

Resf1 Cas9-KO Strategy

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Project Overview

Project Name

Resf1

Project type

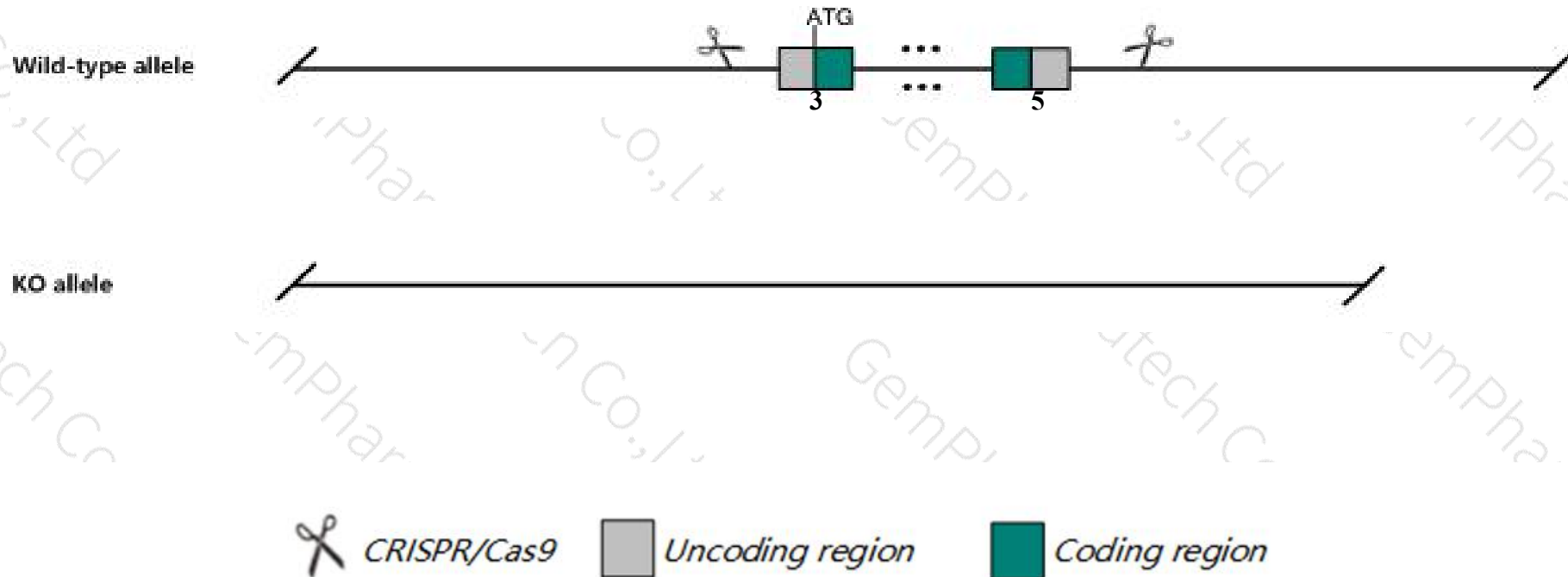
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Resf1* gene has 11 transcripts. According to the structure of *Resf1* gene, exon3-exon5 of *Resf1-201* (ENSMUST00000046689.12) transcript is recommended as the knockout region. The region contains all of the coding sequence. 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: CRISPR/Cas9 system

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

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

Gene ID: 67246, updated on 12-Aug-2019

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	GET; AA536804; AU020969; 2810474O19Rik; 6720435I21Rik
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)

