

***Trim24* Cas9-KO Strategy**

Designer: Xiaojing Li

Reviewer: JiaYu

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Project Overview

Project Name

Trim24

Project type

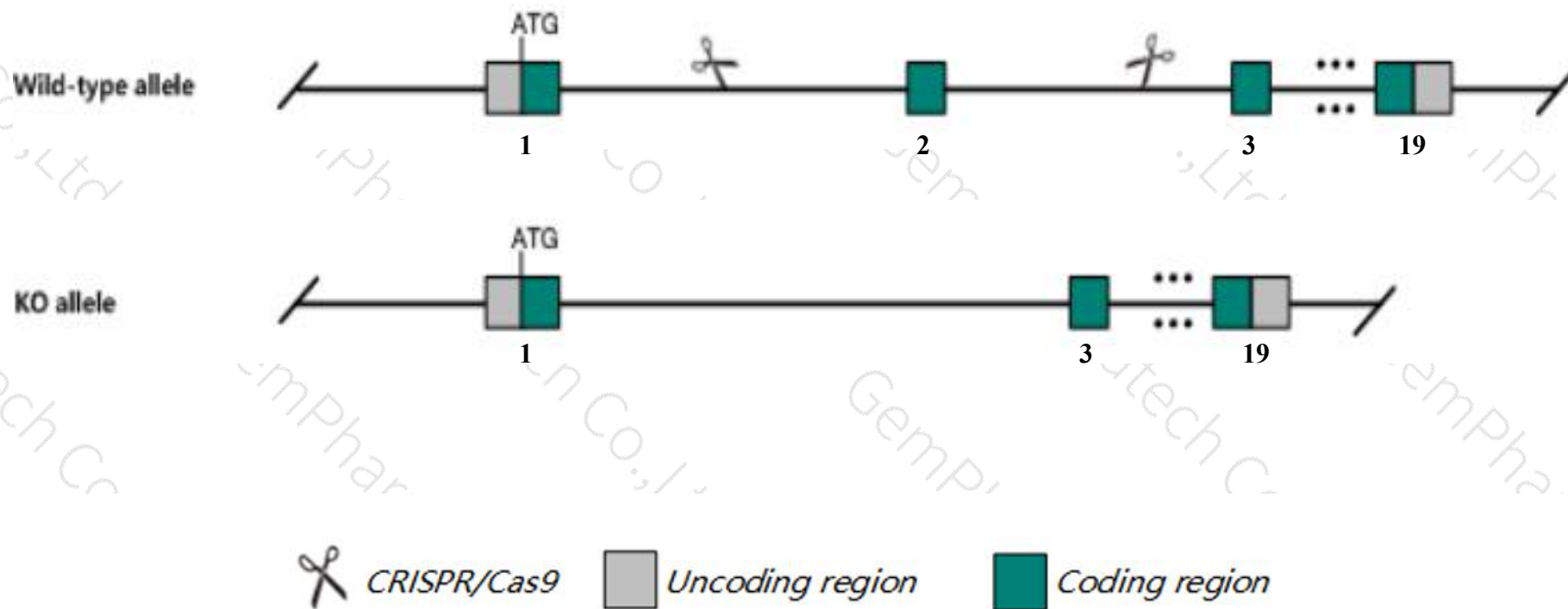
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Trim24* gene. The schematic diagram is as follows:



- The *Trim24* gene has 8 transcripts. According to the structure of *Trim24* gene, exon2 of *Trim24-202* (ENSMUST00000120238.1) transcript is recommended as the knockout region. The region contains 119bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Trim24* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit increased hepatocyte ploidy and uncontrolled hepatocellular proliferation; most adult mice develop malignant hepatocellular carcinomas.
- The *Trim24* 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)

Trim24 tripartite motif-containing 24 [Mus musculus (house mouse)]

