

Mcrs1 Cas9-CKO Strategy

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Project Overview

Project Name

Mcrl

Project type

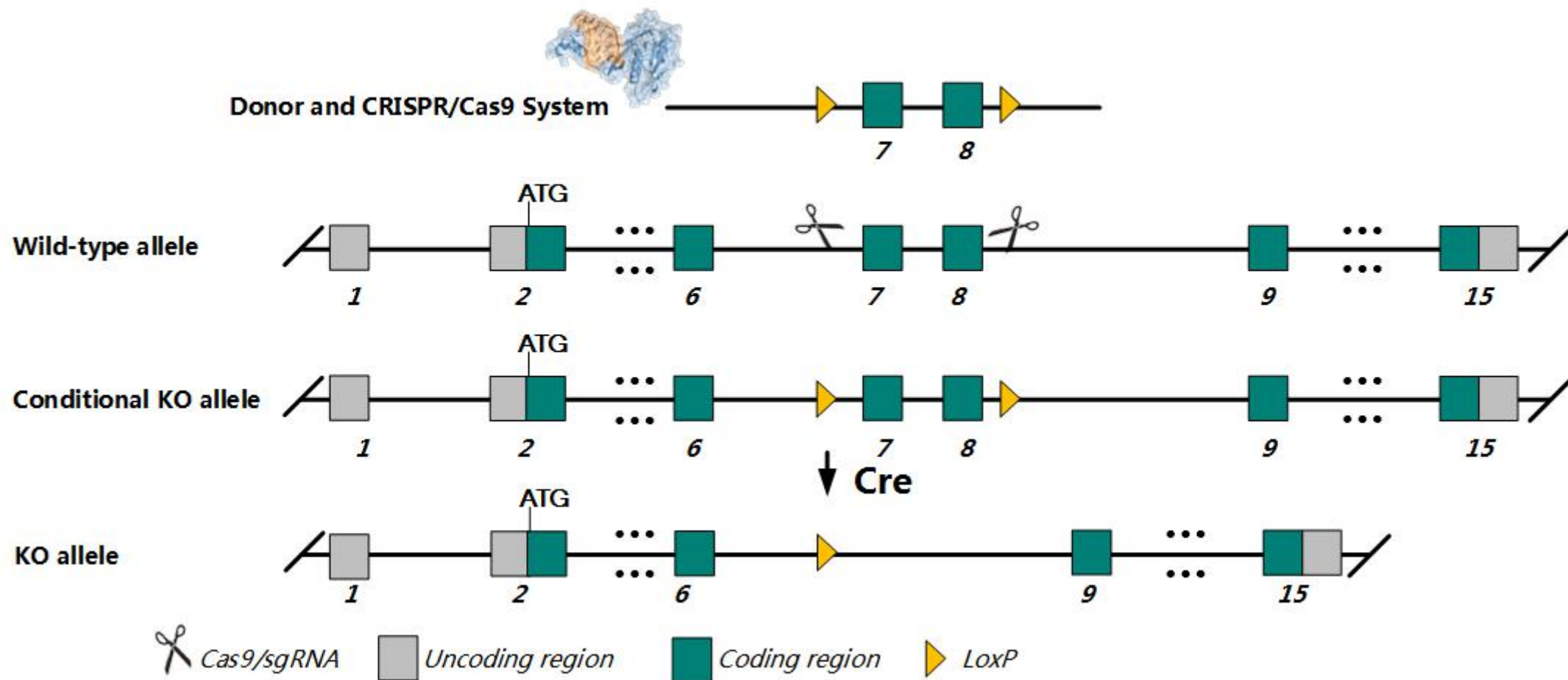
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mcrs1* gene. The schematic diagram is as follows:



- The *Mcrs1* gene has 10 transcripts. According to the structure of *Mcrs1* gene, exon7-exon8 of *Mcrs1*-201 (ENSMUST00000041190.16) transcript is recommended as the knockout region. The region contains 248bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mcrs1* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit early embryonic lethality.
- The *Mcrs1* gene is located on the Chr15. 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.
- Transcript *Mcrs1*-206&210 may not be affected. And the influence of *Mcrs1*-204&207&208 is unknown.
- The N-terminal of *Mcrs1* gene will remain 186aa, it may remain the partial function of *Mcrs1* gene.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)



Mcrs1 microsphere protein 1 [*Mus musculus* (house mouse)]

Gene ID: 51812, updated on 31-Jan-2019

Summary

- Official Symbol

Mcrs1 provided by MGI
- Official Full Name

microsphere protein 1 provided by MGI
- Primary source

[MGI:MGI:1858420](#)
- See related

[Ensembl:ENSMUSG00000037570](#)
- 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

