

Msi2 Cas9-KO Strategy

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Project Overview

Project Name

Msi2

Project type

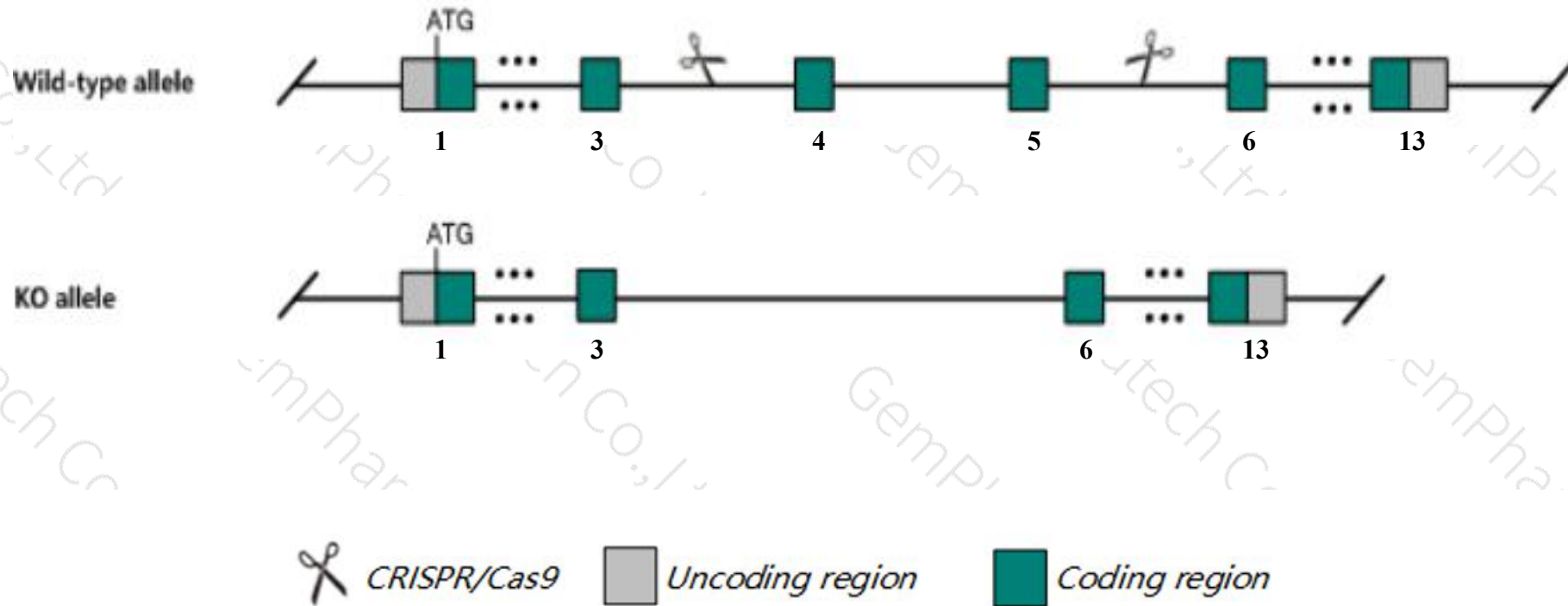
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Msi2* gene. The schematic diagram is as follows:



- The *Msi2* gene has 7 transcripts. According to the structure of *Msi2* gene, exon4-exon5 of *Msi2-201* (ENSMUST00000092794.11) transcript is recommended as the knockout region. The region contains 127bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Msi2* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, mice homozygous for a gene trapped allele exhibit lethality, decreased body size, and decreased hematopoietic stem cells. mice homozygous for a conditional knock-out allele exhibit impaired hematopoietic stem cell physiology upon induction.
- The *Msi2* gene is located on the Chr11. 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)

Msi2 musashi RNA-binding protein 2 [Mus musculus (house mouse)]

