

# *Erfe* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Erfe*

**Project type**

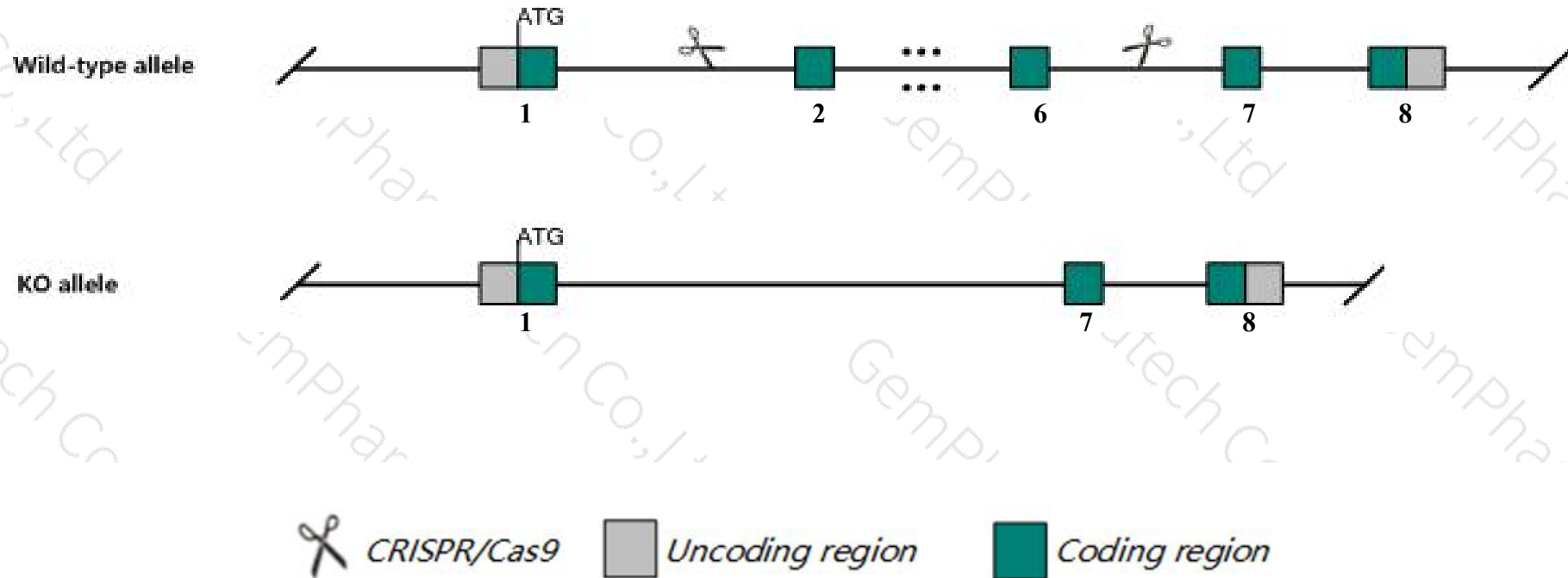
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Erfe* gene has 2 transcripts. According to the structure of *Erfe* gene, exon2-exon6 of *Erfe-201* (ENSMUST00000086861.11) transcript is recommended as the knockout region. The region contains 677bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Erfe* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygous mice exhibit a delay in recovery from blood loss.
- The effect on transcript *Erfe*-202 is unknown.
- The *Erfe* gene is located on the Chr1. 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)

## Erfe erythroferrone [ *Mus musculus* (house mouse) ]

(Gene ID: 227358, updated on 10-Oct-2019)

### Summary

- Official Symbol** Erfe provided by [MGI](#)
- Official Full Name** erythroferrone provided by [MGI](#)
- Primary source** [MGI:MGI:3606476](#)
- See related** [Ensembl:ENSMUSG00000047443](#)
- 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** Fam132b; myonectin; 4832406C22
- Expression** Biased expression in large intestine adult (RPKM 5.6), colon adult (RPKM 5.2) and 14 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

### Genomic context

Location: 1; 1 D

See Erfe in [Genome Data Viewer](#)

Exon count: 9

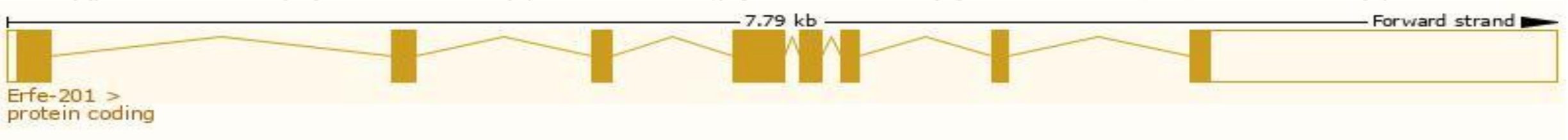
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	1	NC_000067.6 (91366305..91374217)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	1	NC_000067.5 (93263007..93270794)

