

Trrap Cas9-KO Strategy

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Project Overview

Project Name

Trrap

Project type

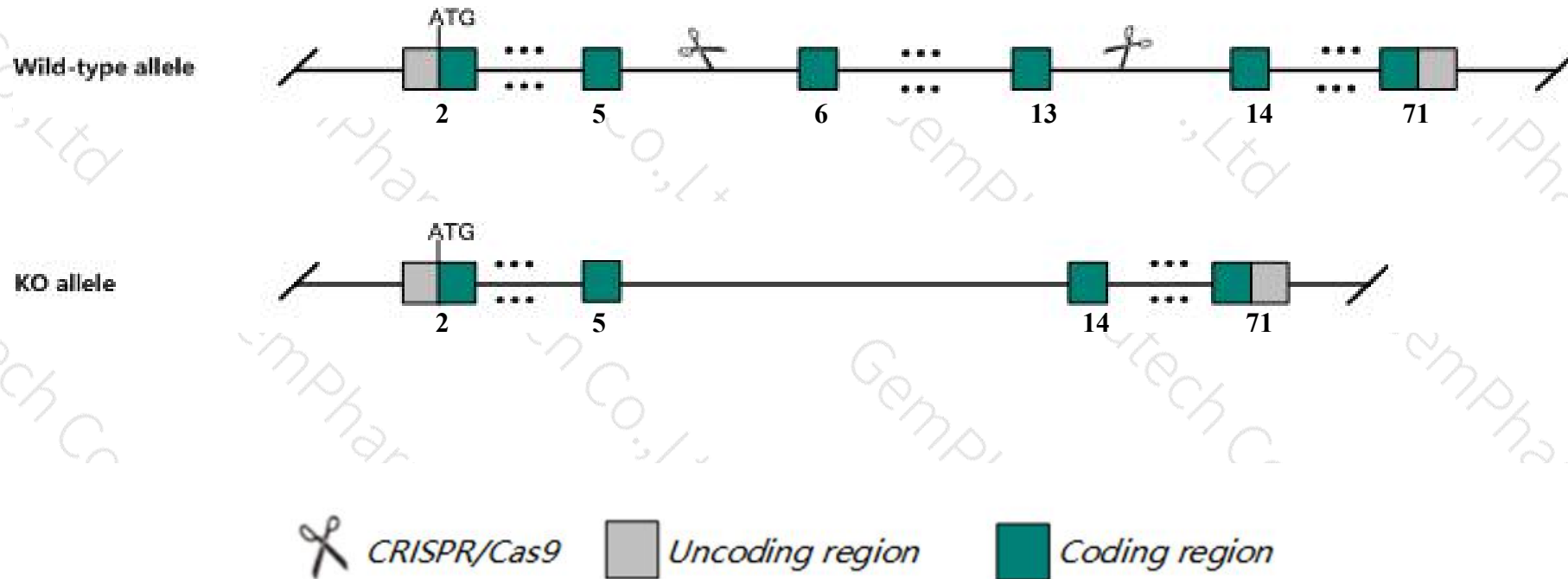
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Trrap* gene has 15 transcripts. According to the structure of *Trrap* gene, exon6-exon13 of *Trrap*-203 (ENSMUST00000100467.9) transcript is recommended as the knockout region. The region contains 749bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Trrap* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous embryos die prior to E3.5 and exhibit embryonic and extraembryonic tissue disorganization. Mitotic abnormalities were also noted in homozygous cells.
- The *Trrap* gene is located on the Chr5. 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)

Trrap transformation/transcription domain-associated protein [*Mus musculus* (house mouse)]

Gene ID: 100683, updated on 12-Aug-2019

Summary

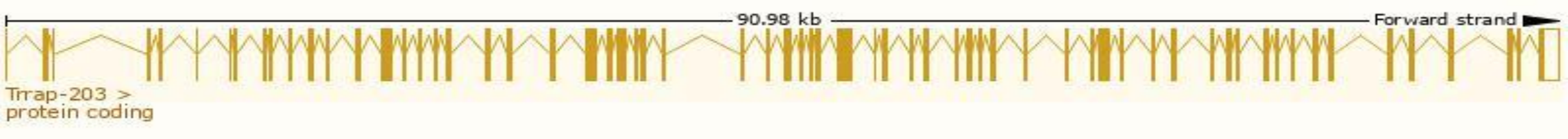
Official Symbol	Trrap provided by MGI
Official Full Name	transformation/transcription domain-associated protein provided by MGI
Primary source	MGI:MGI:2153272
See related	Ensembl:ENSMUSG00000045482
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI481500
Expression	Ubiquitous expression in ovary adult (RPKM 24.1), thymus adult (RPKM 17.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

