

***Taok1* Cas9-KO Strategy**

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Reviewer:

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Project Overview

Project Name

Taok1

Project type

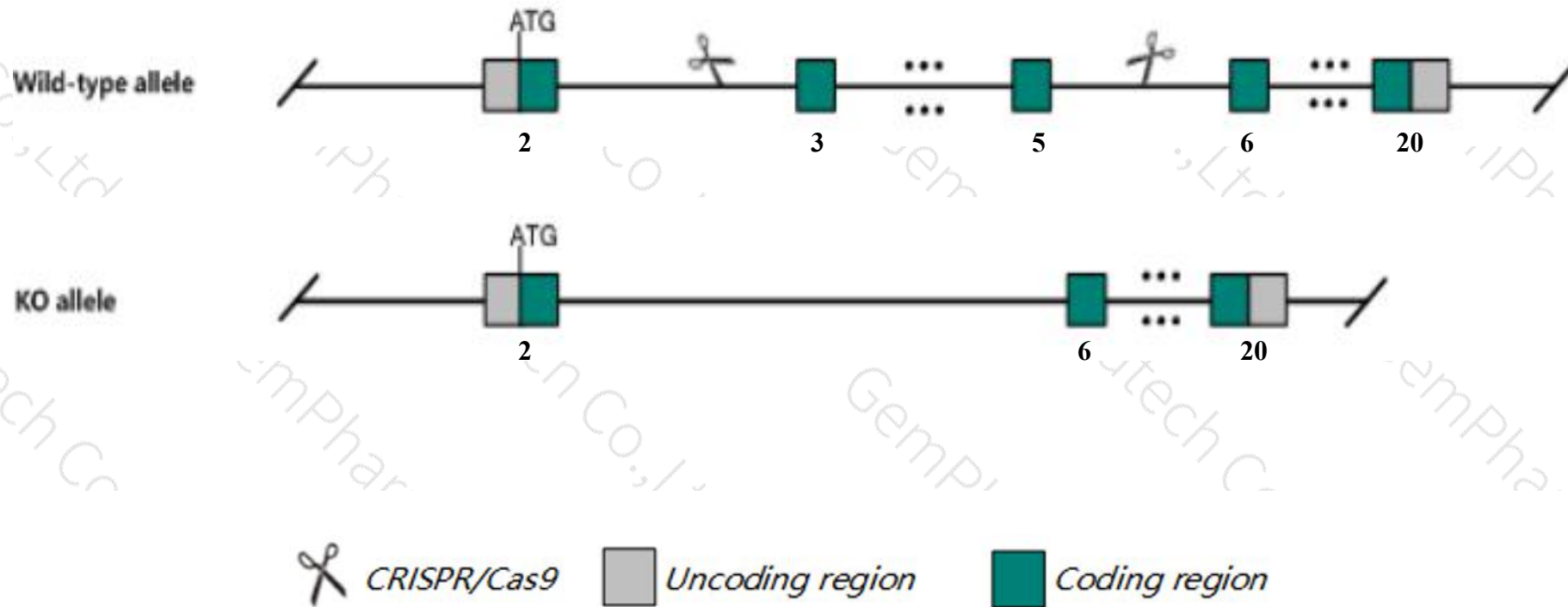
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Taok1* gene. The schematic diagram is as follows:



- The *Taok1* gene has 2 transcripts. According to the structure of *Taok1* gene, exon3-exon5 of *Taok1*-202 (ENSMUST00000058496.7) transcript is recommended as the knockout region. The region contains 220bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Taok1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Taok1* 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)

Taok1 TAO kinase 1 [Mus musculus (house mouse)]

Gene ID: 216965, updated on 13-Mar-2020

Summary



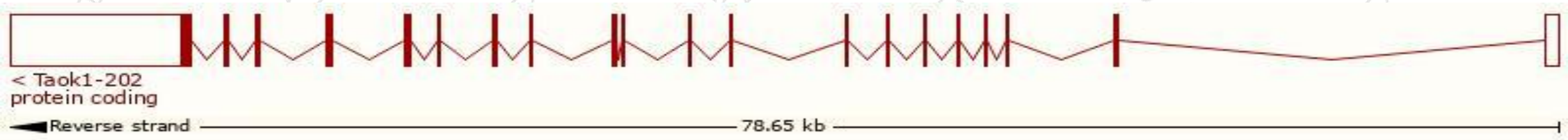
Official Symbol	Taok1 provided by MGI
Official Full Name	TAO kinase 1 provided by MGI
Primary source	MGI:MGI:1914490
See related	Ensembl:ENSMUSG00000017291
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2810468K05Rik, AU020252, D130018F14Rik, Map3k16, Markk, Psk2
Expression	Ubiquitous expression in CNS E18 (RPKM 7.8), frontal lobe adult (RPKM 7.6) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