P78; MSP58; C78274; ICP22BP
- Expression

Ubiquitous expression in whole brain E14.5 (RPKM 38.4), testis adult (RPKM 37.4) and 28 other tissues [See more](#)
- Orthologs

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

Genomic context

Location:

15; 15 F1

See Mcrs1 in [Genome Data Viewer](#)

Exon count:

15

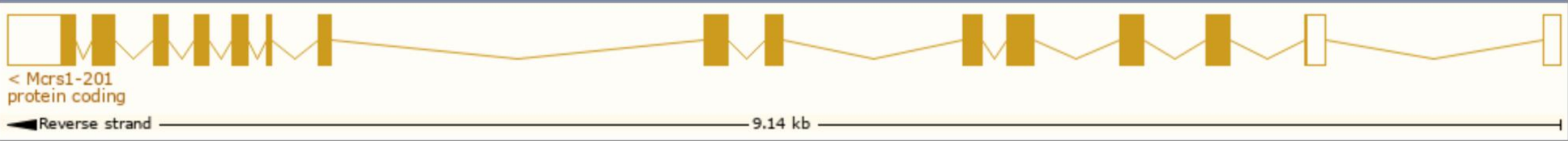
Annotation release	Status	Assembly	Chr	Location
106	current	GRCm38.p4 (GCF_000001635.24)	15	NC_000081.6 (99242817..99251961, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	15	NC_000081.5 (99073248..99082392, complement)

Transcript information (Ensembl)

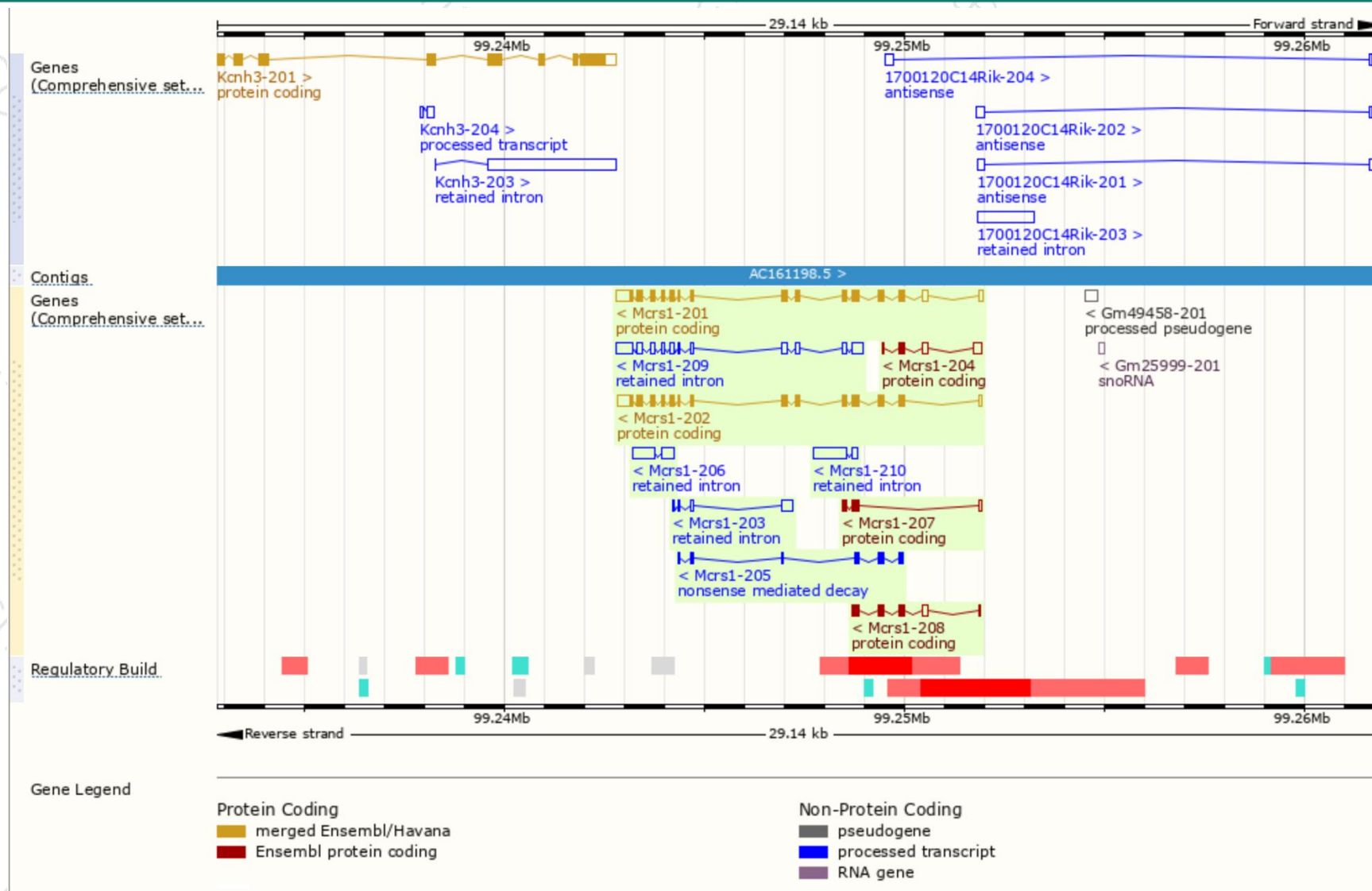
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mcrs1-201	ENSMUST00000041190.16	1916	462aa	Protein coding	CCDS37199	Q99L90	TSL:1 GENCODE basic APPRIS P1
Mcrs1-202	ENSMUST00000163506.2	1771	449aa	Protein coding	CCDS49728	Q3TJY1	TSL:1 GENCODE basic
Mcrs1-208	ENSMUST00000229926.1	598	133aa	Protein coding	-	A0A2R8VH87	CDS 3' incomplete
Mcrs1-204	ENSMUST00000229359.1	551	69aa	Protein coding	-	A0A2R8VHY5	CDS 3' incomplete
Mcrs1-207	ENSMUST00000229671.1	354	88aa	Protein coding	-	A0A2R8VJX8	CDS 3' incomplete
Mcrs1-205	ENSMUST00000229399.1	485	135aa	Nonsense mediated decay	-	A0A2R8VHY8	CDS 5' incomplete
Mcrs1-209	ENSMUST00000230444.1	1521	No protein	Retained intron	-	-	-
Mcrs1-210	ENSMUST00000231020.1	960	No protein	Retained intron	-	-	-
Mcrs1-206	ENSMUST00000229656.1	885	No protein	Retained intron	-	-	-
Mcrs1-203	ENSMUST00000229143.1	407	No protein	Retained intron	-	-	-

