

Resf1-HA Cas9-CKO Strategy

Designer: Jia Yu

Reviewer: Yanhua Shen

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Project Overview

Project Name

Resf1-HA

Project type

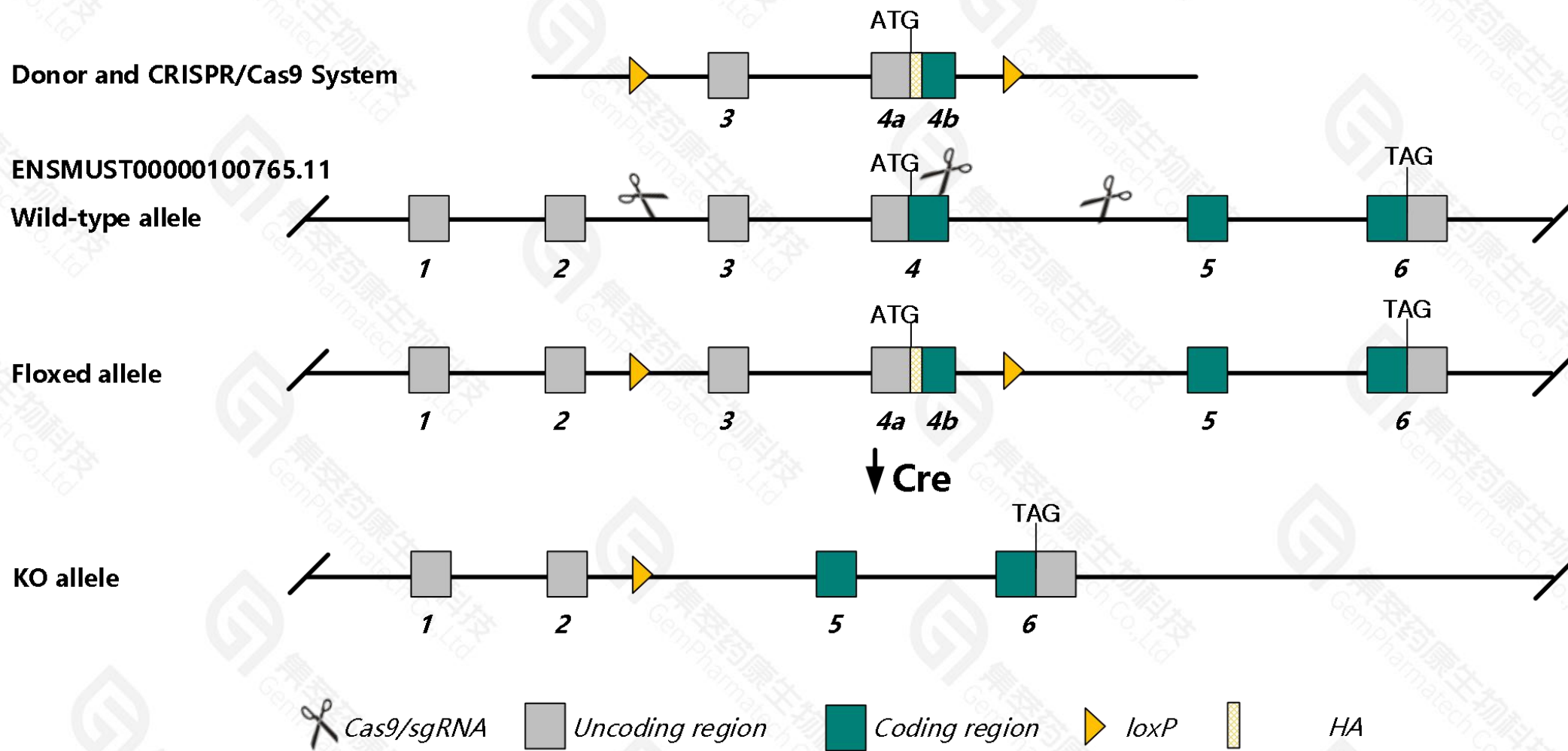
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Resf1* gene. The schematic diagram is as follows:



Technical routes

- The *Resf1* gene has 11 transcripts. According to the structure of *Resf1* gene, exon3-exon4 of *Resf1*-202(ENSMUST00000100765.11) transcript is recommended as the knockout region. The region contains 4327bp coding sequence. While, HA tag will be inserted after ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Resf1* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor was constructed. Cas9, sgRNA 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 was 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.