Gene ID: 76626, updated on 13-Mar-2020

Summary



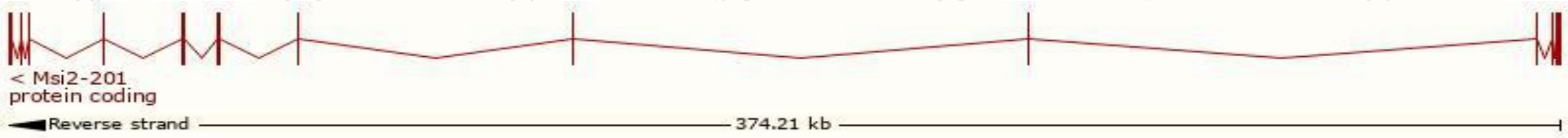
Official Symbol	Msi2 provided by MGI
Official Full Name	musashi RNA-binding protein 2 provided by MGI
Primary source	MGI:MGI:1923876
See related	Ensembl:ENSMUSG00000069769
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1700105C15Rik, AI451722, AI563628, AW489193, Msi2h
Expression	Ubiquitous expression in CNS E11.5 (RPKM 15.7), whole brain E14.5 (RPKM 15.6) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

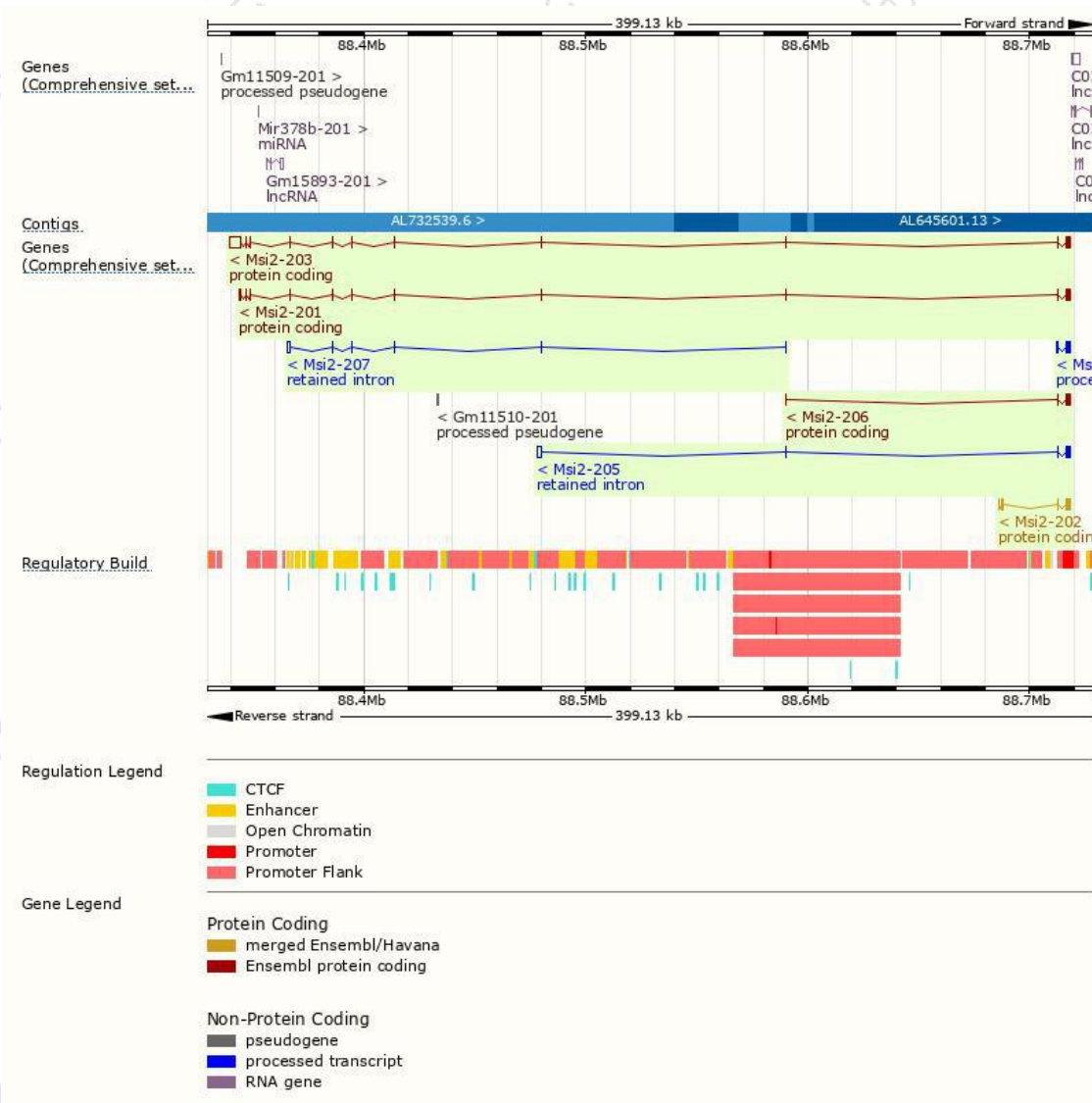
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Msi2-201	ENSMUST00000092794.11	1855	346aa	Protein coding	CCDS56796	Q3TE41 Q920Q6	TSL:1 GENCODE basic APPRIS P2
Msi2-202	ENSMUST00000107908.1	695	158aa	Protein coding	CCDS48882	B1AT13	TSL:5 GENCODE basic
Msi2-203	ENSMUST00000107909.7	6436	328aa	Protein coding	-	Q2M2Q8 Q920Q6	TSL:1 GENCODE basic APPRIS ALT2
Msi2-206	ENSMUST00000144699.7	405	113aa	Protein coding	-	B1AT10	CDS 3' incomplete TSL:3
Msi2-204	ENSMUST00000126293.1	684	No protein	Processed transcript	-	-	TSL:1
Msi2-205	ENSMUST00000138790.7	2516	No protein	Retained intron	-	-	TSL:1
Msi2-207	ENSMUST00000148013.7	1748	No protein	Retained intron	-	-	TSL:3