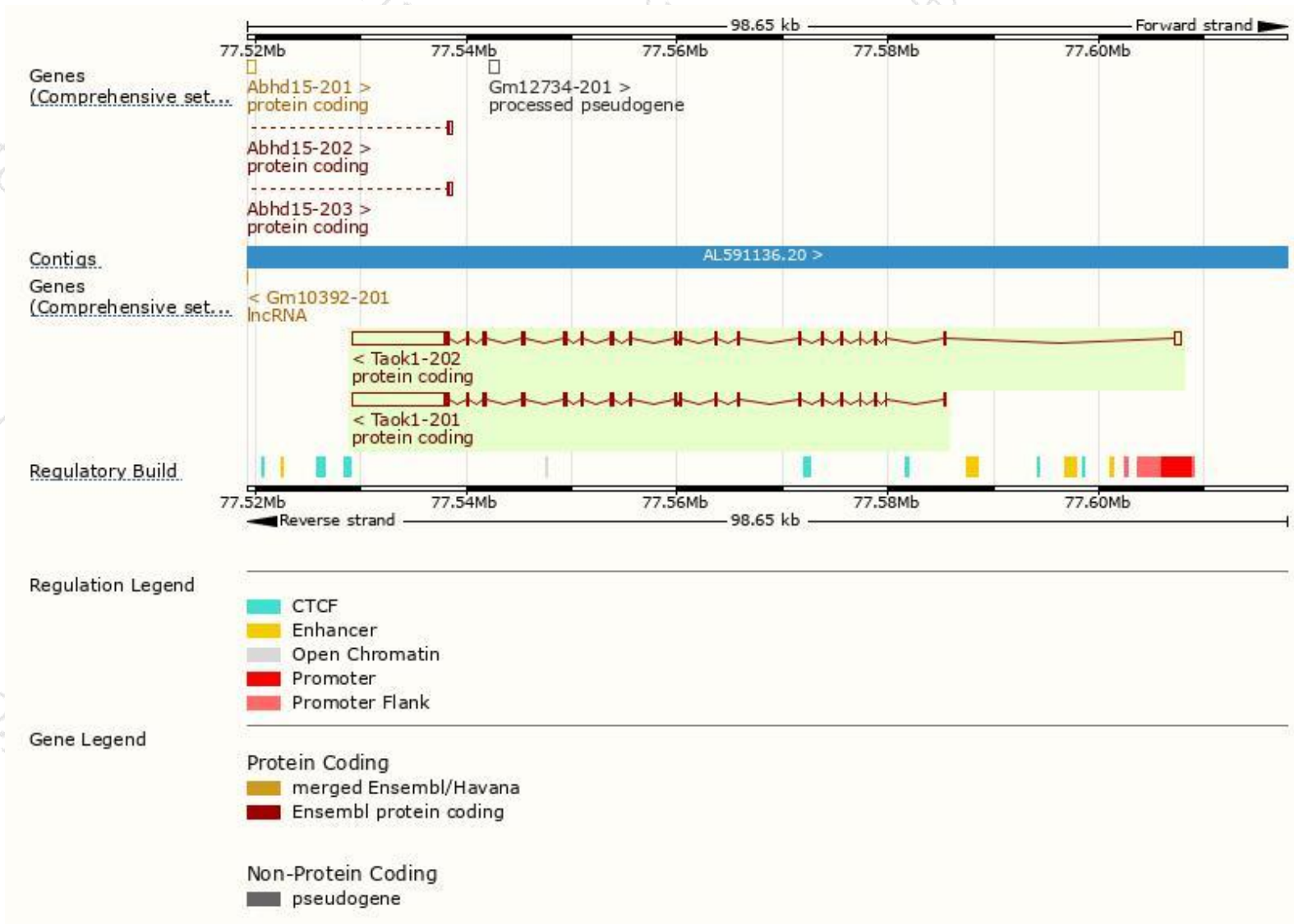
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Taok1-202	ENSMUST00000058496.7	12409	1001aa	Protein coding	CCDS36235	B2RX66_Q5F2E8	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Taok1-201	ENSMUST00000017435.10	11813	1001aa	Protein coding	CCDS36235	B2RX66_Q5F2E8	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