- The *Resf1* gene is located on the Chr6. 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 loxp and HA insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Resf1 retroelement silencing factor 1 [Mus musculus (house mouse)]

Gene ID: 67246, updated on 17-Dec-2020

Summary



Official Symbol Resf1 provided by [MGI](#)

Official Full Name retroelement silencing factor 1 provided by [MGI](#)

Primary source [MGI:MGI:1914496](#)

See related [Ensembl:ENSMUSG00000032712](#)

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 2810474O19Rik, 6720435I21Rik, AA536804, AU020969, GET

Expression Ubiquitous expression in bladder adult (RPKM 4.3), ovary adult (RPKM 3.6) and 28 other tissues [See more](#)

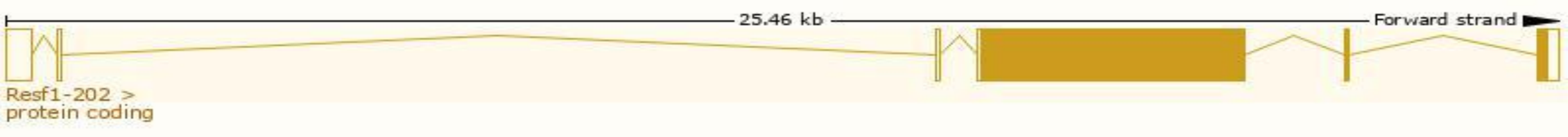
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

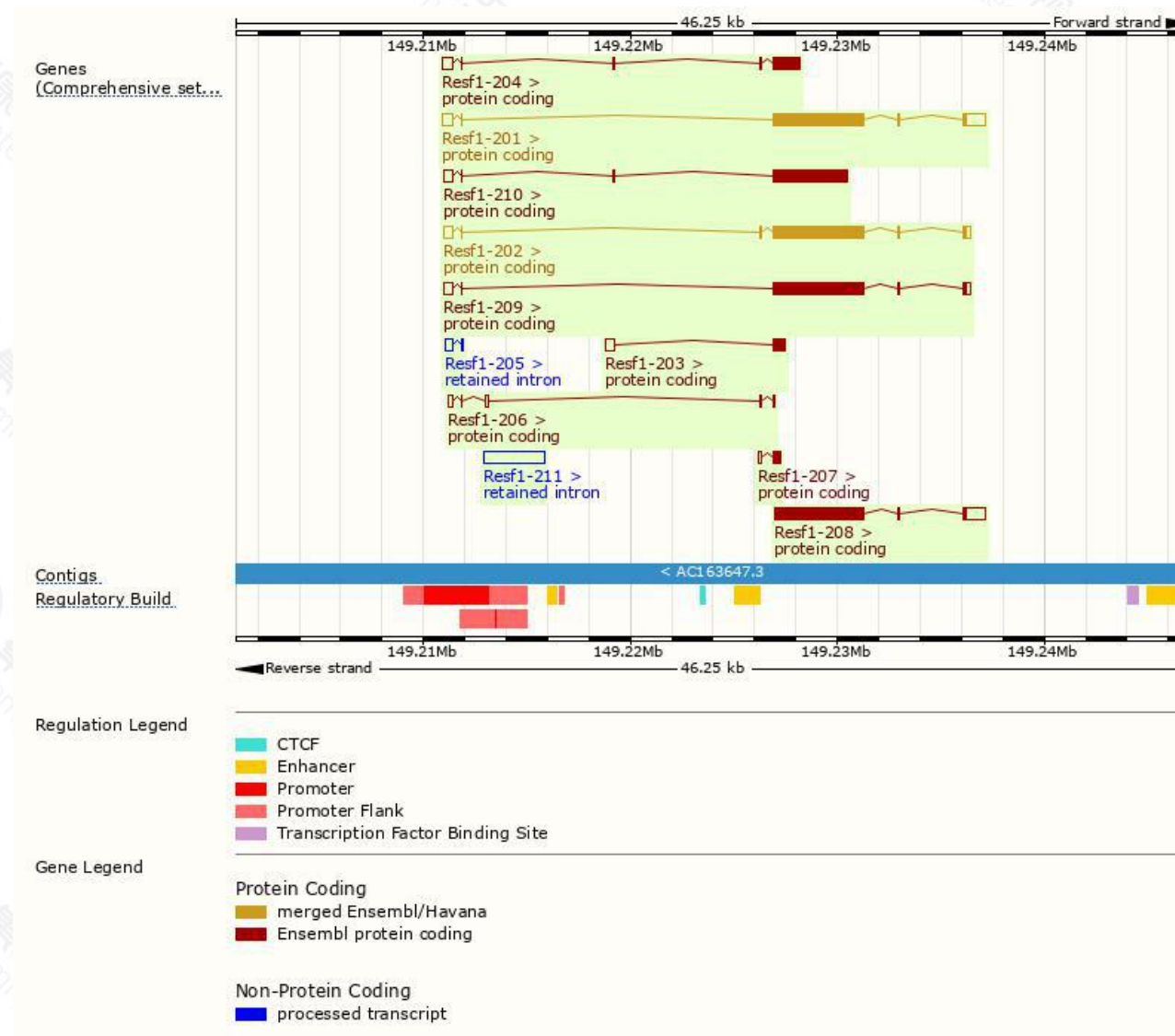
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Resf1-201	ENSMUST00000046689.13	6066	1521aa	Protein coding	CCDS20717		TSL:1 , GENCODE basic , APPRIS P2 ,
Resf1-202	ENSMUST00000100765.11	5356	1521aa	Protein coding	CCDS20717		TSL:1 , GENCODE basic , APPRIS P2 ,
Resf1-209	ENSMUST00000189932.7	5269	1521aa	Protein coding	CCDS20717		TSL:1 , GENCODE basic , APPRIS P2 ,
Resf1-208	ENSMUST00000189837.2	5469	1519aa	Protein coding	-		TSL:1 , GENCODE basic , APPRIS ALT2 ,
Resf1-210	ENSMUST00000190785.7	4152	1173aa	Protein coding	-		CDS 3' incomplete , TSL:1 ,
Resf1-204	ENSMUST00000130664.8	1957	404aa	Protein coding	-		CDS 3' incomplete , TSL:1 ,
Resf1-203	ENSMUST00000127680.2	938	170aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Resf1-207	ENSMUST00000187881.2	514	105aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Resf1-206	ENSMUST00000185930.2	511	10aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Resf1-211	ENSMUST00000203348.2	2951	No protein	Retained intron	-		TSL:NA ,
Resf1-205	ENSMUST00000137983.2	466	No protein	Retained intron	-		TSL:2 ,