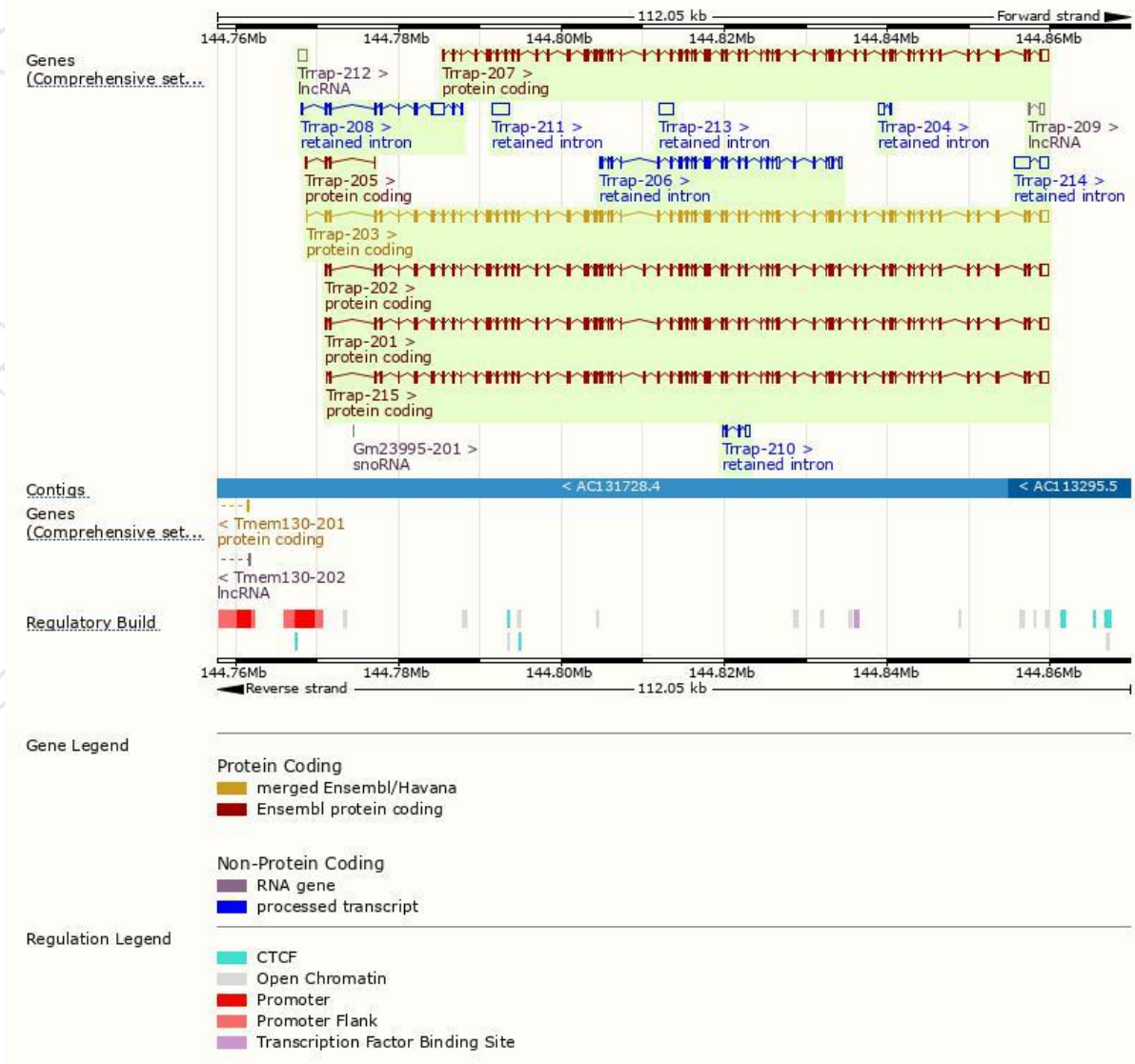
The gene has 15 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Trrap-203	ENSMUST00000100467.9	12479	3847aa	Protein coding	CCDS39379	E9QLK7	TSL:1 GENCODE basic APPRIS P2
Trrap-202	ENSMUST00000094120.8	12456	3858aa	Protein coding	-	E9PWT1	TSL:5 GENCODE basic APPRIS ALT2
Trrap-215	ENSMUST00000213013.1	12398	3859aa	Protein coding	-	A0A1D5RLL4	TSL:5 GENCODE basic APPRIS ALT2
Trrap-201	ENSMUST00000038980.12	12344	3829aa	Protein coding	-	E9PZA7	TSL:5 GENCODE basic APPRIS ALT2
Trrap-207	ENSMUST00000132925.1	11581	3587aa	Protein coding	-	F7CGG2	CDS 5' incomplete TSL:5
Trrap-205	ENSMUST00000128550.7	415	58aa	Protein coding	-	D3YY11	CDS 3' incomplete TSL:3
Trrap-206	ENSMUST00000132347.7	4781	No protein	Retained intron	-	-	TSL:1
Trrap-214	ENSMUST00000198524.1	3101	No protein	Retained intron	-	-	TSL:1
Trrap-208	ENSMUST00000136379.1	2621	No protein	Retained intron	-	-	TSL:1
Trrap-211	ENSMUST00000196258.1	2193	No protein	Retained intron	-	-	TSL:NA
Trrap-213	ENSMUST00000197834.1	1752	No protein	Retained intron	-	-	TSL:NA
Trrap-210	ENSMUST00000143357.1	796	No protein	Retained intron	-	-	TSL:3
Trrap-204	ENSMUST00000124909.1	719	No protein	Retained intron	-	-	TSL:3
Trrap-212	ENSMUST00000197741.1	960	No protein	lncRNA	-	-	TSL:NA
Trrap-209	ENSMUST00000138589.1	888	No protein	lncRNA	-	-	TSL:5

