

***Utp4* Cas9-KO Strategy**

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Project Overview

Project Name

Utp4

Project type

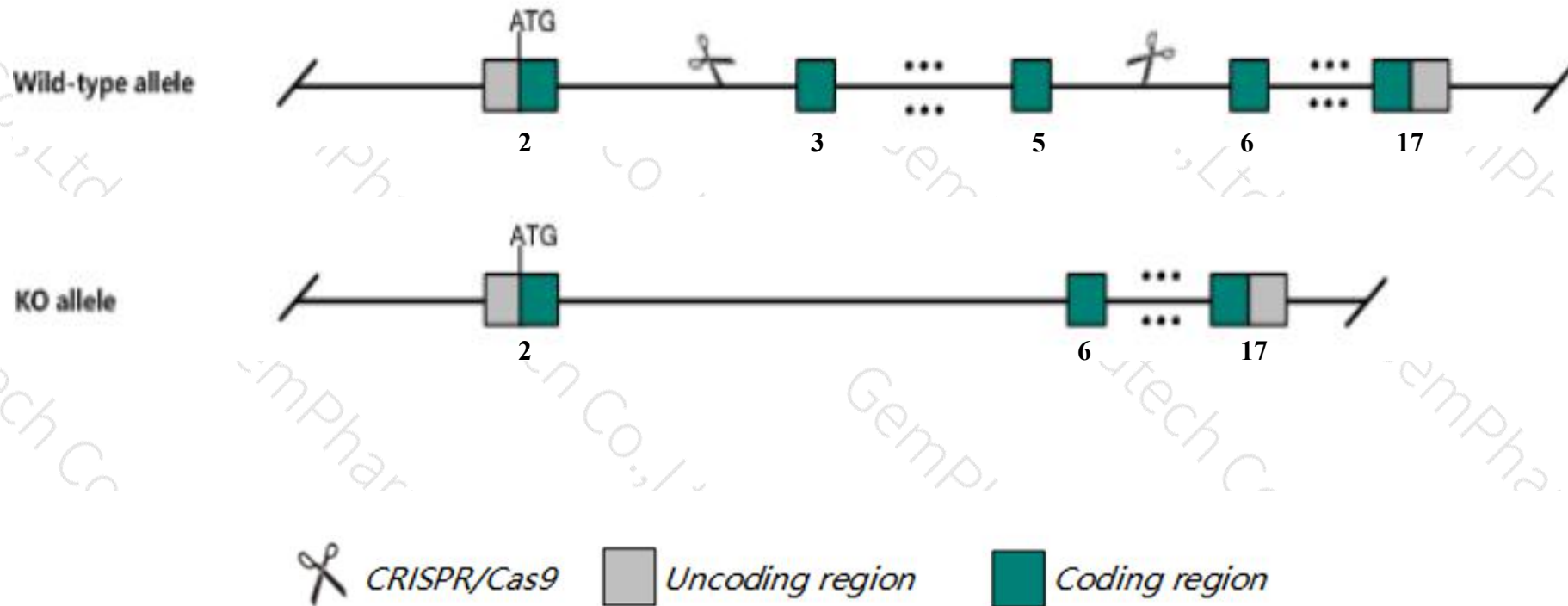
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Utp4* gene. The schematic diagram is as follows:



- The *Utp4* gene has 3 transcripts. According to the structure of *Utp4* gene, exon3-exon5 of *Utp4*-201(ENSMUST00000047629.6) transcript is recommended as the knockout region. The region contains 367bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Utp4* gene. The brief process is as follows: CRISPR/Cas9 system 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- The *Utp4* gene is located on the Chr8. 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)

Utp4 UTP4 small subunit processome component [Mus musculus (house mouse)]

Gene ID: 21771, updated on 13-Mar-2020

Summary



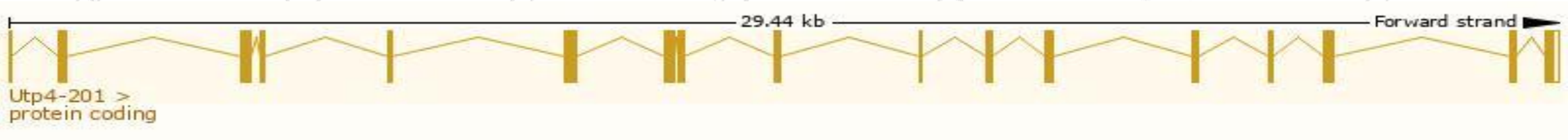
Official Symbol	Utp4 provided by MGI
Official Full Name	UTP4 small subunit processome component provided by MGI
Primary source	MGI:MGI:1096573
See related	Ensembl:ENSMUSG00000041438
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cirh1a, Cirhin, Naic, Teg-292, Tex292
Expression	Ubiquitous expression in liver E14.5 (RPKM 18.0), liver E14 (RPKM 17.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