The strategy is based on the design of *Resf1-202* transcript,the transcription is shown below:



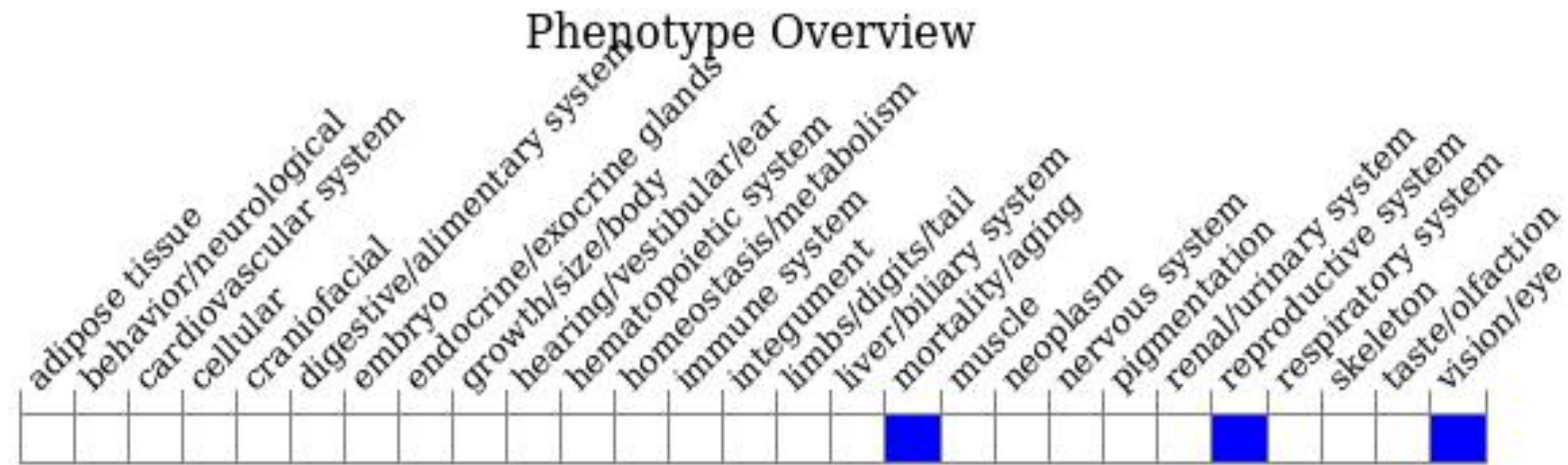
Genomic location distribution



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/>).

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

Tel: 025-5864 1534

