Trim37 Cas9-KO Strategy

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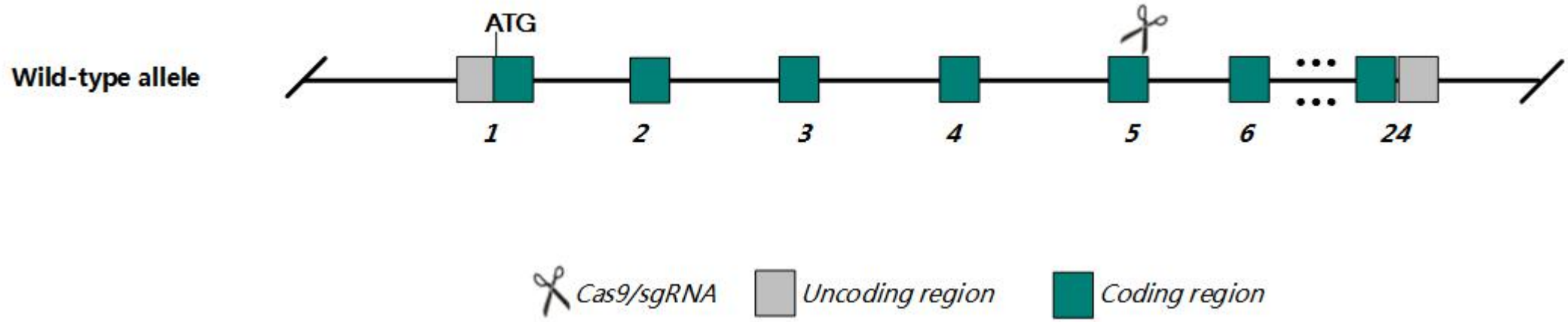
Project Overview

Project Name	***Trim37***
Project type	**Cas9-KO**
Strain background	**C57BL/6N**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Trim37* gene. The schematic diagram is as follows:



Technical routes

- In this project we use CRISPR/Cas9 technology to modify *Trim37* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6N mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6N mice.

Notice

➢ According to MGI, Mice homozygous for a knock-out allele are infertile due to gonadal degeneration and exhibit late-onset weight loss, smaller skull size, non-compaction cardiomyopathy, hepatomegaly, fatty liver, altered glucose metabolism, splenomegaly, and increased tumor incidence..

➢ The *Trim37* gene is located on the Chr11, 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）

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Trim37 tripartite motif-containing 37 [*Mus musculus* (house mouse)]

Gene ID: 68729, updated on 12-Aug-2019

Summary

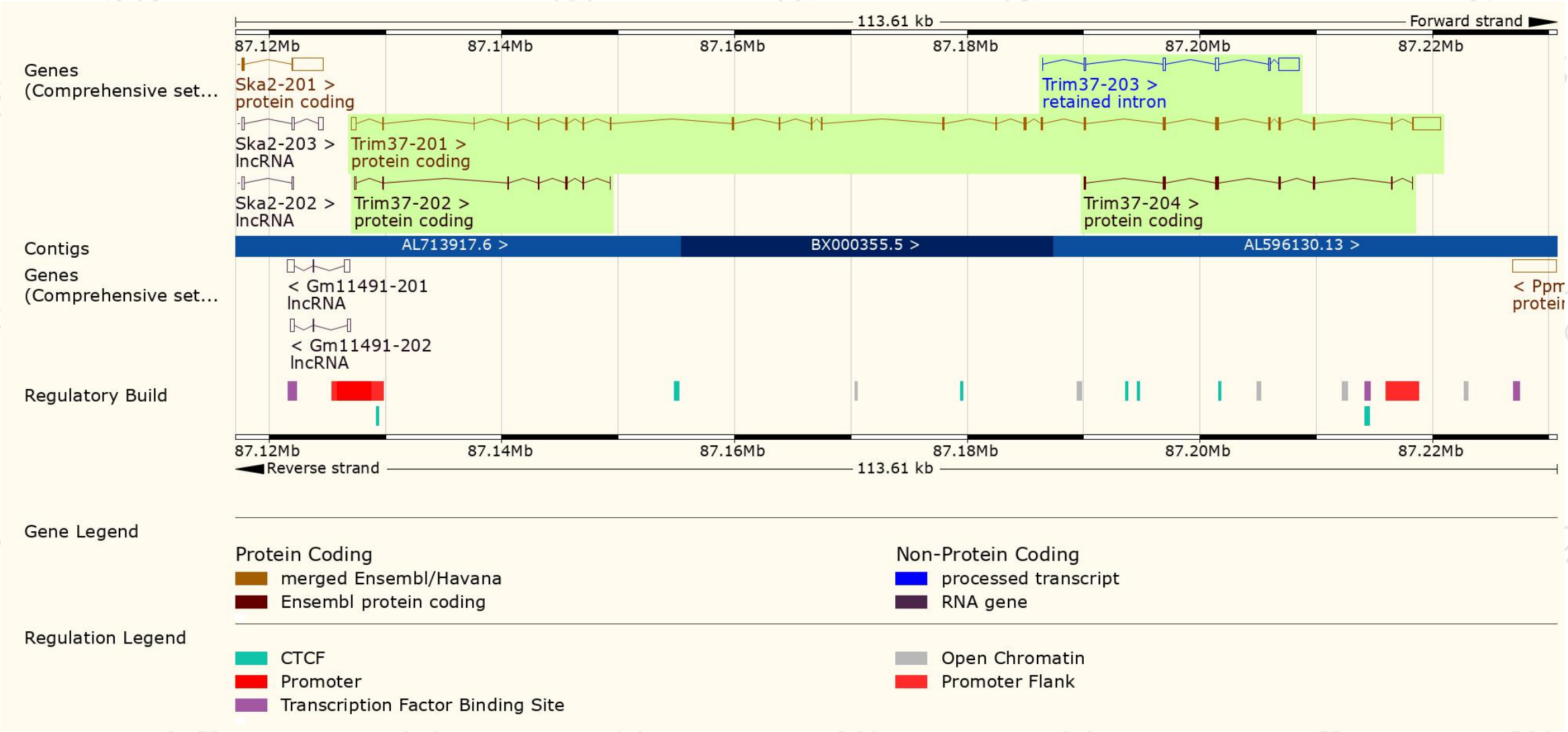
Official Symbol	Trim37 provided by MGI
Official Full Name	tripartite motif-containing 37 provided by MGI
Primary source	MGI:MGI:2153072
See related	Ensembl:ENSMUSG00000018548
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	MUL; TEF3; AI848587; AU043018; 1110032A10Rik; 2810004E07Rik
Summary	The protein encoded by this gene is part of the tripartite-motif containing family (TRIM), which is typified by the RING, B-box type 1, B-box type 2, and coiled-coil region domains. In mouse this protein is proposed to oligomerize through its coiled coil domain and has been reported to be expressed in neural crest-derived tissues as well as in tissues whose development is regulated by mesenchymal-epithelial interactions. In humans, mutations in this gene are associated with mulibrey (muscle-liver-brain-eye) nanism, an autosomal recessive disorder characterized by prenatal onset growth failure, cardiomyopathy and dysmorphic features. [provided by RefSeq, Jan 2013]
Expression	Biased expression in cortex adult (RPKM 34.0), testis adult (RPKM 33.1) and 14 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