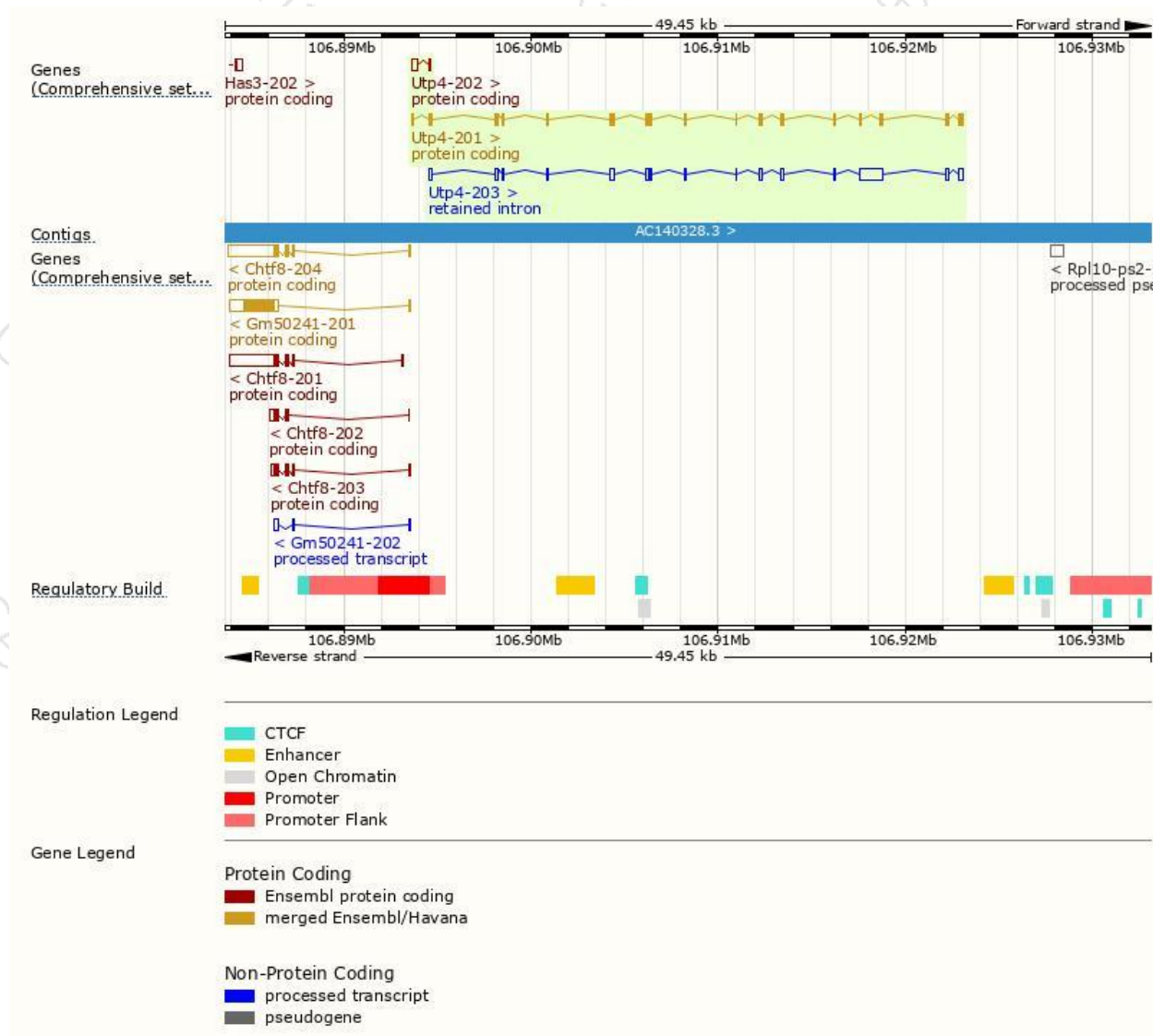
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Utp4-201	ENSMUST00000047629.6	2232	686aa	Protein coding	CCDS52664	Q8R2N2	TSL:1 GENCODE basic APPRIS P1
Utp4-202	ENSMUST00000212272.1	373	11aa	Protein coding	-	A0A1D5RLM4	CDS 3' incomplete TSL:2
Utp4-203	ENSMUST00000212718.1	3113	No protein	Retained intron	-	-	TSL:5

