Trip13 Cas9-KO Strategy

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Design Date: 2019-11-25

Project Overview

Project Name	***Trip13***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Trip13* gene. The schematic diagram is as follows:

Technical routes

➢ The *Trip13* gene has 3 transcripts. According to the structure of *Trip13* gene, exon3 of *Trip13-201* (ENSMUST00000022053.10) transcript is recommended as the knockout region.The region contains 130bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Trip13* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,Mice homozygous for a gene trapped allele exhibit postnatal lethality, infertility, reduced gonad size, tail defects and meiotic arrest of sperm and oocytes associated with unrepaired double strand breaks.

➢ The *Trip13* gene is located on the Chr13. 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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Trip13 thyroid hormone receptor interactor 13 [Mus musculus (house mouse)]

Gene ID: 69716, updated on 31-Jan-2019

Summary

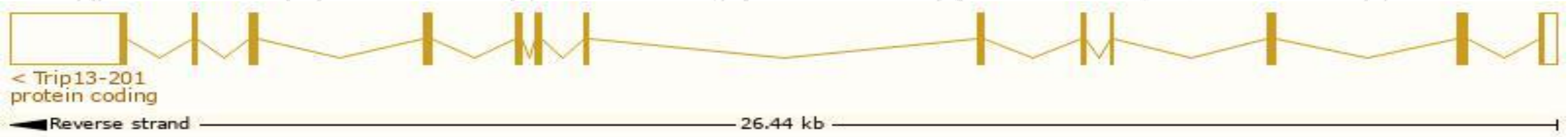
Official Symbol	Trip13 provided by MGI
Official Full Name	thyroid hormone receptor interactor 13 provided by MGI
Primary source	MGI:MGI:1916966
See related	Ensembl:ENSMUSG00000021569
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410002G23Rik, D13Ertd328e
Expression	Biased expression in CNS E11.5 (RPKM 11.3), placenta adult (RPKM 8.5) and 11 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

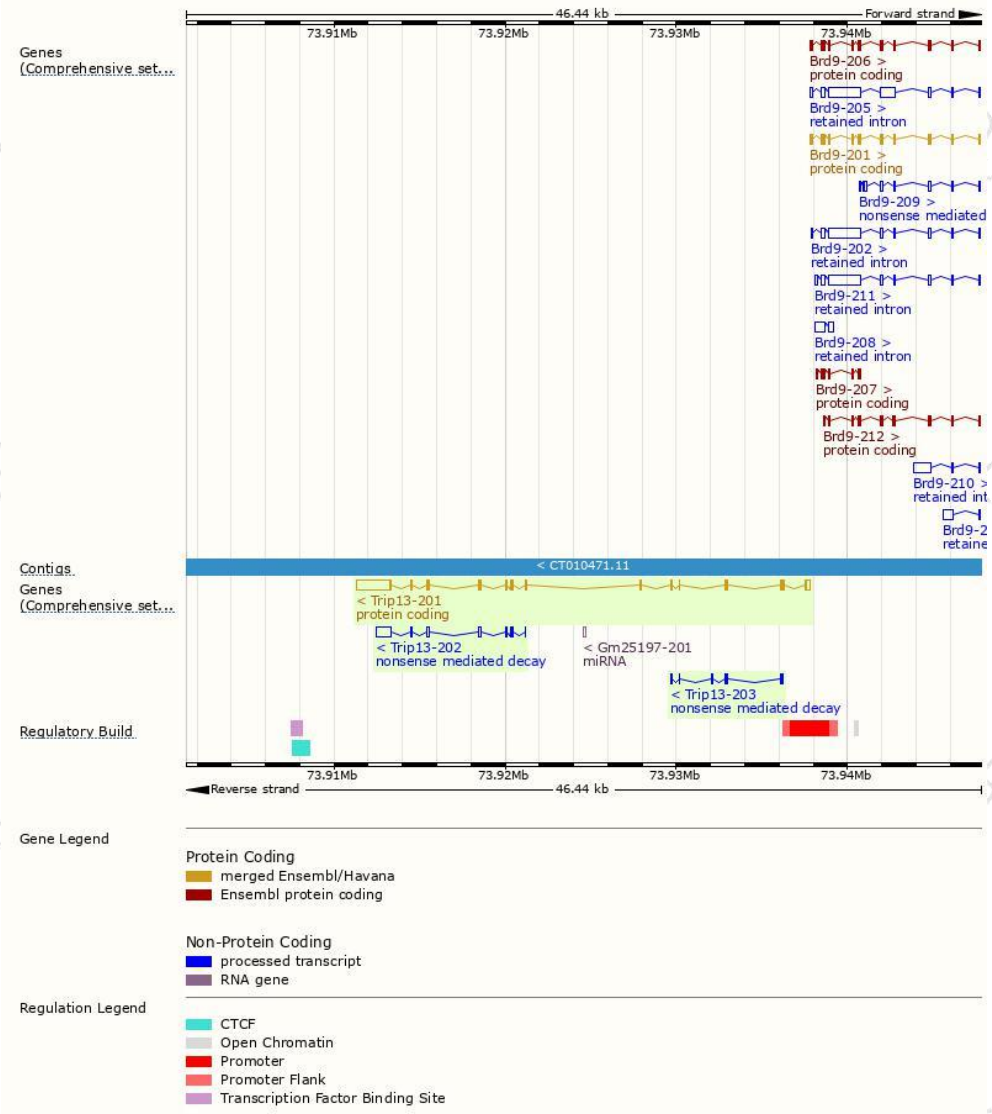
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Trip13-201	ENSMUST00000022053.10	3399	432aa	Protein coding	CCDS26637	Q3UA06	TSL:1 GENCODE basic APPRIS P1
Trip13-202	ENSMUST00000222156.1	1469	23aa	Nonsense mediated decay	-	A0A1Y7VK03	CDS 5' incomplete TSL:1
Trip13-203	ENSMUST00000223017.1	382	80aa	Nonsense mediated decay	-	A0A1Y7VLR4	CDS 5' incomplete TSL:1