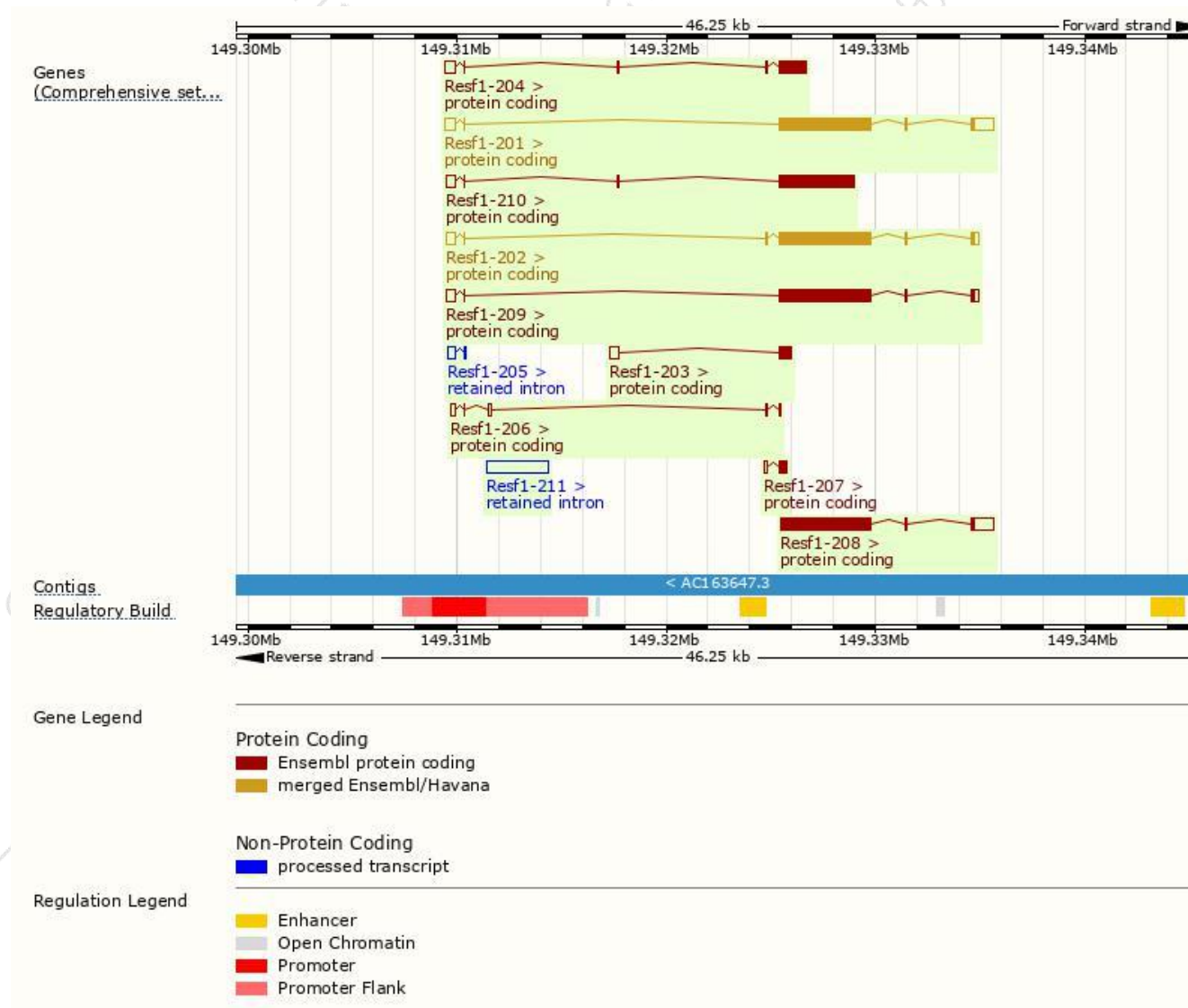
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Resf1-201	ENSMUST00000046689.12	6066	1521aa	Protein coding	CCDS20717	B2KFD2 Q5DTW7	TSL:1 GENCODE basic APPRIS P2
Resf1-202	ENSMUST00000100765.10	5356	1521aa	Protein coding	CCDS20717	B2KFD2 Q5DTW7	TSL:1 GENCODE basic APPRIS P2
Resf1-209	ENSMUST00000189932.6	5269	1521aa	Protein coding	CCDS20717	B2KFD2 Q5DTW7	TSL:1 GENCODE basic APPRIS P2
Resf1-208	ENSMUST00000189837.1	5469	1519aa	Protein coding	-	A0A087WP74	TSL:1 GENCODE basic APPRIS ALT2
Resf1-210	ENSMUST00000190785.6	4152	1173aa	Protein coding	-	A0A087WP47	CDS 3' incomplete TSL:1
Resf1-204	ENSMUST00000130664.7	1957	404aa	Protein coding	-	A0A140T8R9	CDS 3' incomplete TSL:1
Resf1-203	ENSMUST00000127680.1	938	170aa	Protein coding	-	B2KFD0	CDS 3' incomplete TSL:3
Resf1-207	ENSMUST00000187881.1	514	105aa	Protein coding	-	A0A087WR65	CDS 3' incomplete TSL:3
Resf1-206	ENSMUST00000185930.1	511	10aa	Protein coding	-	A0A140T8W0	CDS 3' incomplete TSL:3
Resf1-211	ENSMUST00000203348.1	2951	No protein	Retained intron	-	-	TSL:NA
Resf1-205	ENSMUST00000137983.1	466	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Resf1-201* transcript,The transcription is shown below



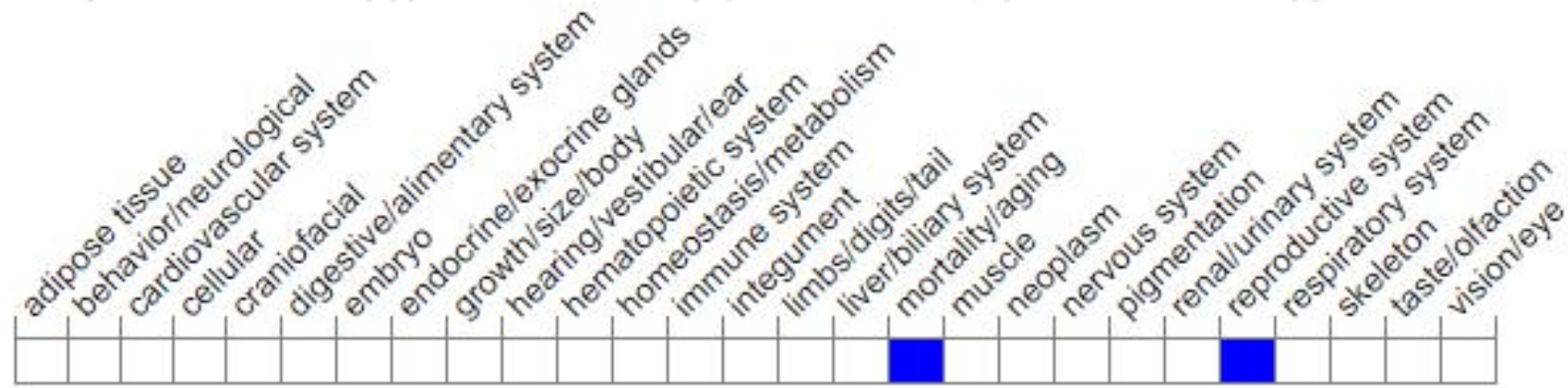
Genomic location distribution



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/>).

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

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