

# Trim42 Cas9-CKO Strategy

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Design Date: 2023-06-07

### Overview

### Target Gene Name

• Trim42

Project Type

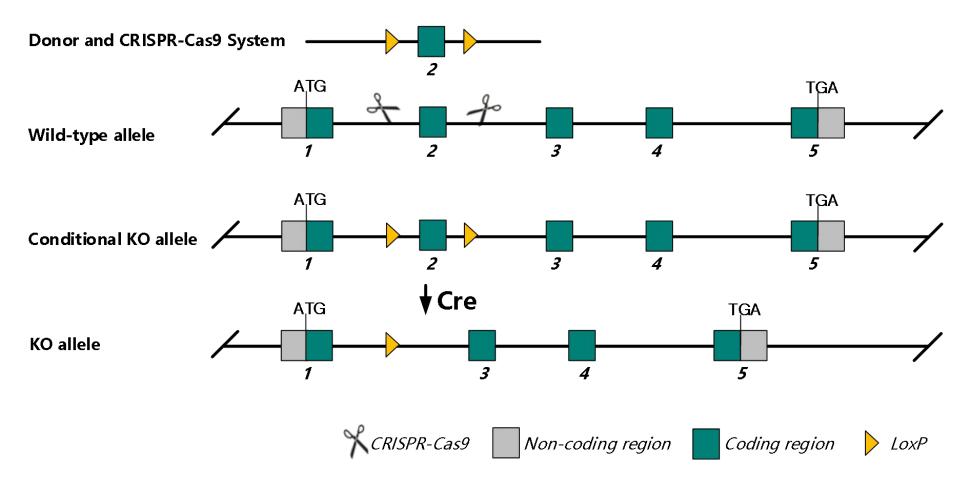
• Cas9-CKO

Genetic Background

• C57BL/6JGpt



## Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the Trim42 gene.

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# Technical Information

- The *Trim42* gene has 1 transcript. According to the structure of *Trim42* gene, exon2 of *Trim42*-201 (ENSMUST0000035026.5) transcript is recommended as the knockout region. The region contains 698bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Trim42* gene. The brief process is as follows: CRISPR-Cas9 system 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- The flox mice will be 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.

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## Gene Information

#### Trim42 tripartite motif-containing 42 [ Mus musculus (house mouse) ]

Gene ID: 78911, updated on 31-May-2023

#### Summary

Official SymbolTrim42 provided by MGIOfficial Full Nametripartite motif-containing 42 provided by MGIPrimary sourceMGI:MGI:1926161See relatedEnsembl:ENSMUSG0000032451 AllianceGenome:MGI:1926161Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea;<br/>Muridae; Murinae; Mus; MusAlso knownas4930486B16RikSummaryPredicted to enable ubiquitin-protein transferase activity. Predicted to be involved in positive regulation of transcription, DNA-templated. Predicted to be<br/>active in chromatin and nucleoplasm. Orthologous to human TRIM42 (tripartite motif containing 42). [provided by Alliance of Genome Resources, Apr 2022]ExpressionRestricted expression toward testis adult (RPKM 24.6) See more<br/>OrthologOrthologhuman all

Source: https://www.ncbi.nlm.nih.gov/gene/78911

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Download Datasets

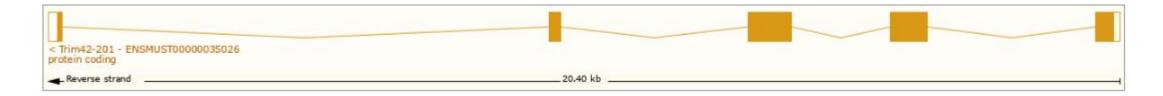
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# Transcript Information

The gene has 1 transcript, all transcripts are shown below:

Transcript ID	Name 🍦	bp 🛊	Protein 💧	Biotype 💧	CCDS 🕴	UniProt Match	Flags			
ENSMUST0000035026.5	Trim42-201	2463	<u>723aa</u>	Protein coding	CCDS23422@	<u>Q9D2H5</u> ଜ	Ensembl Canonical	GENCODE basic	APPRIS P1	TSL:1

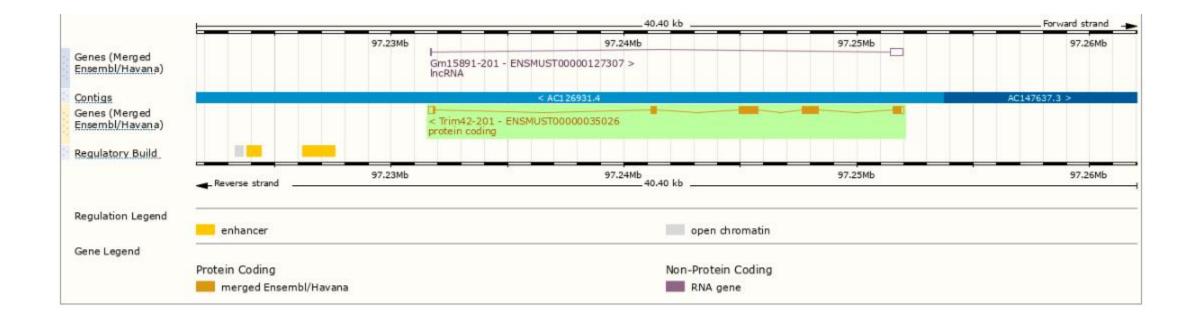
### The strategy is based on the design of *Trim42*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org



## Genomic Information





Source: : https://www.ensembl.org

# Protein Information

ENSMUSP00000035026 Low complexity (Seg)	.5								
AFDB-ENSP mappings Superfamily		55F57850	SSR	5/845			9	Fibronectin type II	II supertamily
SMART		Zinc linger, RNG-type	B-box-type zinc fing	per				Hbronectin type	
Pfam		and inget fails type	8-6	ox-type zinc finger				Hbronectin ty	/pe 111
PROSITE profiles		Zinc tinger, RING-type	BHDR	ox-type zinc finger	CUS doma	ID		Fibronectin type	
PROSITE patterns	DTHR2546515F13	Zinc finger, RING-tyr	pe, conserved site						
	PTRR25465								
Gene3D			.830.40 3.30.1	10.60				Immunoglobuli	
CDD		TRIM42, RING-HC finger						Fibronectin ty)	SE 111
All sequence SNPs/	Sequence variants (EVA and all other	er sources)	-	01.0 1.0	11 1 11 11 100	10.4	(E)	1 0	0.004
Variant Legend	stop gained				frameshift variant				
	missense variant				synonymous variant				
Scale bar	0 80	160	240	320	400	480	560	640	723

Source: : https://www.ensembl.org

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## Important Information

- The knockout region is overlapped with the predictd gene *Gm15891*. The expression of *Gm15891* gene may be affected.
- *Trim42* is located on Chr9. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