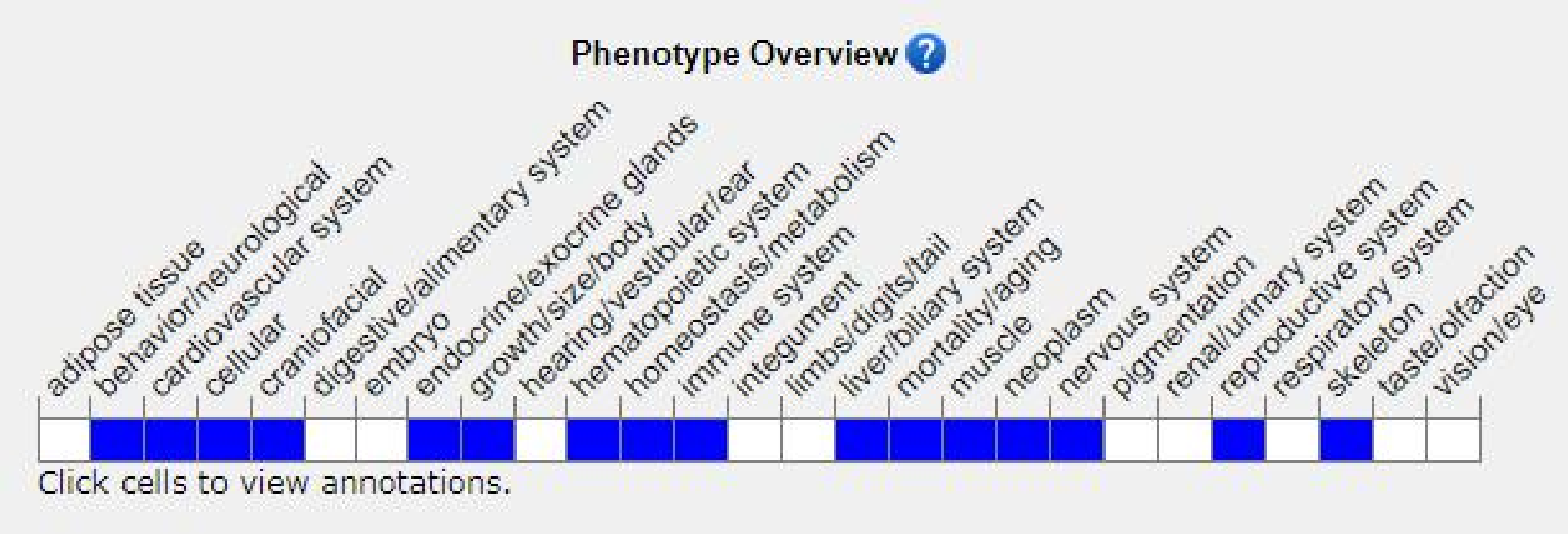
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Trim37-201	ENSMUST00000041282.12	5632	961aa	Protein coding	CCDS25210	Q6PCX9	TSL:1 GENCODE basic APPRIS P1
Trim37-202	ENSMUST00000139532.1	766	197aa	Protein coding	-	Q5SQY9	CDS 3' incomplete TSL:5
Trim37-203	ENSMUST00000152637.1	2488	No protein	Retained intron	-	-	TSL:5
Trim37-204	ENSMUST00000154138.1	1017	339aa	Protein coding	-	F6XMH5	CDS 5' and 3' incomplete TSL:5

Genomic location distribution



Mouse phenotype description(MGI)



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

Mice homozygous for a knock-out allele are infertile due to gonadal degeneration and exhibit late-onset weight loss, smaller skull size, non-compaction cardiomyopathy, hepatomegaly, fatty liver, altered glucose metabolism, splenomegaly, and increased tumor incidence.

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

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