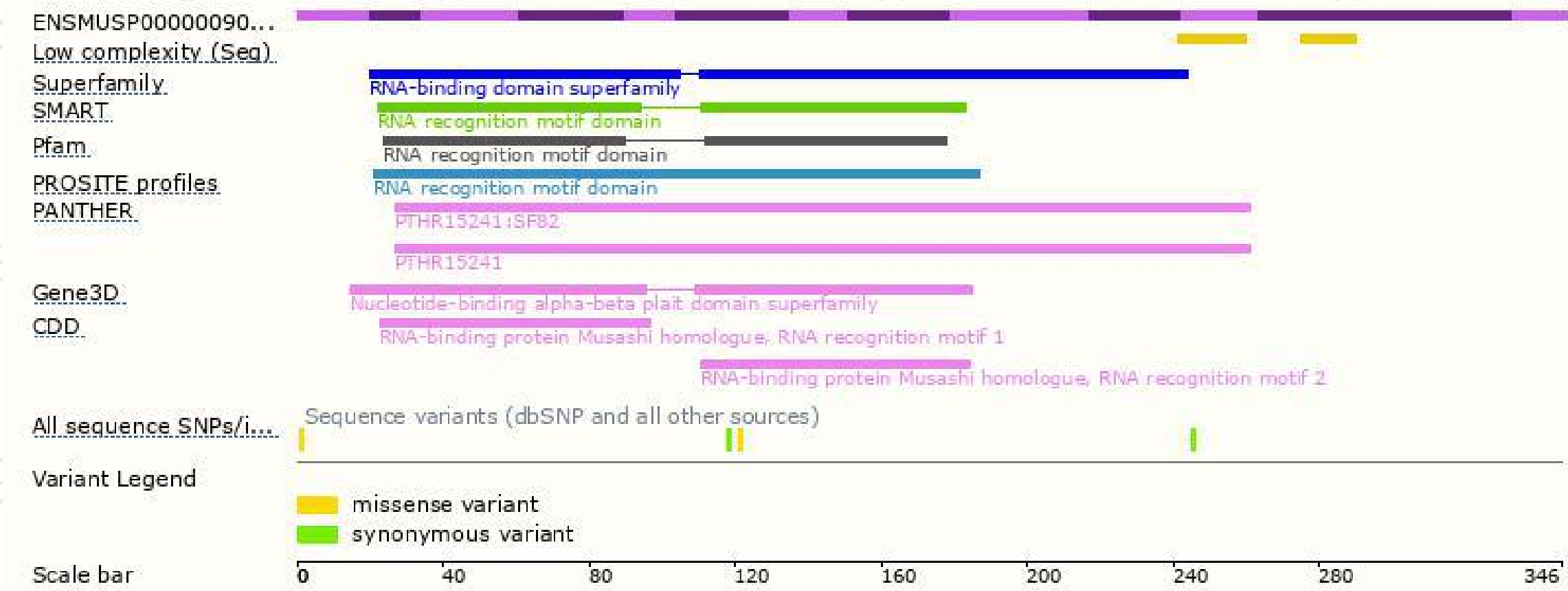
The strategy is based on the design of *Msi2-201* transcript,the transcription is shown below:



