Treh Cas9-KO Strategy

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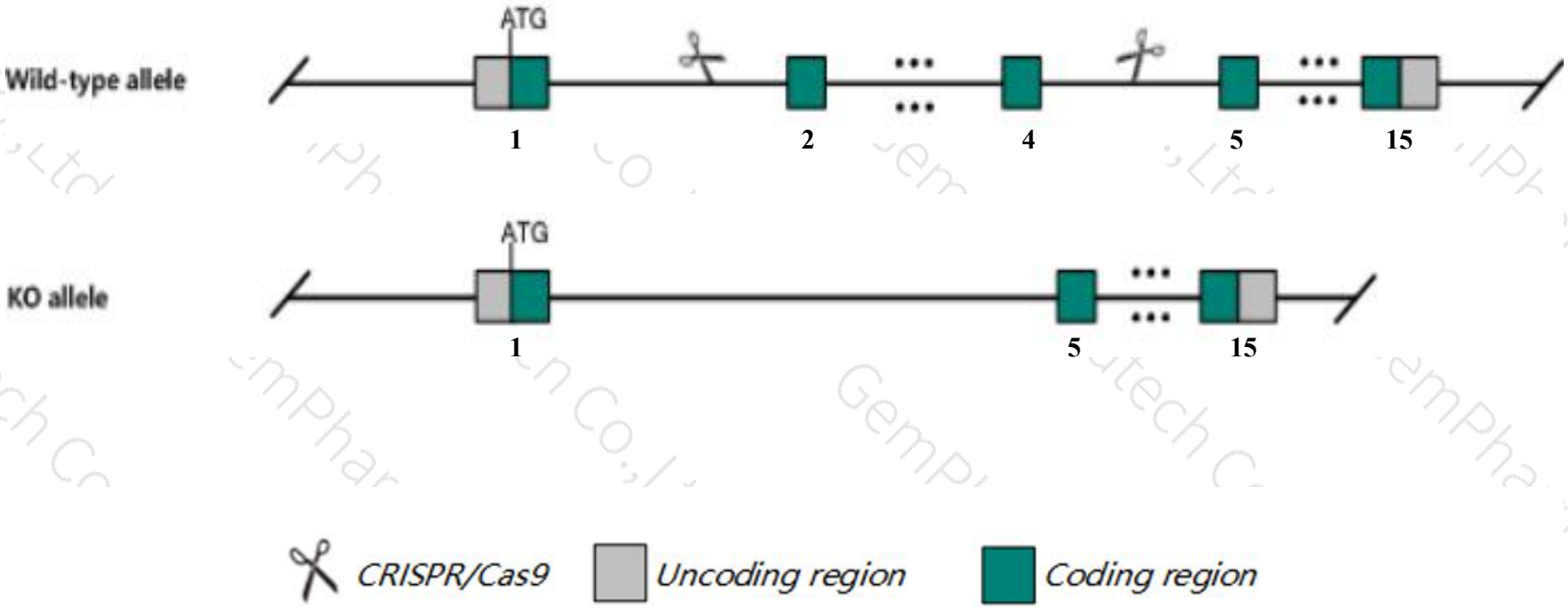
Project Overview

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

Knockout strategy

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



Technical routes

➢ The *Treh* gene has 4 transcripts. According to the structure of *Treh* gene, exon2-exon4 of *Treh-201* (ENSMUST00000034609.10) transcript is recommended as the knockout region.The region contains 334bp coding sequence. Knock out the region will result in disruption of protein function.

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

Notice

- According to the existing MGI data,mice homozygous for a knock-out allele fail to exhibit a rapid increase in blood glucose levels following oral trehalose administration.
- The *Treh* gene is located on the Chr9. 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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Treh trehalase (brush-border membrane glycoprotein) [Mus musculus (house mouse)]

Gene ID: 58866, updated on 31-Jan-2019

Summary

Official Symbol	Treh provided by MGI
Official Full Name	trehalase (brush-border membrane glycoprotein) provided by MGI
Primary source	MGI:MGI:1926230
See related	Ensembl:ENSMUSG00000032098
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	2210412M19Rik
Summary	This gene belongs to the alpha-glucosidase family, whose members encode enzymes that carry out hydrolysis of alpha-glucoside bonds of a variety of carbohydrates. The enzyme encoded by this gene uses the disaccharide trehalose as a highly specific substrate and converts it into two glucose molecules. Alternative splicing of this gene results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Apr 2013]
Expression	Biased expression in duodenum adult (RPKM 127.9), small intestine adult (RPKM 63.2) and 2 other tissuesSee more
Orthologs	human all