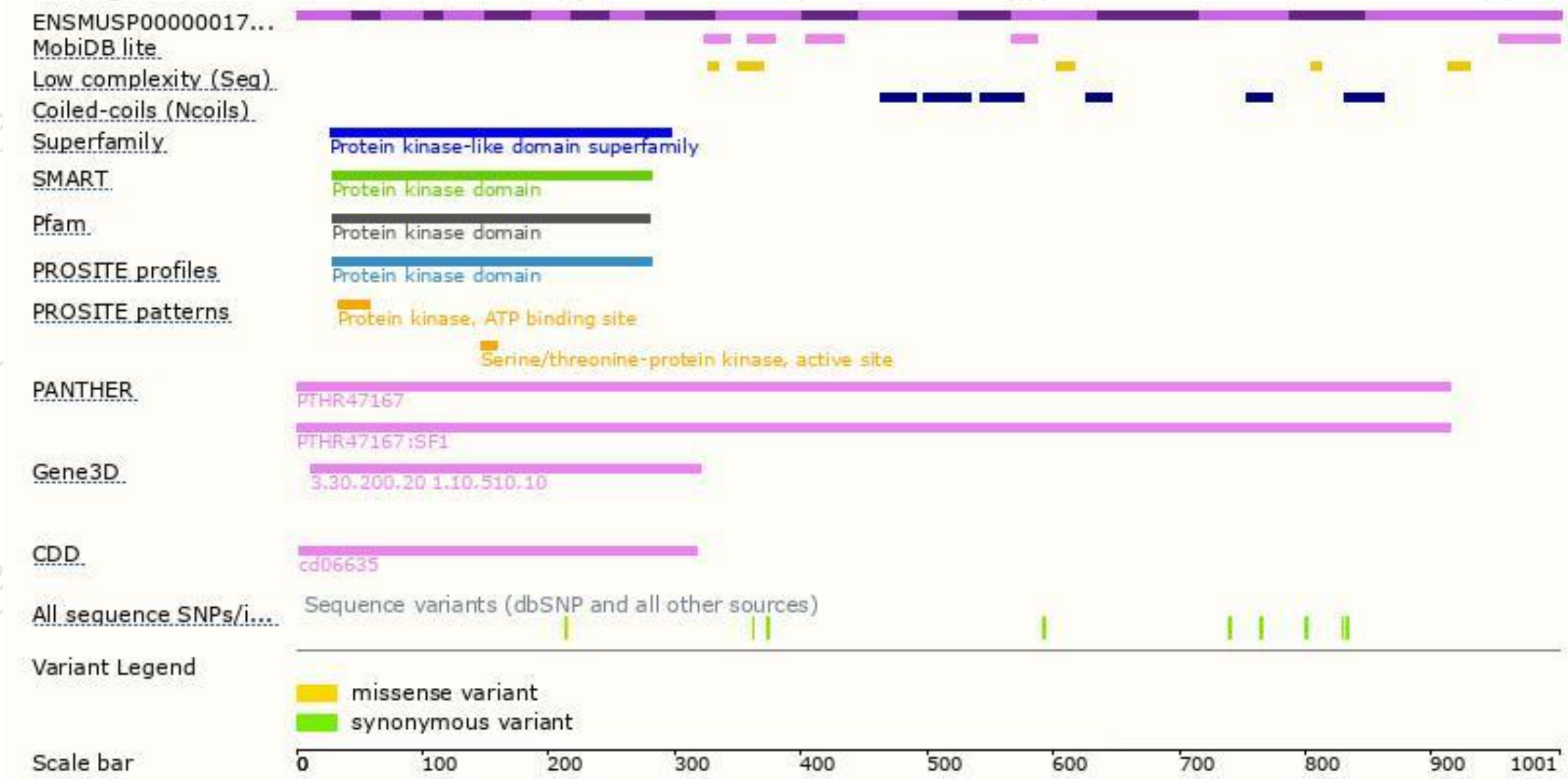
The strategy is based on the design of *Taok1-202* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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