

Ezr Cas9-KO Strategy

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Project Overview

Project Name

Ezr

Project type

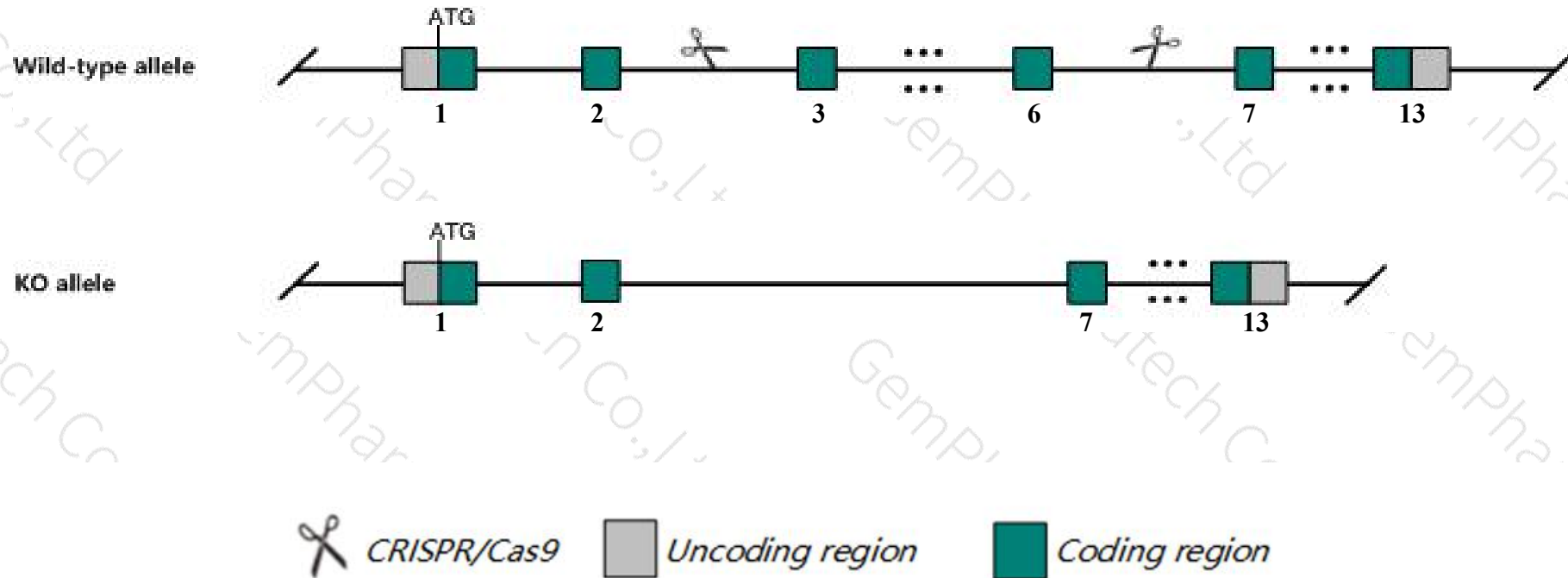
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Ezr* gene has 2 transcripts. According to the structure of *Ezr* gene, exon3-exon6 of *Ezr-201* (ENSMUST00000064234.6) transcript is recommended as the knockout region. The region contains 602bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ezr* gene. The brief process is as follows: CRISPR/Cas9 system will

- According to the existing MGI data, Homozygous null mice display postnatal lethality with abnormal intestinal villi morphology. Mice homozygous for a knock-down allele exhibit growth retardation, partial postnatal lethality, achlorhydria, and abnormal gastric parietal cell morphology and response to histamine stimulation.
- The *Ezr* gene is located on the Chr17. 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)

Ezr ezrin [Mus musculus (house mouse)]