Gene ID: 21848, updated on 31-Jan-2019

Summary



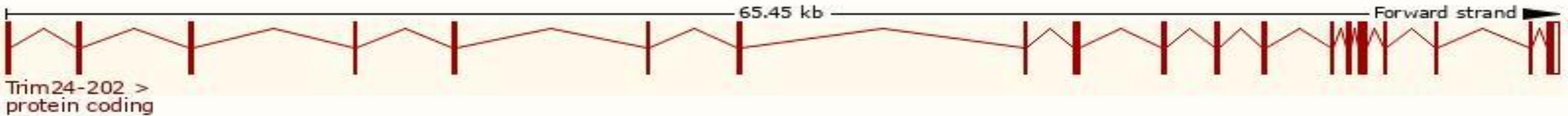
Official Symbol	Trim24 provided by MGI
Official Full Name	tripartite motif-containing 24 provided by MGI
Primary source	MGI:MGI:109275
See related	Ensembl:ENSMUSG00000029833
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A130082H20Rik, A1447469, D430004I05Rik, TIF1, TIF1-alpha, TIF1alpha, Tif1a
Summary	The protein encoded by this gene is part of the tripartite-motif containing family (TRIM), which are typified by the RING, B-box type 1, B-box type 2, and coiled-coil region domains. This protein, which also contains a PHD/TTC finger and bromodomain important for regulating nuclear receptors and binding chromatin, has important roles in differentiation, development, and tissue homeostasis. This protein has been reported to regulate the activity of the tumor suppressor p53 and of the retinoic acid receptor. A translocation event between this gene and Braf transforming gene, which results in the fusion protein T18, has been reported in hepatocellular carcinomas. Alternative splicing results in multiple transcript variants that encode different protein isoforms. [provided by RefSeq, Jan 2013]
Expression	Ubiquitous expression in testis adult (RPKM 15.5), CNS E11.5 (RPKM 8.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

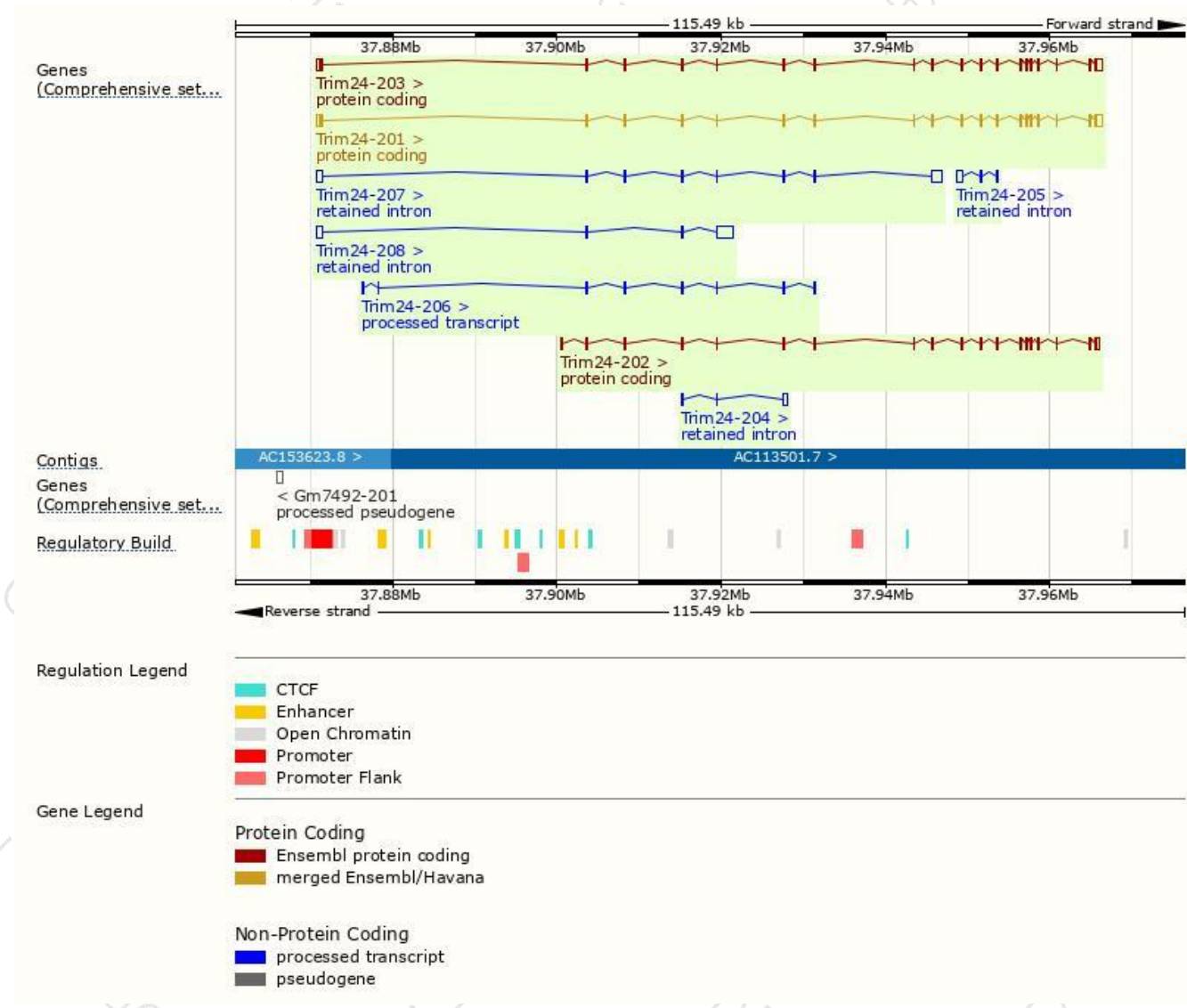
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Trim24-201	ENSMUST00000031859.13	4042	1051aa	Protein coding	CCDS20008	Q64127	TSL:1 GENCODE basic APPRIS P3
Trim24-203	ENSMUST00000120428.7	3940	1017aa	Protein coding	CCDS71751	Q64127	TSL:1 GENCODE basic APPRIS ALT2
Trim24-202	ENSMUST00000120238.1	3258	981aa	Protein coding	CCDS71752	E9Q1U8	TSL:1 GENCODE basic APPRIS ALT2
Trim24-206	ENSMUST00000149561.7	941	No protein	Processed transcript	-	-	TSL:3
Trim24-208	ENSMUST00000153004.7	3048	No protein	Retained intron	-	-	TSL:1
Trim24-207	ENSMUST00000149828.7	2722	No protein	Retained intron	-	-	TSL:1
Trim24-205	ENSMUST00000135387.1	1151	No protein	Retained intron	-	-	TSL:2
Trim24-204	ENSMUST00000123007.1	677	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Trim24-202* transcript,the transcription is shown below:



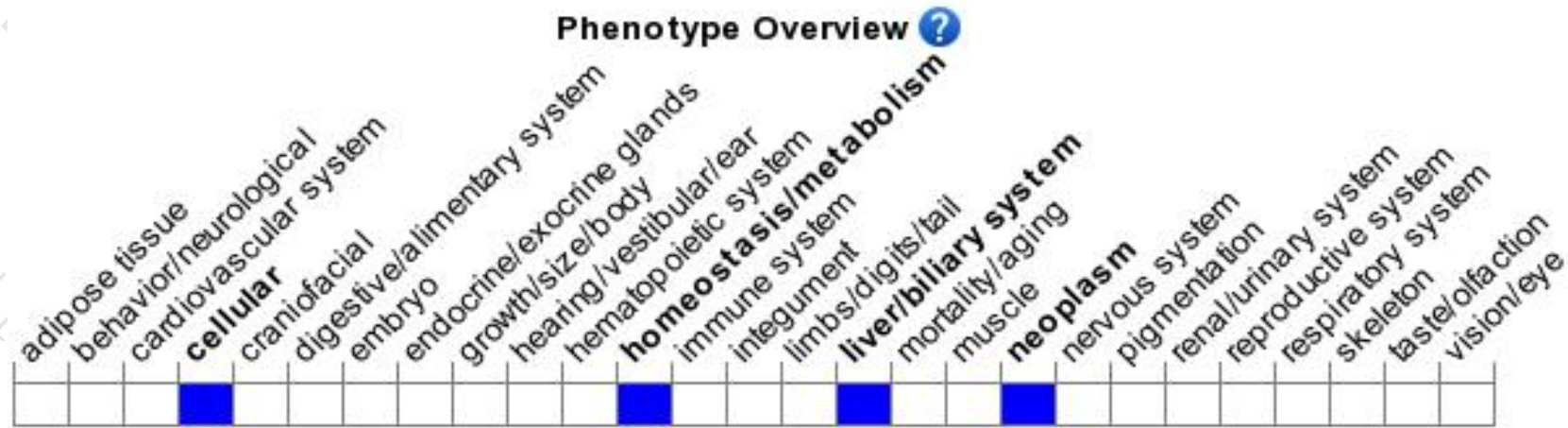
Genomic location distribution



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/>).

According to the existing MGI data, mice homozygous for a knock-out allele exhibit increased hepatocyte ploidy and uncontrolled hepatocellular proliferation; most adult mice develop malignant hepatocellular carcinomas.

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

Tel: 400-9660890