The strategy is based on the design of *Mcrs1-201* transcript,The transcription is shown below



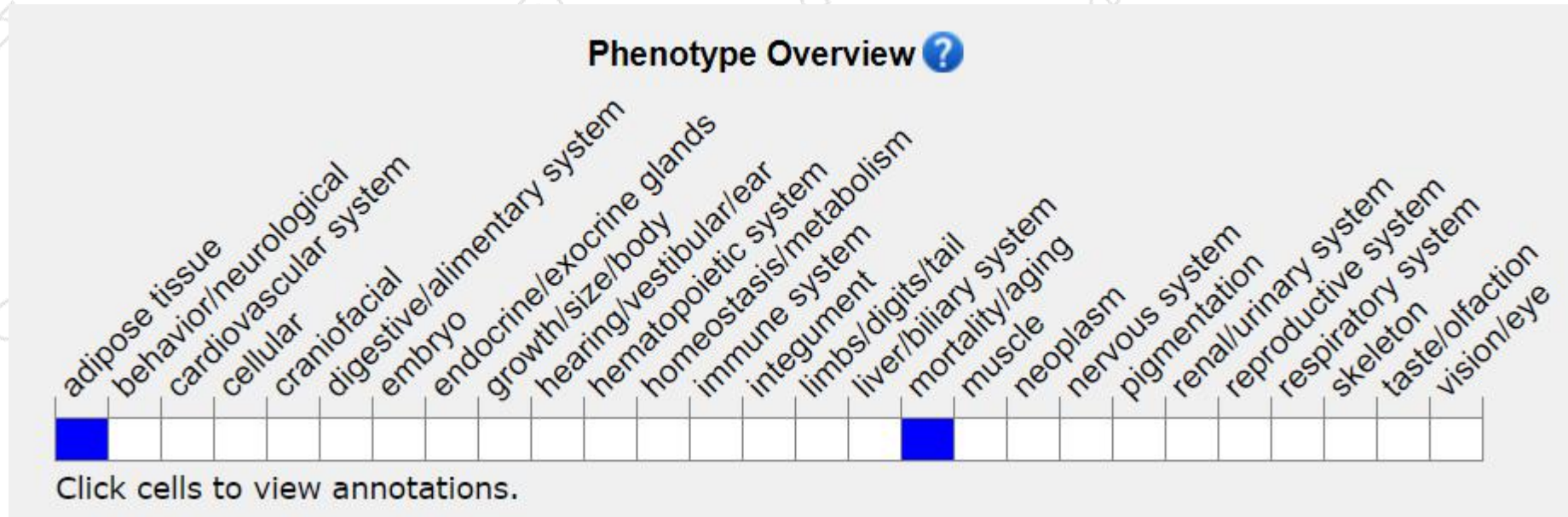
Genomic location distribution



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/>).

Mice homozygous for a knock-out allele exhibit early embryonic lethality.

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

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