Gene ID: 22350, updated on 19-Mar-2019

Summary



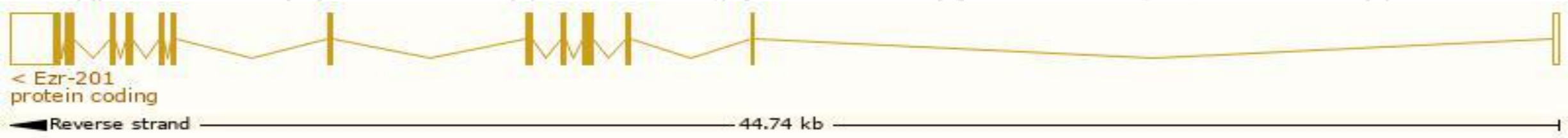
Official Symbol	Ezr provided by MGI
Official Full Name	ezrin provided by MGI
Primary source	MGI:MGI:98931
See related	Ensembl:ENSMUSG00000052397
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW146364, R75297, Vil2, p81
Expression	Broad expression in large intestine adult (RPKM 105.7), small intestine adult (RPKM 102.3) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

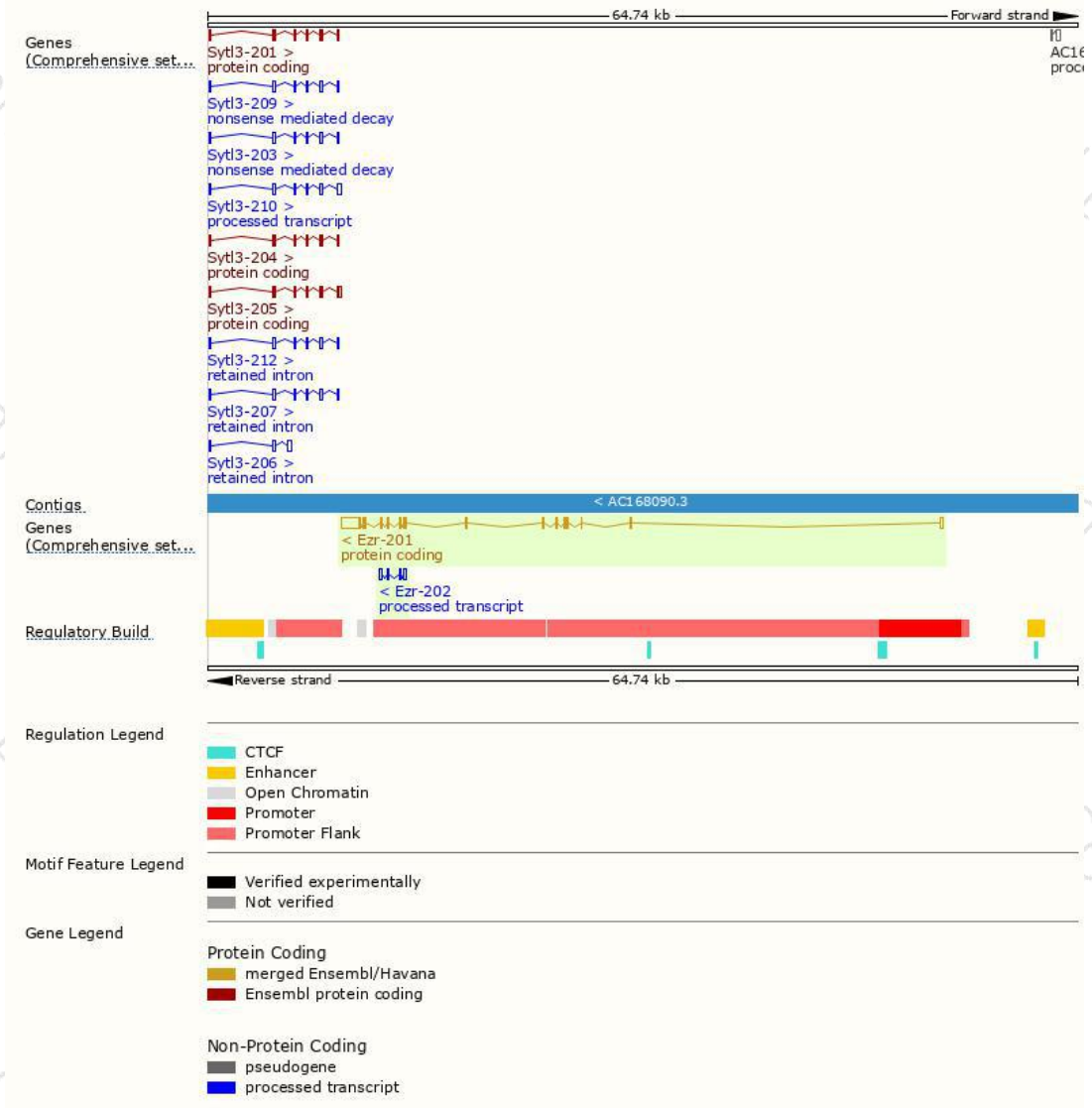
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ezr-201	ENSMUST00000064234.6	3164	586aa	Protein coding	CCDS37428	P26040 Q4KML7	TSL:1 GENCODE basic APPRIS P1
Ezr-202	ENSMUST00000131131.1	643	No protein	Processed transcript	-	-	TSL:3

