

# Mc1r Cas9-KO Strategy

Designer: Lingyan Wu

Reviewer: Rui Xiong

Design Date: 2023-12-26

# Overview

## Target Gene Name

- Mc1r

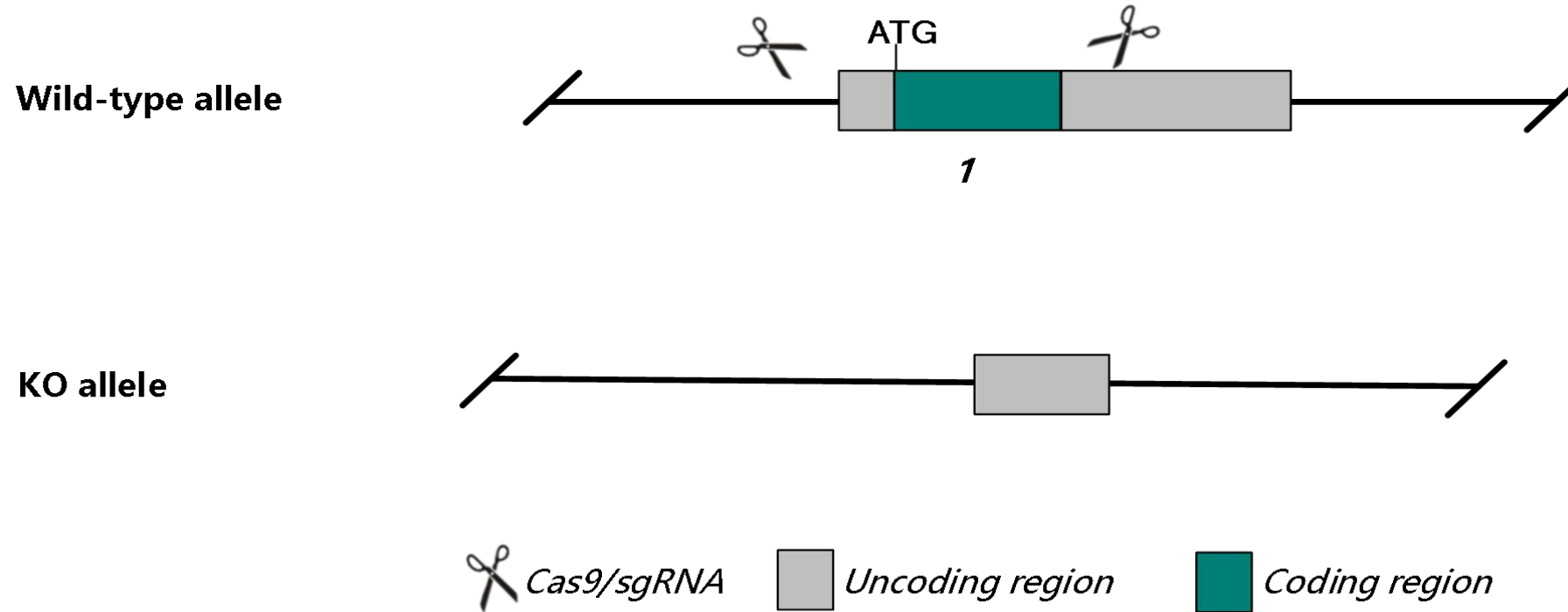
## Project Type

- Cas9-KO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Mclr* gene.

# Technical Information

- The *Mclr* gene has 1 transcript. According to the structure of *Mclr* gene, exon1 of *Mclr*-201 (ENSMUST00000098324.4) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Mclr* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

# Gene Information

**Mc1r melanocortin 1 receptor [ *Mus musculus* (house mouse) ]**

[Download Datasets](#)

Gene ID: 17199, updated on 23-Nov-2023

## Summary

<b>Official Symbol</b>	Mc1r provided by <a href="#">MGI</a>
<b>Official Full Name</b>	melanocortin 1 receptor provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:99456</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000074037</a> <a href="#">AllianceGenome:MGI:99456</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	e; Tob; Mcr1; Mshra
<b>Summary</b>	Enables melanocyte-stimulating hormone receptor activity. Involved in intracellular signal transduction; positive regulation of intracellular signal transduction; and positive regulation of transcription by RNA polymerase II. Acts upstream of or within melanin biosynthetic process; pigmentation; and sensory perception of pain. Predicted to be located in membrane. Predicted to be integral component of membrane. Predicted to be active in cytoplasm and plasma membrane. Is expressed in ductus deferens; epididymis; esophagus; and skin. Human ortholog(s) of this gene implicated in familial melanoma; major depressive disorder; melanoma; oculocutaneous albinism type II; and pigmentation disease. Orthologous to human MC1R (melanocortin 1 receptor). [provided by Alliance of Genome Resources, Apr 2022]
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>
<b>NEW</b>	Try the new <a href="#">Gene table</a> Try the new <a href="#">Transcript table</a>

