

Msrb1 Cas9-KO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

Design Date:

2020-2-14

Project Overview

Project Name

Msrb1

Project type

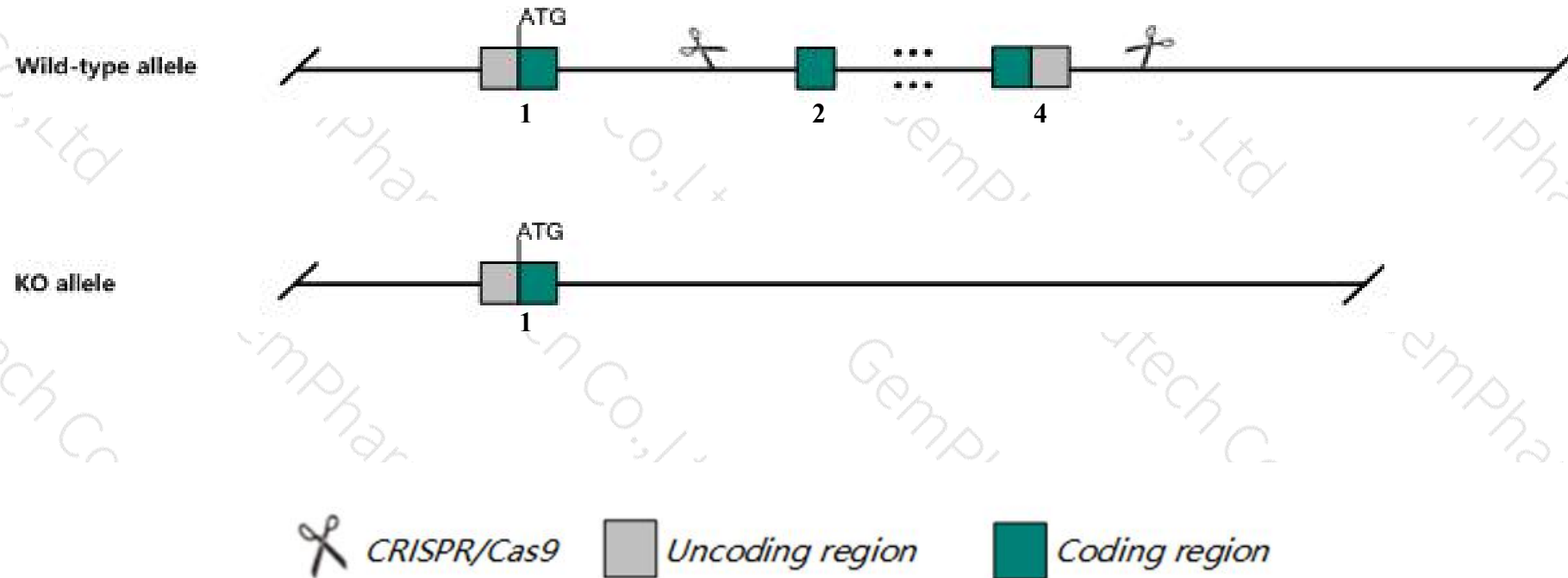
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Msrb1* gene has 2 transcripts. According to the structure of *Msrb1* gene, exon2-exon4 of *Msrb1-201* (ENSMUST00000101800.5) transcript is recommended as the knockout region. The region contains 296bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Msrb1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a gene trap allele exhibit oxidative stress.
- The *Msrbl* gene is located on the Chr17. 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)

Msrb1 methionine sulfoxide reductase B1 [Mus musculus (house mouse)]

Gene ID: 27361, updated on 3-Feb-2019

Summary

Official Symbol Msrb1 provided by [MGI](#)

Official Full Name methionine sulfoxide reductase B1 provided by [MGI](#)

Primary source [MGI:MGI:1351642](#)

See related [Ensembl:ENSMUSG00000075705](#)

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 D17Wsu82e, SELX, SelR, Sepr, Sepx1

Summary The protein encoded by this gene belongs to the methionine-R-sulfoxide reductase B (MsrB) family. Members of this family function as repair enzymes that protect proteins from oxidative stress by catalyzing the reduction of methionine-R-sulfoxides to methionines. This protein is highly expressed in liver and kidney, and is localized to the nucleus and cytosol. It is the only member of the MsrB family that is a selenoprotein, containing a selenocysteine (Sec) residue at its active site. It also has the highest methionine-R-sulfoxide reductase activity compared to other members containing cysteine in place of Sec. Sec is encoded by the UGA codon, which normally signals translation termination. The 3' UTRs of selenoprotein mRNAs contain a conserved stem-loop structure, designated the Sec insertion sequence (SECIS) element, that is necessary for the recognition of UGA as a Sec codon, rather than as a stop signal. Alternatively spliced transcript variants have been described for this gene. [provided by RefSeq, Oct 2016]

Expression Ubiquitous expression in liver adult (RPKM 166.6), bladder adult (RPKM 66.9) and 25 other tissues [See more](#)