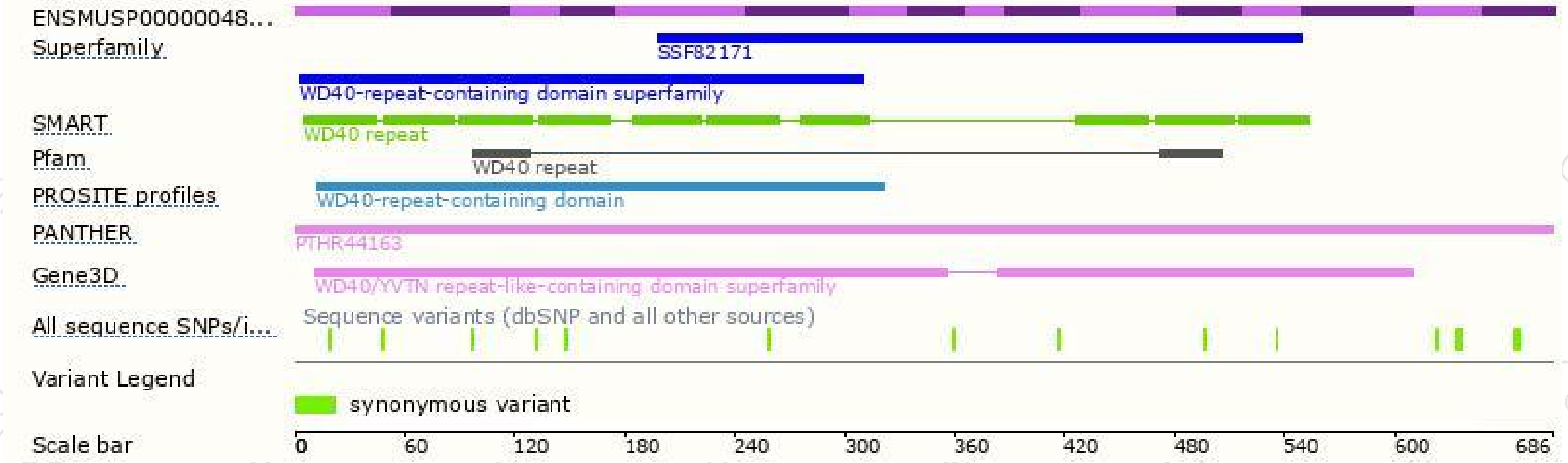
The strategy is based on the design of *Utp4-201* transcript,the transcription is shown below:



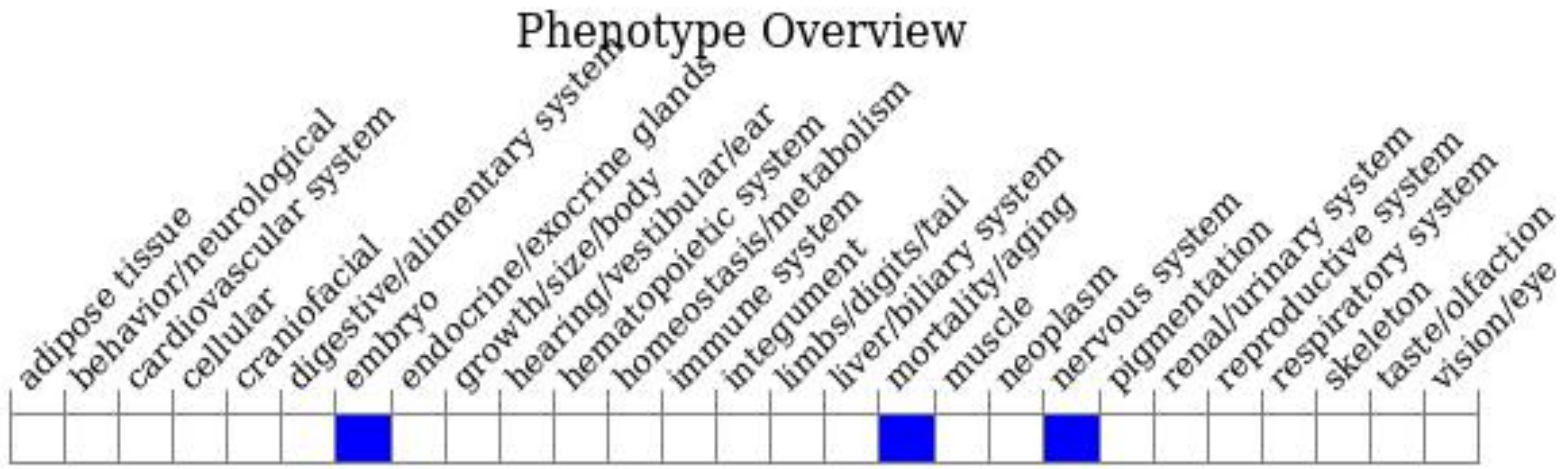
Genomic location distribution



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/>).

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

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