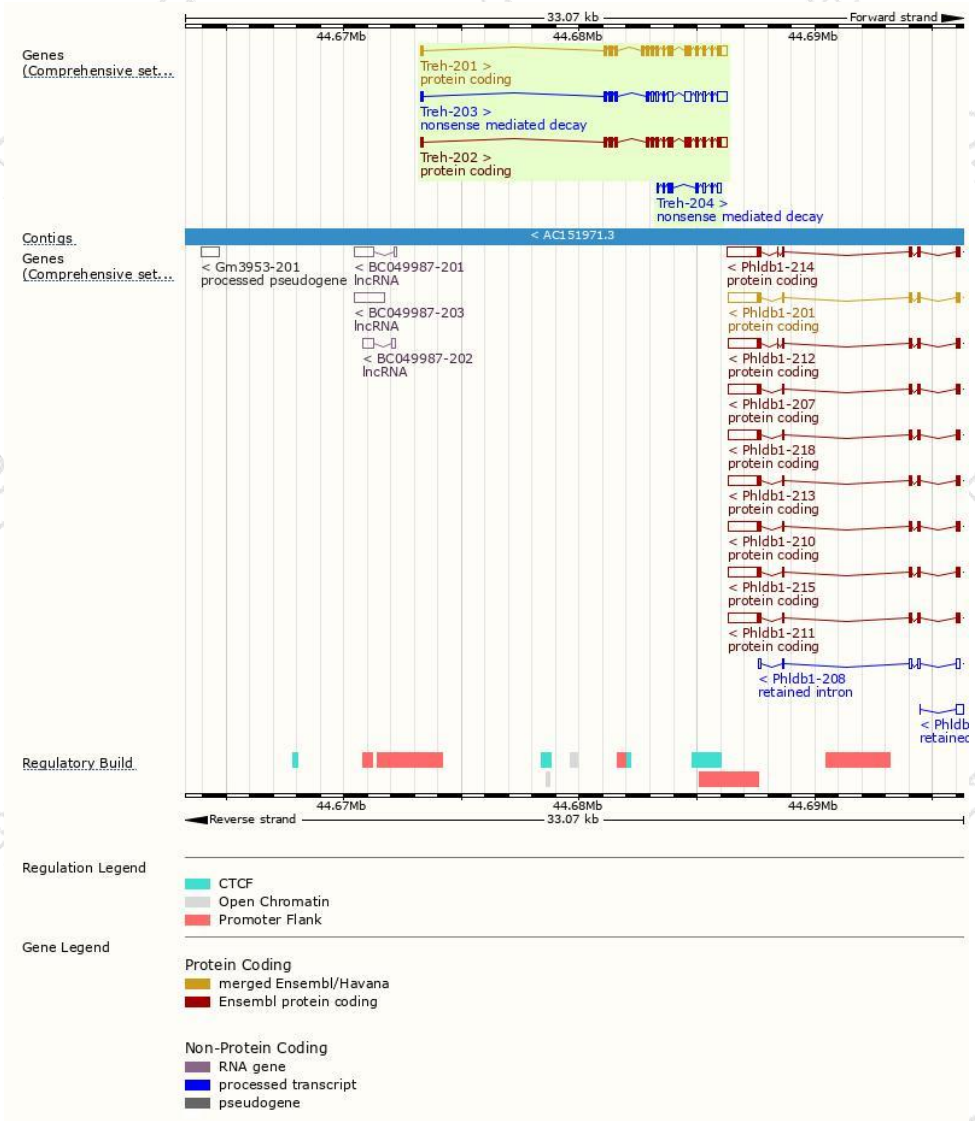
Transcript information（Ensembl）

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

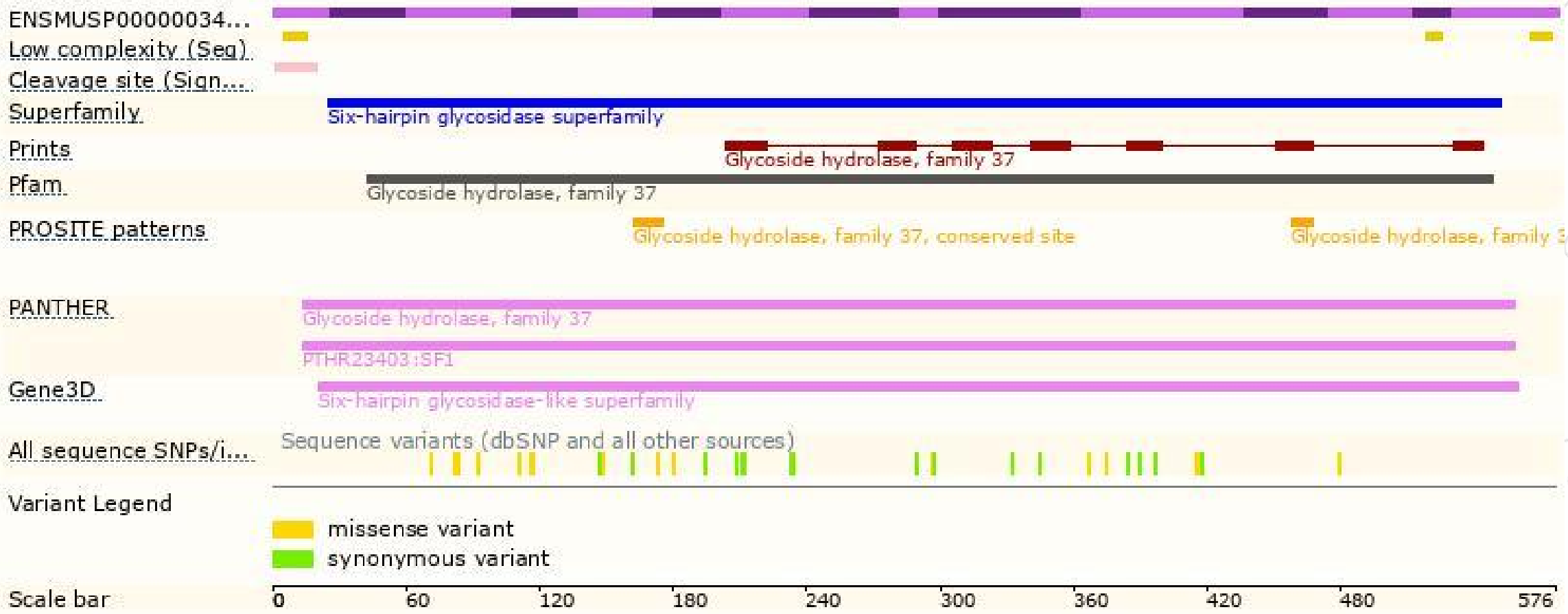
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Treh-201	ENSMUST00000034609.10	2048	576aa	Protein coding	CCDS23117	Q9JLT2	TSL:1 GENCODE basic APPRIS P1
Treh-202	ENSMUST00000071219.11	1927	541aa	Protein coding	CCDS72222	E9PYP7	TSL:1 GENCODE basic