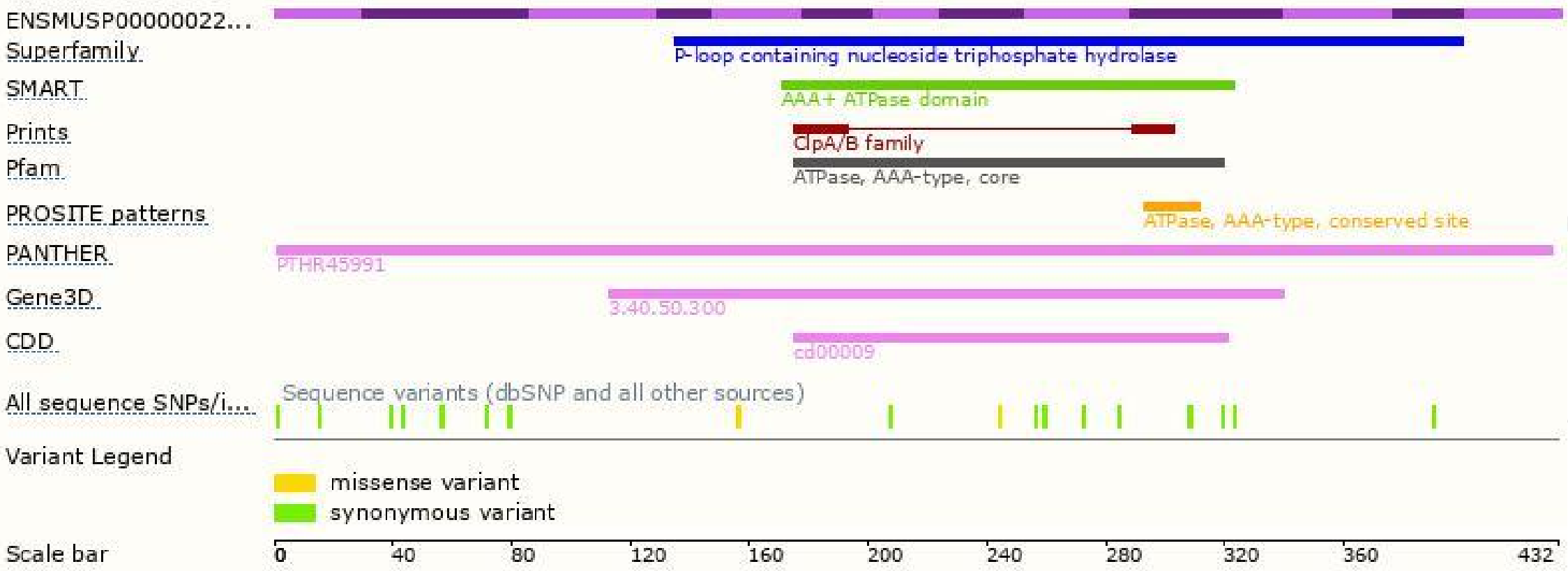
The strategy is based on the design of *Trip13-201* transcript,The transcription is shown below



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,Mice homozygous for a gene trapped allele exhibit postnatal lethality, infertility, reduced gonad size, tail defects and meiotic arrest of sperm and oocytes associated with unrepaired double strand breaks.

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

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