# Transcript information (Ensembl)

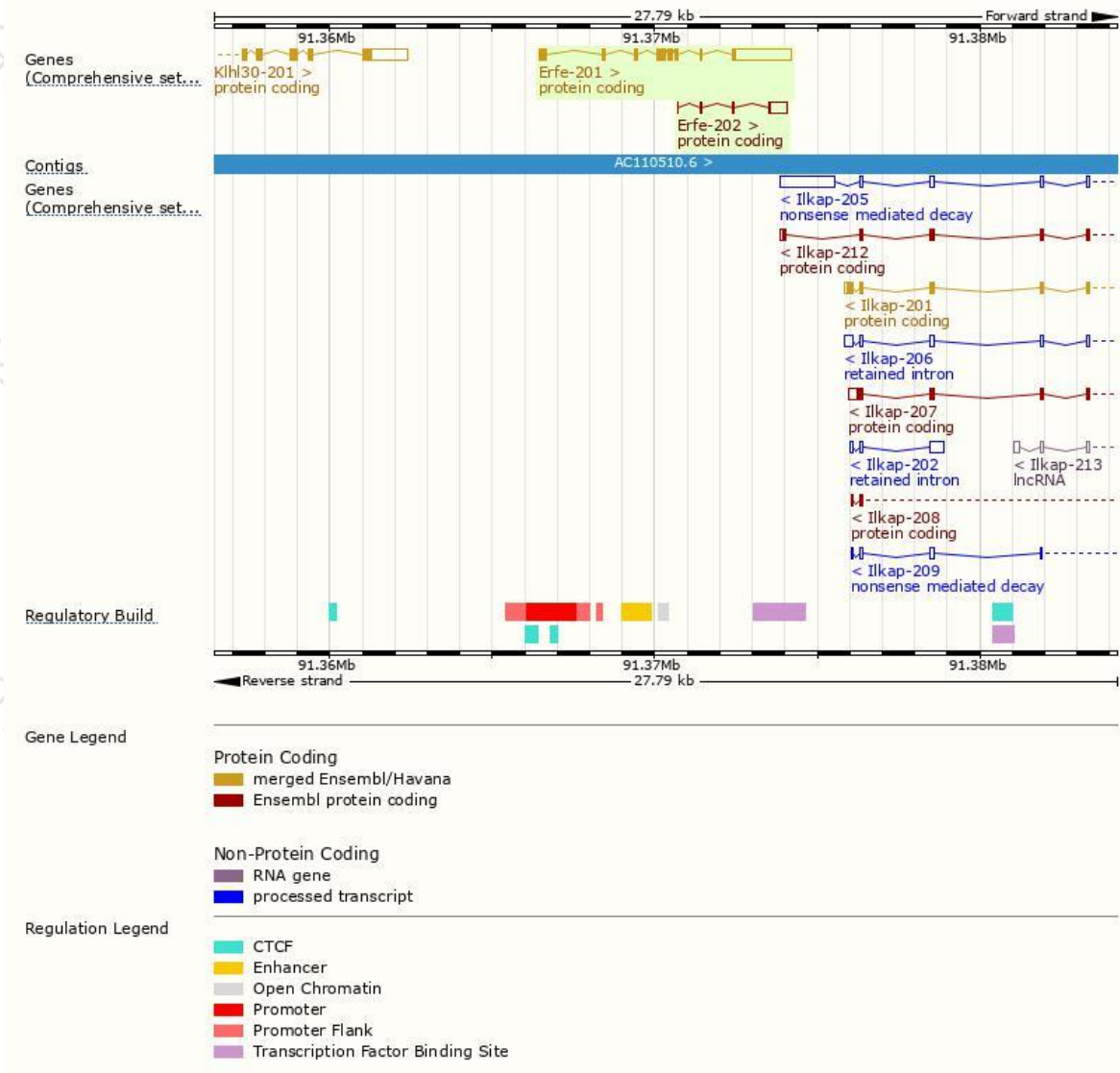
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Erfe-201	<a href="#">ENSMUST00000086861.11</a>	2815	<a href="#">340aa</a>	Protein coding	<a href="#">CCDS48323</a>	<a href="#">Q6PGN1</a>	TSL:1 GENCODE basic APPRIS P1
Erfe-202	<a href="#">ENSMUST00000190998.1</a>	715	<a href="#">56aa</a>	Protein coding	-	<a href="#">A0A087WR80</a>	CDS 5' incomplete TSL:5