Treh-203	ENSMUST00000139389.7	1944	150aa	Nonsense mediated decay	-	D6RI51	TSL:1
Treh-204	ENSMUST00000150822.1	745	124aa	Nonsense mediated decay	-	F6XTD2	CDS 5' incomplete TSL:3

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

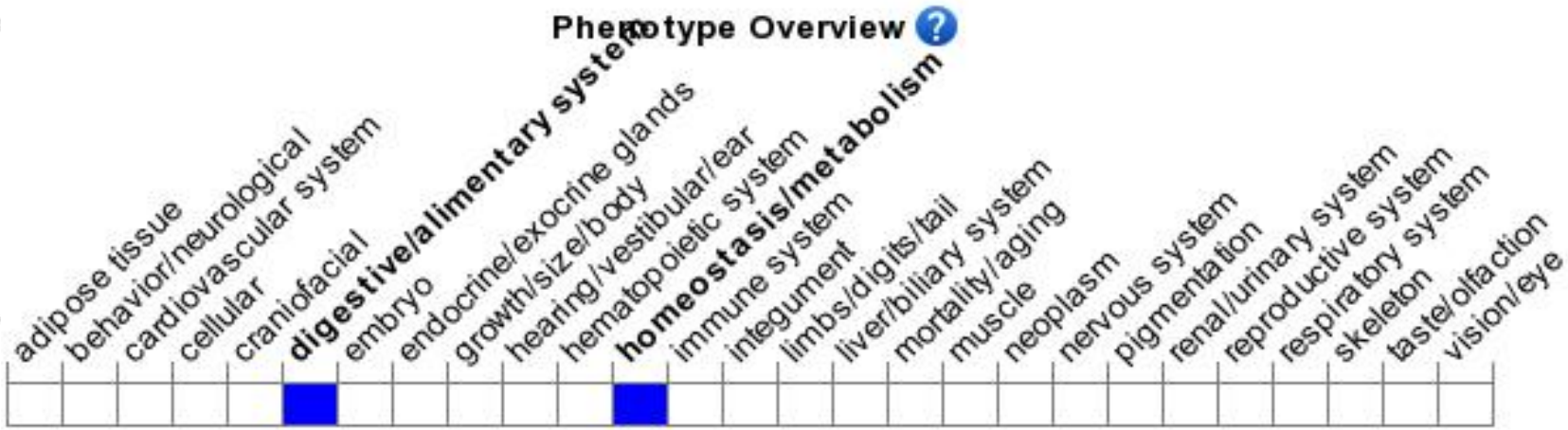
Genomic location distribution



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/).

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

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