

# Hrasls Cas9-KO Strategy

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# **Project Overview**



**Project Name** 

Hrasls

**Project type** 

Cas9-KO

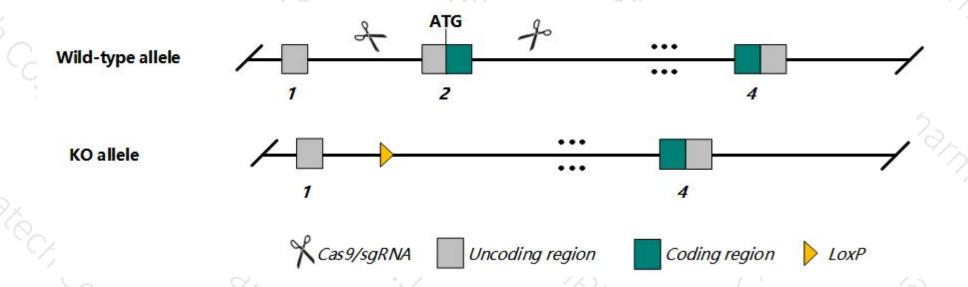
Strain background

C57BL/6JGpt

# **Knockout strategy**



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



### **Technical routes**



- ➤ The *Hrasls* gene has 4 transcripts. According to the structure of *Hrasls* gene, exon2 of *Hrasls-201* (ENSMUST00000089824.10) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Hrasls* gene. The brief process is as follows: CRISPR/Cas9 system

### **Notice**



- > The *Hrasls* gene is located on the Chr16. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

## Gene information (NCBI)



#### HrasIs HRAS-like suppressor [Mus musculus (house mouse)]

Gene ID: 27281, updated on 31-Jan-2019

#### Summary

☆ ?

Official Symbol Hrasls provided by MGI

Official Full Name HRAS-like suppressor provided by MGI

Primary source MGI:MGI:1351473

See related Ensembl: ENSMUSG00000022525

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 2810012B06Rik, A-C1, HRSL1, Hrasrs

Expression Biased expression in testis adult (RPKM 44.5), heart adult (RPKM 3.7) and 2 other tissuesSee more

Orthologs <u>human</u> all

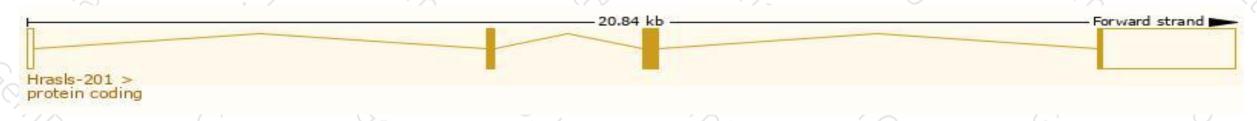
# Transcript information (Ensembl)



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

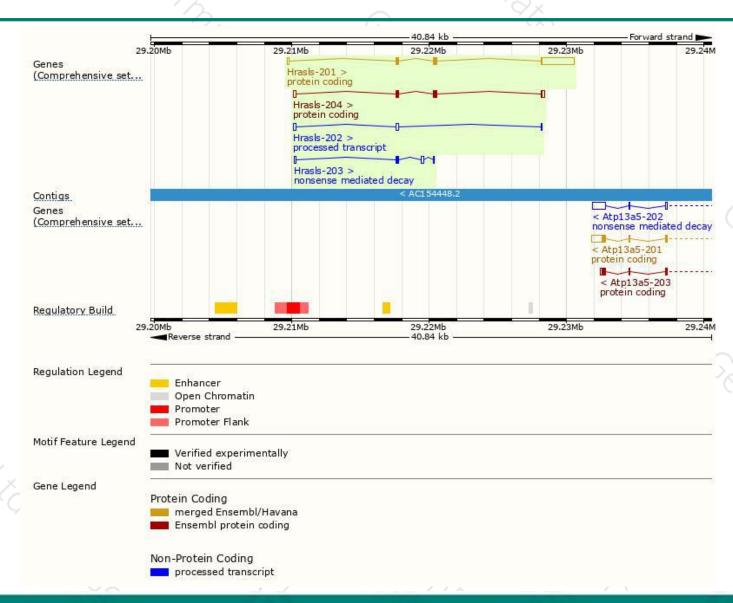
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000089824.10	2916	<u>167aa</u>	Protein coding	CCDS28094	A0A0R4J130	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000162747.7	854	<u>167aa</u>	Protein coding	CCDS28094	A0A0R4J130	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000161294.1	478	<u>50aa</u>	Nonsense mediated decay	ū	E0CYE9	TSL:3
ENSMUST00000160794.1	412	No protein	Processed transcript	2	100	TSL:2
	ENSMUST00000089824.10 ENSMUST00000162747.7 ENSMUST00000161294.1	ENSMUST00000089824.10 2916 ENSMUST00000162747.7 854 ENSMUST00000161294.1 478	ENSMUST000000162747.7 854 167aa ENSMUST00000161294.1 478 50aa	ENSMUST00000089824.10         2916         167aa         Protein coding           ENSMUST00000162747.7         854         167aa         Protein coding           ENSMUST00000161294.1         478         50aa         Nonsense mediated decay	ENSMUST00000089824.10         2916         167aa         Protein coding         CCDS28094           ENSMUST00000162747.7         854         167aa         Protein coding         CCDS28094           ENSMUST00000161294.1         478         50aa         Nonsense mediated decay         -	ENSMUST00000089824.10         2916         167aa         Protein coding         CCDS28094         A0A0R4J130           ENSMUST00000162747.7         854         167aa         Protein coding         CCDS28094         A0A0R4J130           ENSMUST00000161294.1         478         50aa         Nonsense mediated decay         -         E0CYE9

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



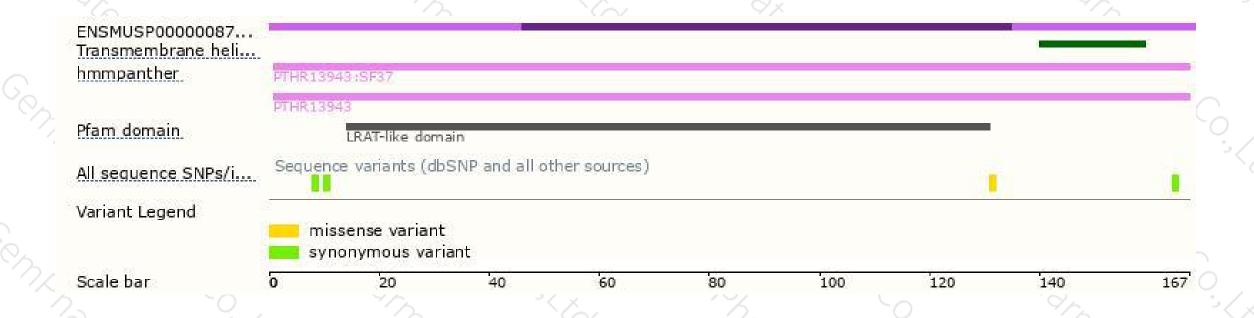
### Genomic location distribution





### Protein domain







If you have any questions, you are welcome to inquire. Tel: 400-9660890