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

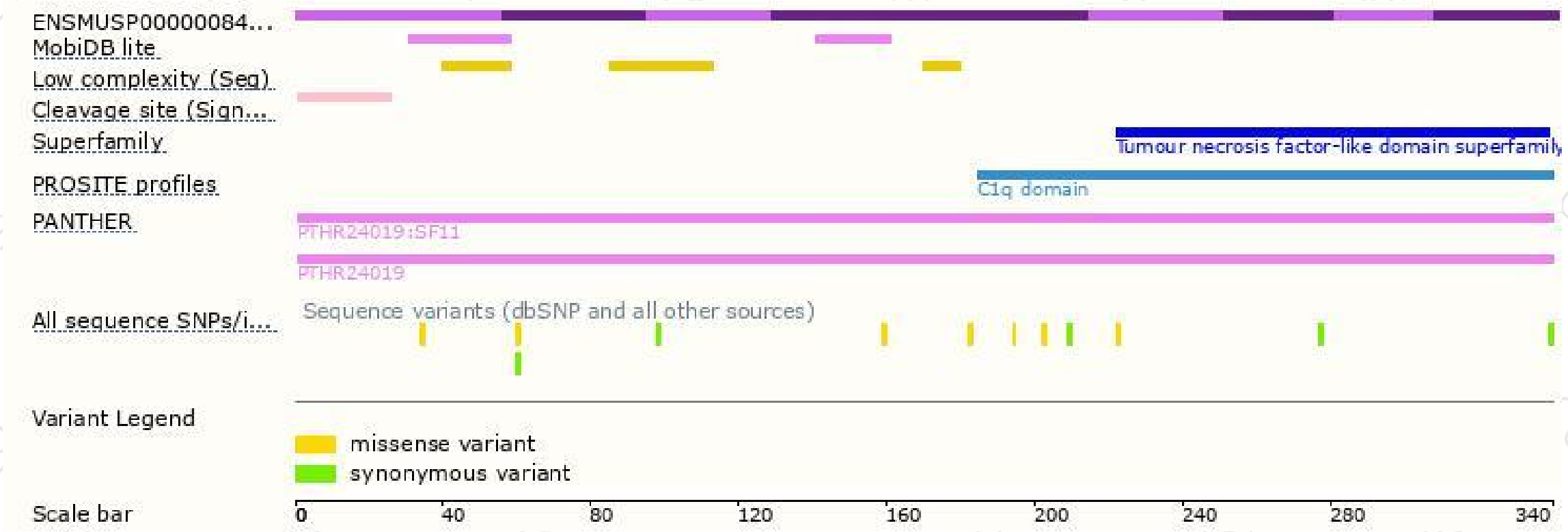


# Genomic location distribution

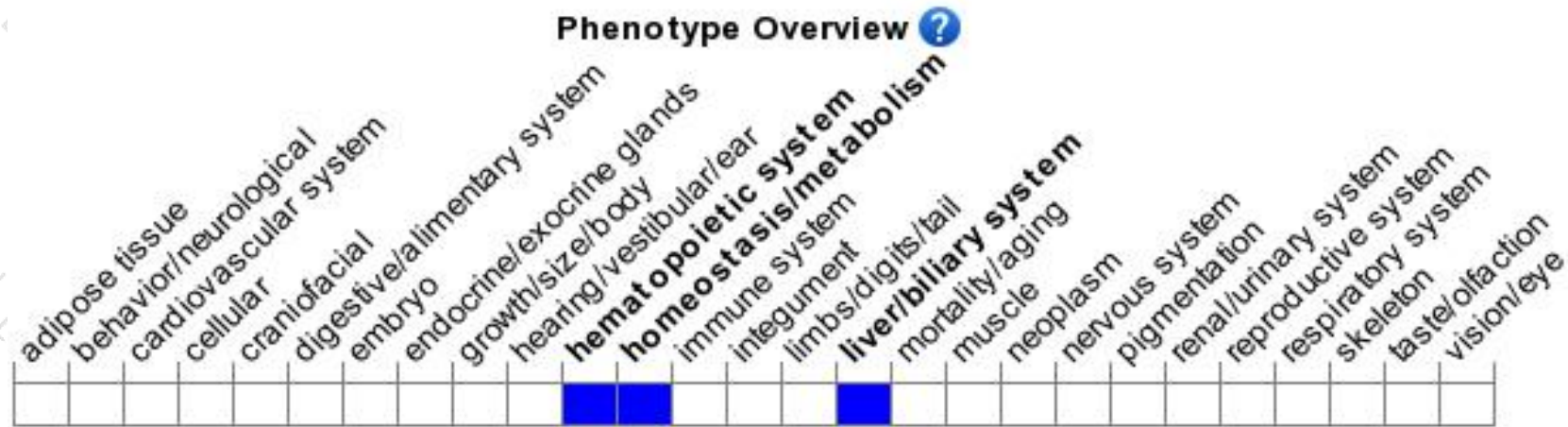




# Protein domain



# Mouse phenotype description(MGI )



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

According to the existing MGI data, Homozygous mice exhibit a delay in recovery from blood loss.

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

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