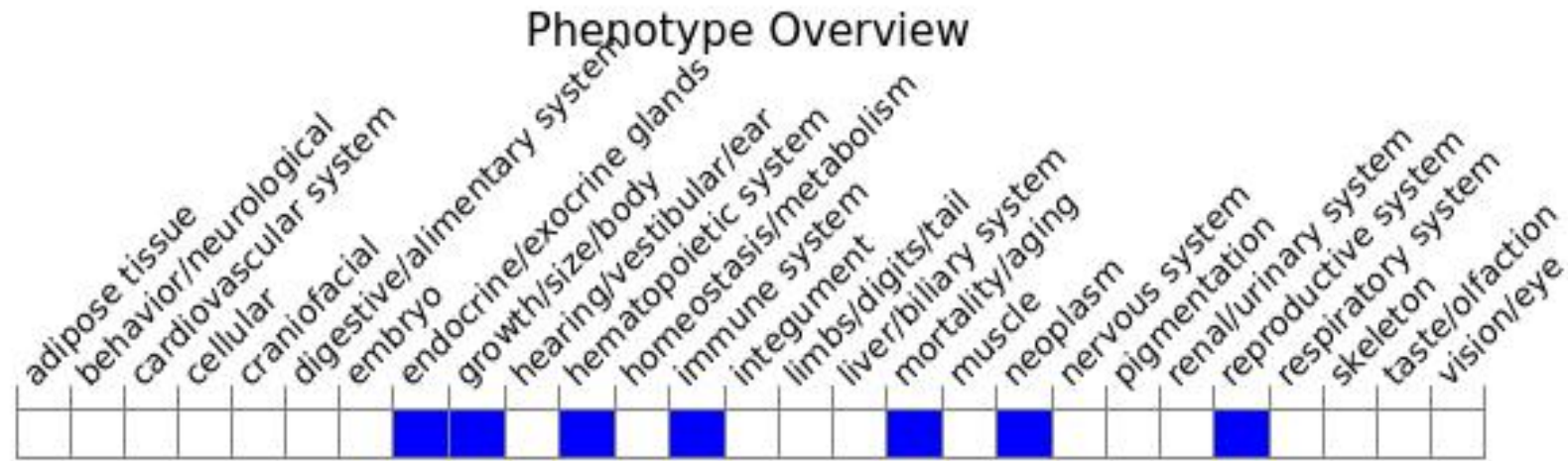
Genomic location distribution



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 trapped allele exhibit lethality, decreased body size, and decreased hematopoietic stem cells. Mice homozygous for a conditional knock-out allele exhibit impaired hematopoietic stem cell physiology upon induction.

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

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