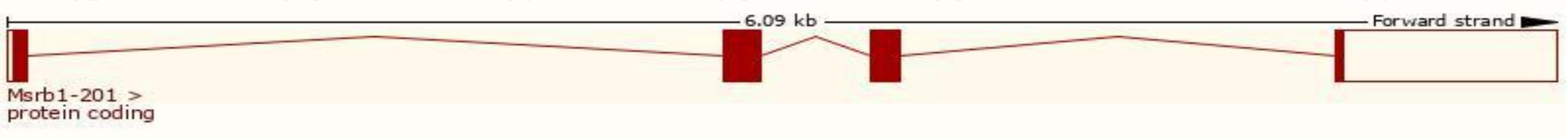
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

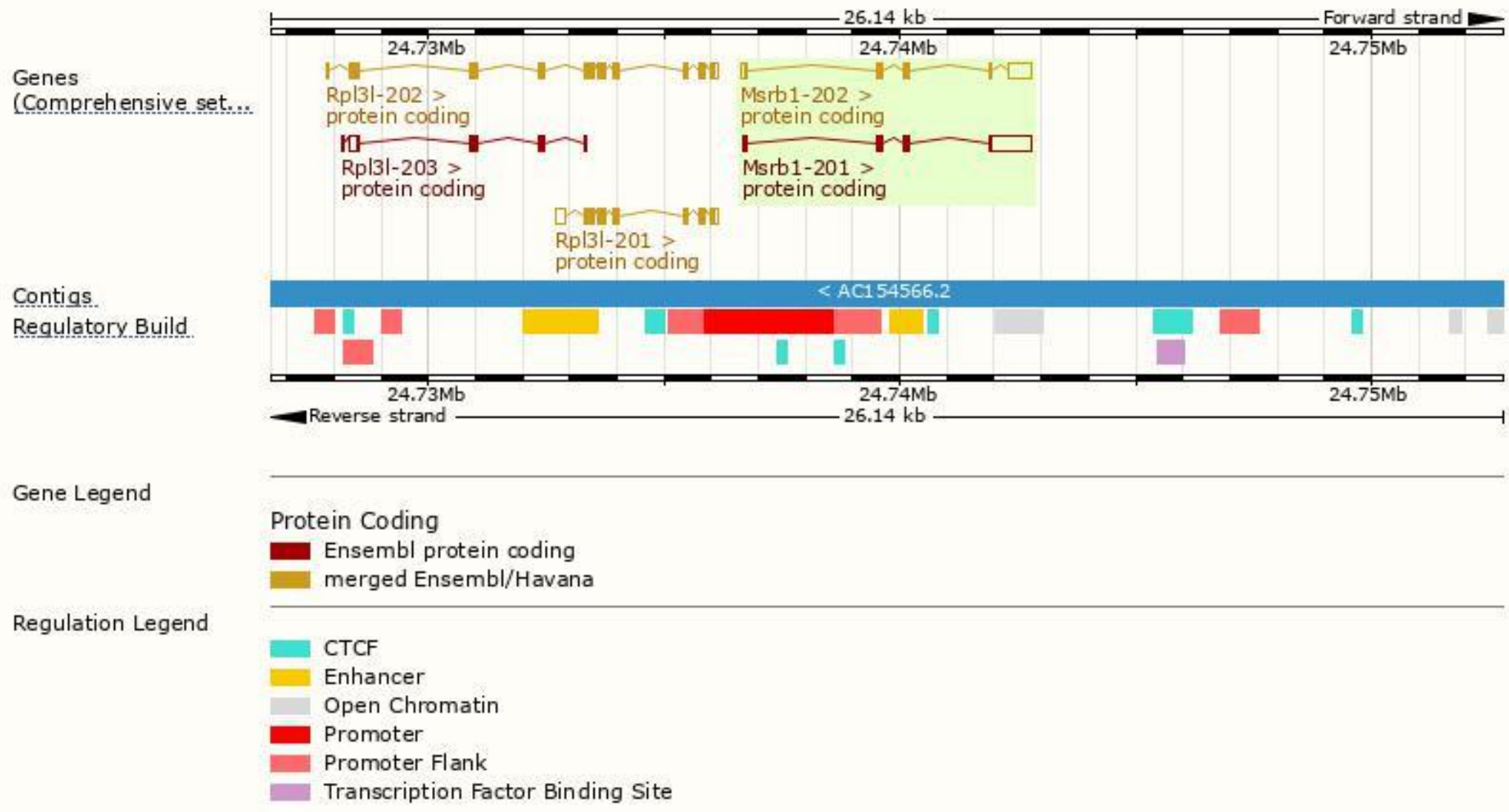
The gene has 2 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|--------------------------------------|------|-----------------------|----------------|---------------------------|------------------------|-------------------------------|
| Msrb1-201 | ENSMUST00000101800.5 | 1211 | 116aa | Protein coding | CCDS28495 | Q9JLC3 | TSL:1 GENCODE basic APPRIS P1 |
| Msrb1-202 | ENSMUST00000115262.7 | 886 | 116aa | Protein coding | CCDS28495 | Q9JLC3 | TSL:1 GENCODE basic APPRIS P1 |