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



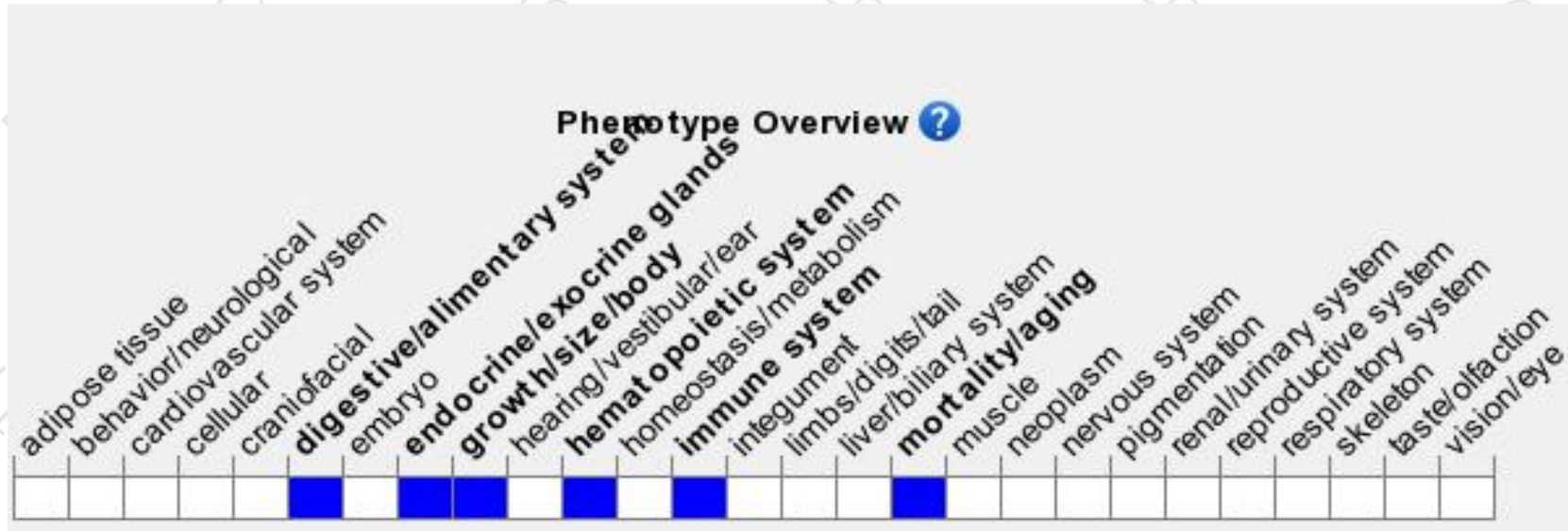
Genomic location distribution



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/>).

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

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