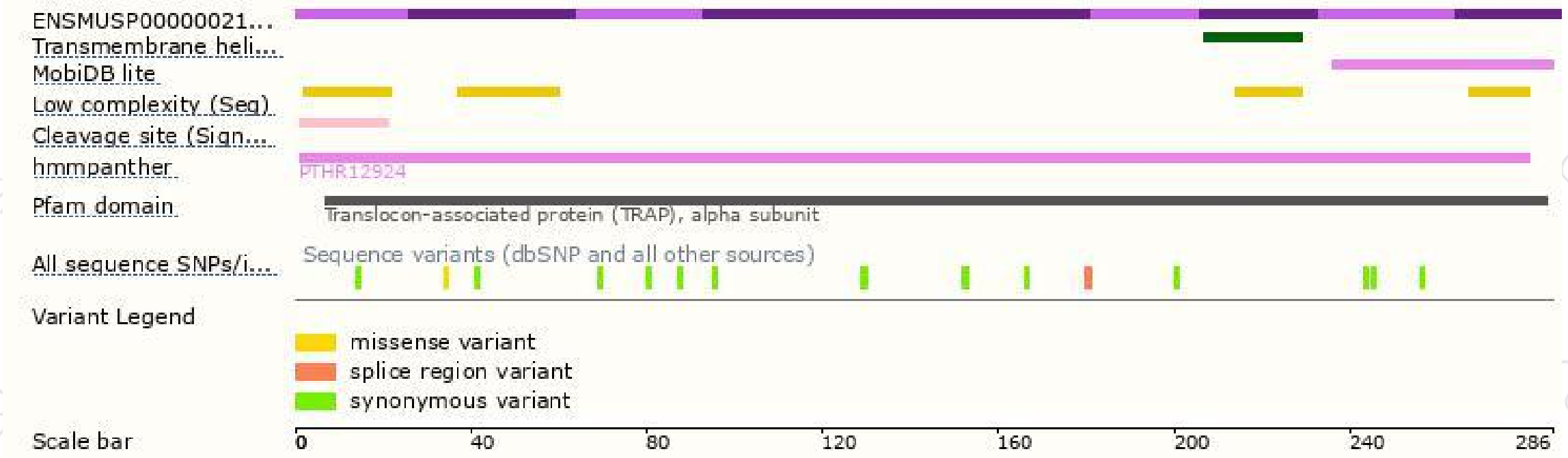
The strategy is based on the design of *Ssr1-201* transcript,The transcription is shown below



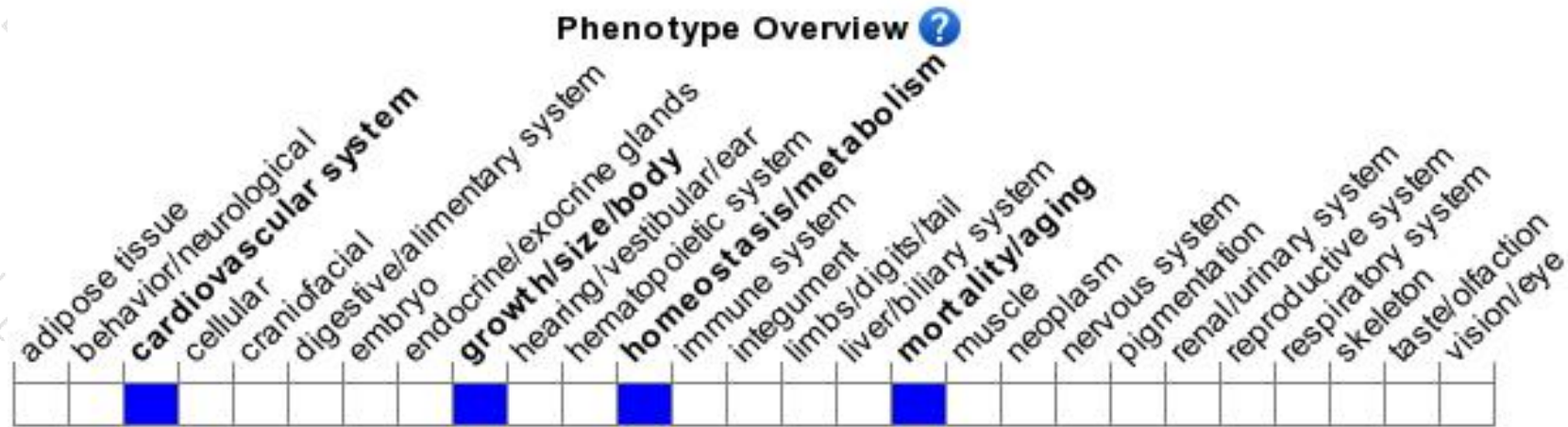
Genomic location distribution



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, Homozygous mutation of this gene results in neonatal lethality, subcutaneous edema, and cardiac defects, including absence of septation of the proximal part of the outflow tract, double outlet right ventricle, persistent truncus arteriosus, and abnormal development of the endocardial cushion.

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

Tel: 400-9660890