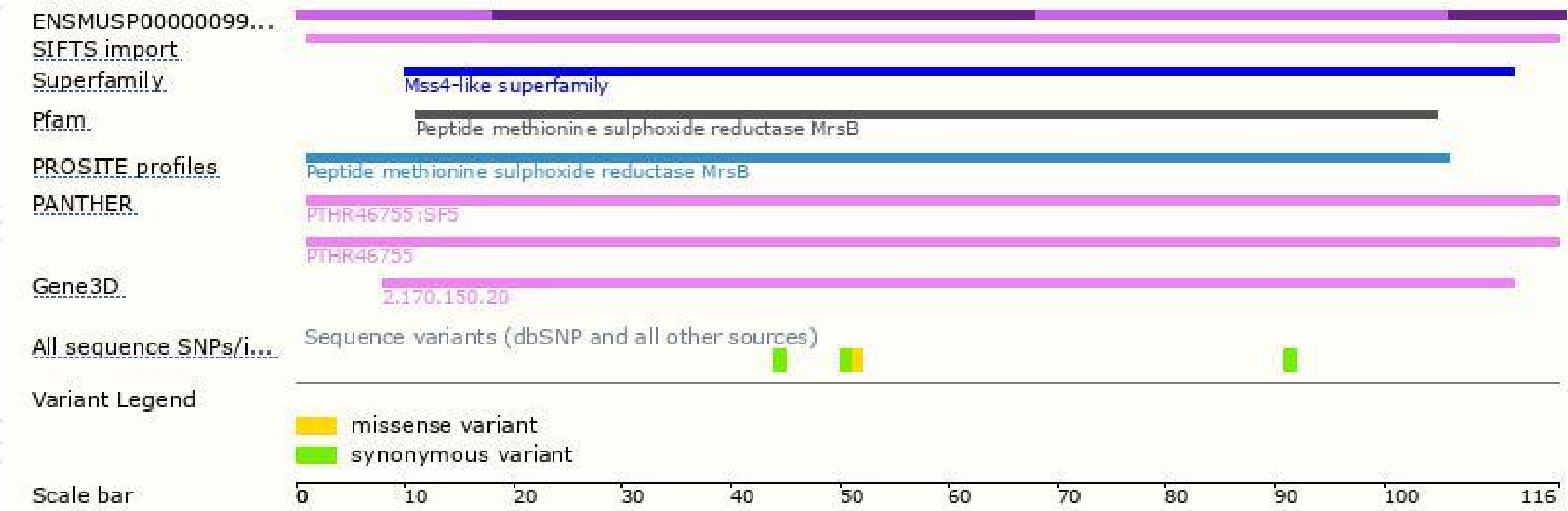
The strategy is based on the design of *Msrb1-201* transcript,The transcription is shown below



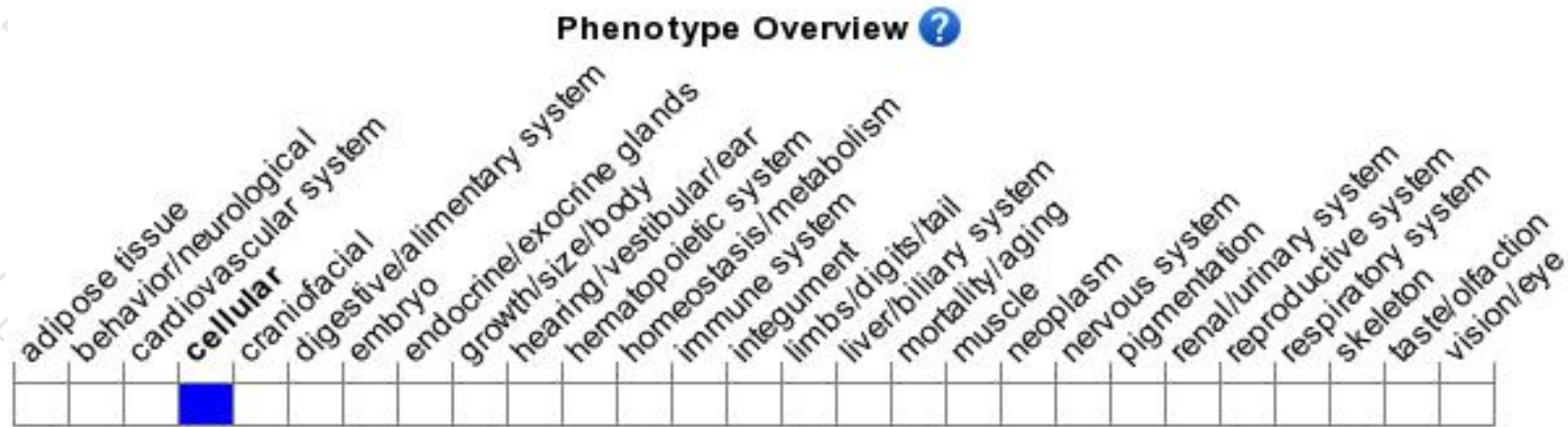
Genomic location distribution



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, Mice homozygous for a gene trap allele exhibit oxidative stress.

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

Tel: 400-9660890