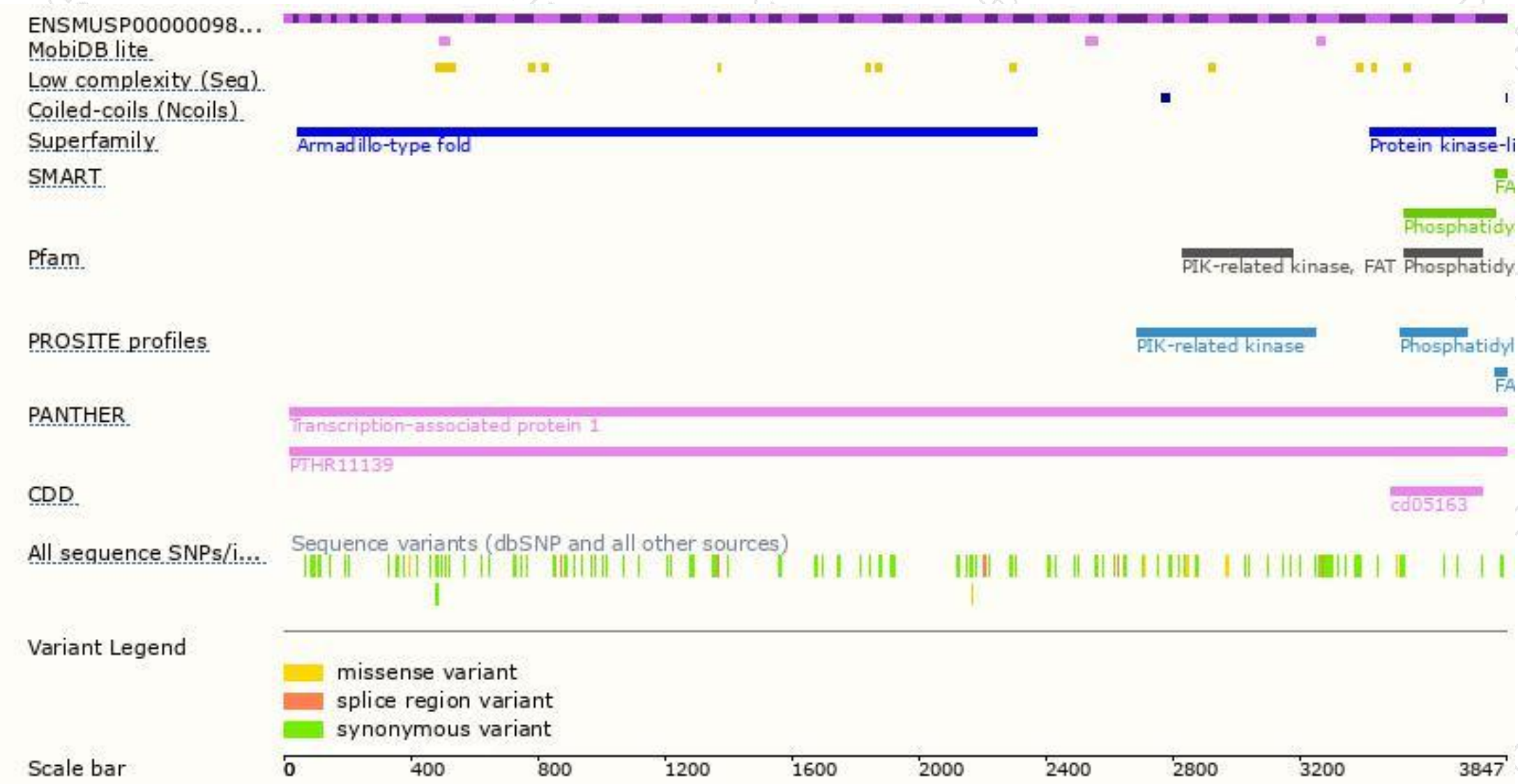
The strategy is based on the design of *Trrap-203* transcript,The transcription is shown below