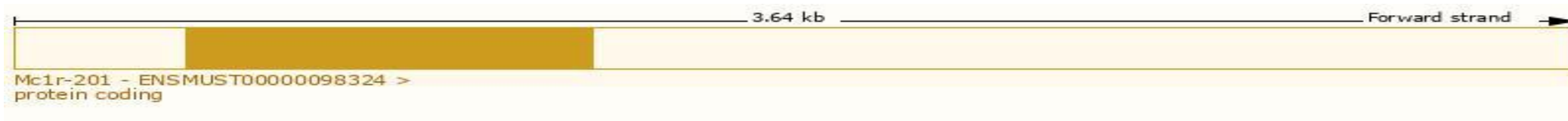
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

The gene has 1 transcript, and the transcript is shown below:

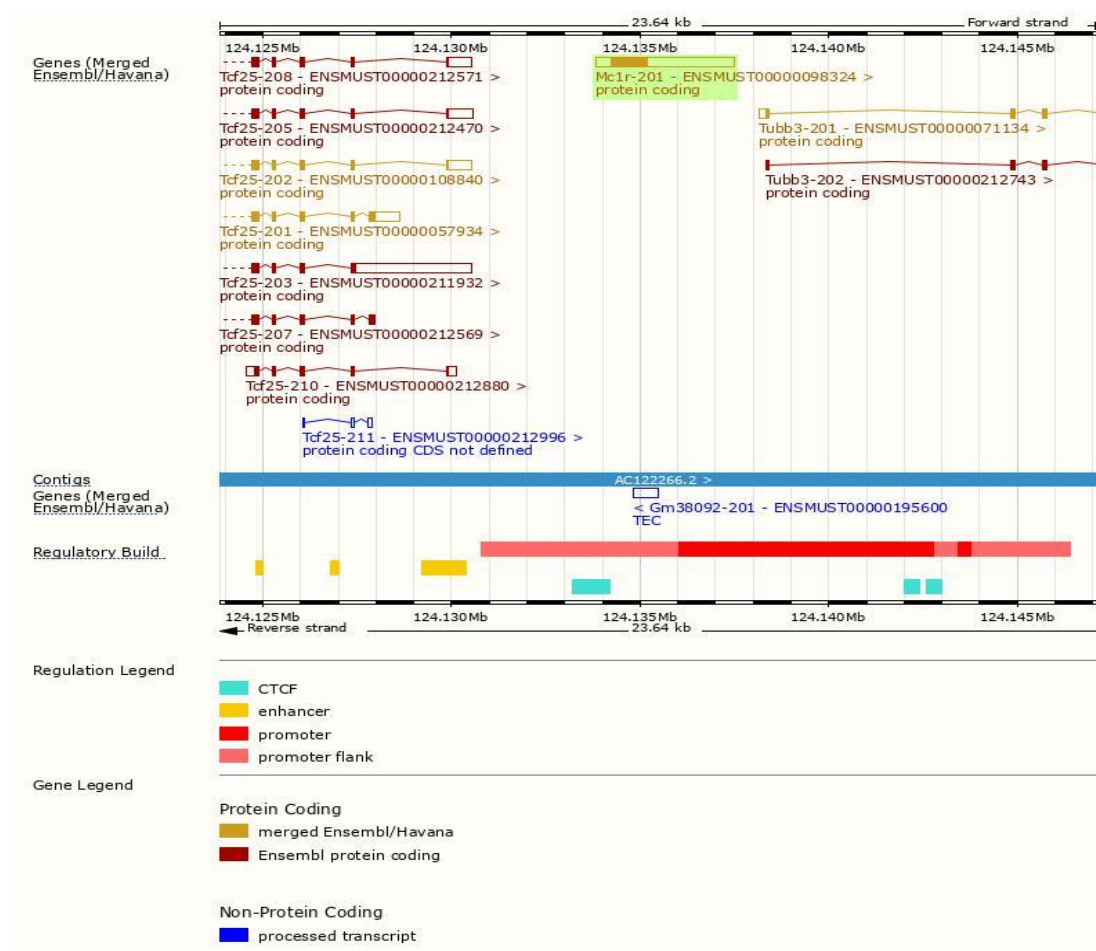
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
<a href="#">ENSMUST00000098324.4</a>	Mc1r-201	3638	<a href="#">315aa</a>	Protein coding	<a href="#">CCDS22756</a>	<a href="#">A0A0B6VTJ4</a> <a href="#">Q01727</a>	Ensembl Canonical Gencode basic APPRIS P1 TSL:NA

The strategy is based on the design of *Mc1r*-201 transcript, the transcription is shown below:



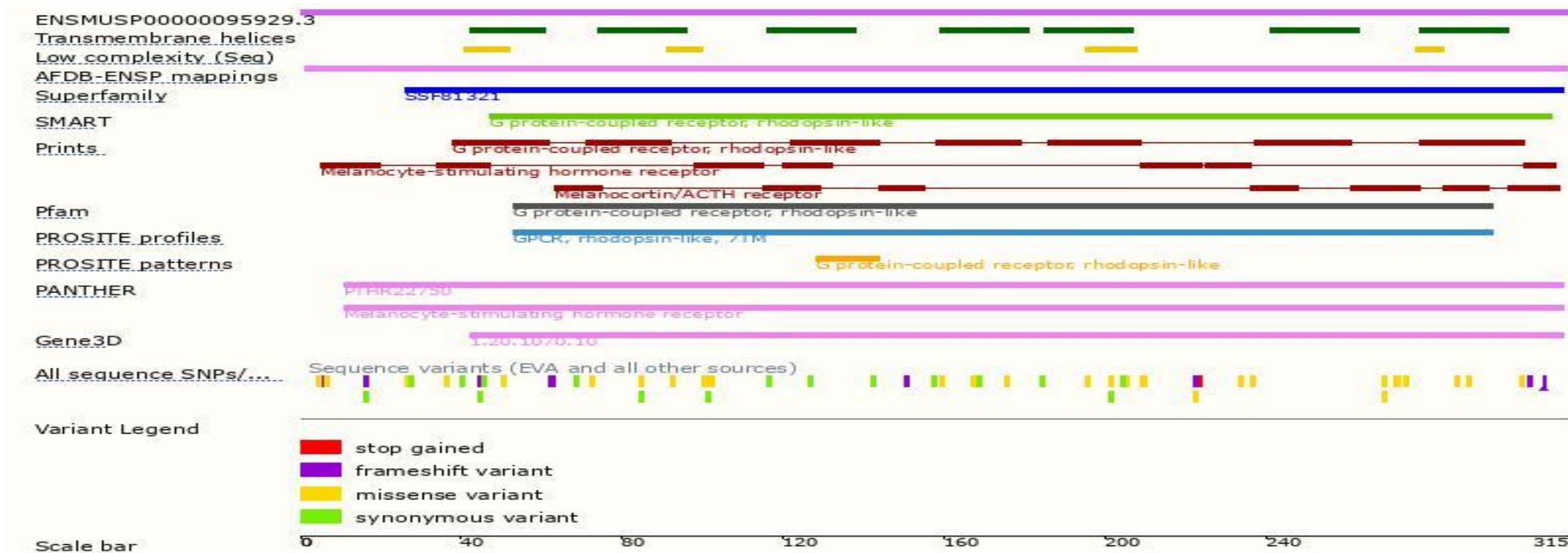
Source: <https://www.ensembl.org>

# Genomic Information



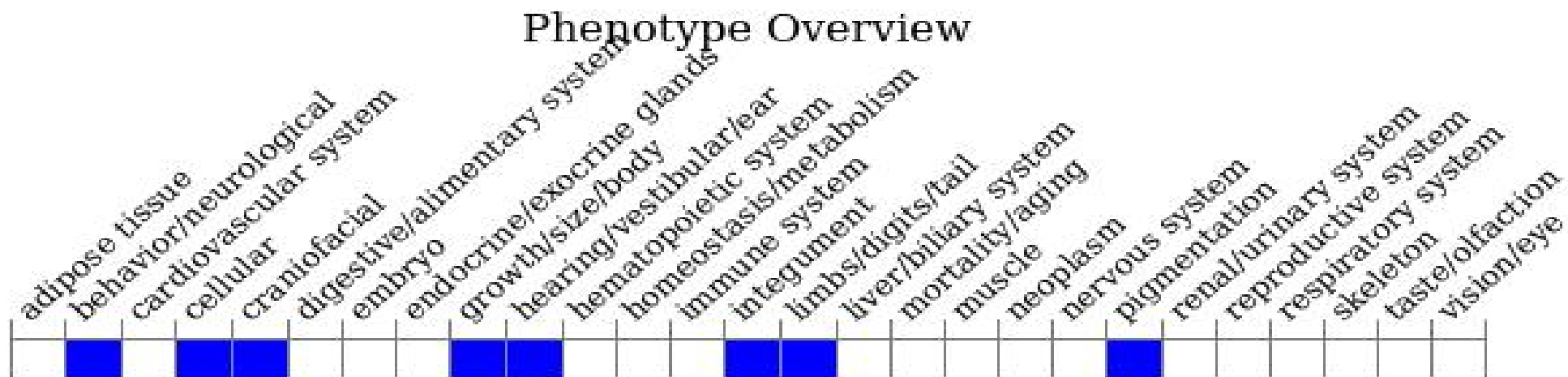


# Protein Information





# Mouse Phenotype Information (MGI)



- Mutant alleles at this locus extend or restrict the amount of black pigment (eumelanin) in hair with the opposite effect on yellow pigment (phaeomelanin). Some variants affect pain sensitivity.

# Important Information

- According to MGI information, mutant alleles at this locus extend or restrict the amount of black pigment (eumelanin) in hair with the opposite effect on yellow pigment (phaeomelanin). Some variants affect pain sensitivity.
- The KO region is about ~2.5kb away from the N-terminal of *Tubb3* gene, this strategy may influence the regulatory function of the N-terminal of *Tubb3* gene.
- *Gm38092* gene may be deleted.
- *Mc1r* is located on Chr8. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.