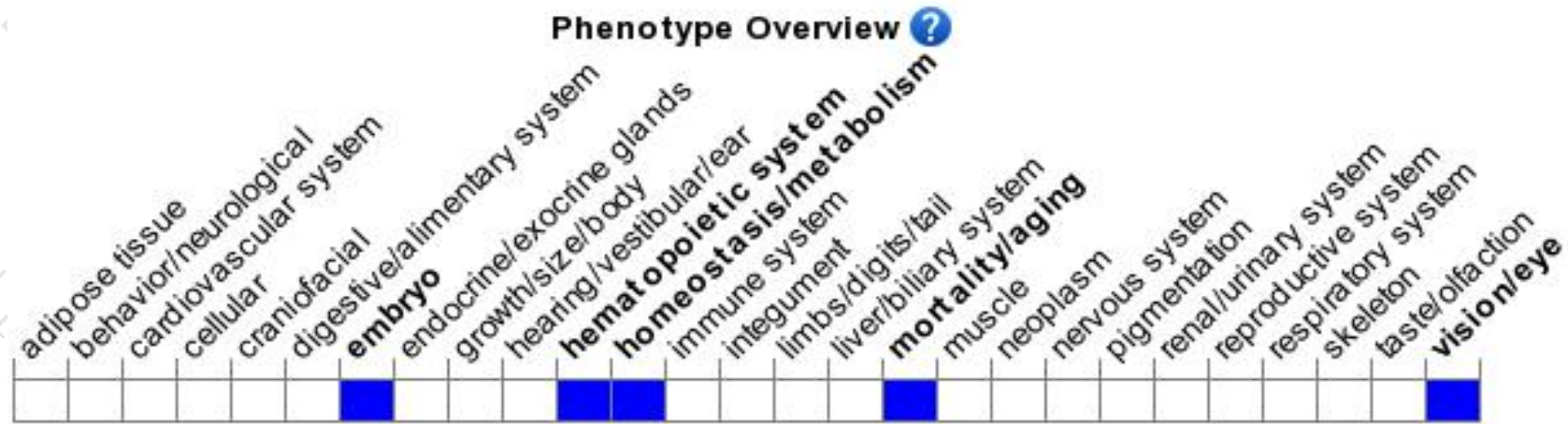
Genomic location distribution



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, Homozygous embryos die prior to E3.5 and exhibit embryonic and extraembryonic tissue disorganization. Mitotic abnormalities were also noted in homozygous cells.

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

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