

Otol1 Cas9-KO Strategy

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Project Overview

Project Name

Otol1

Project type

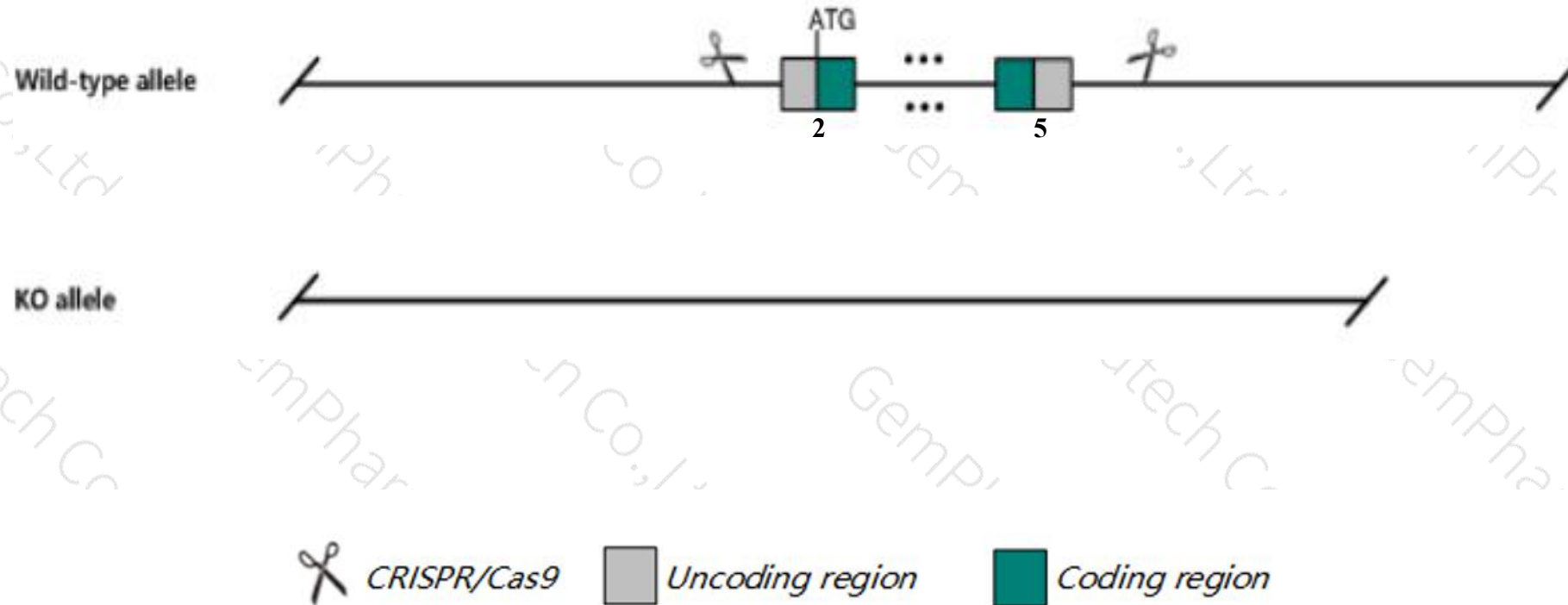
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Otol1* gene. The schematic diagram is as follows:



- The *Otol1* gene has 1 transcript. According to the structure of *Otol1* gene, exon2-exon5 of *Otol1-201* (ENSMUST00000053013.5) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Otol1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Otol1* gene is located on the Chr3. 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)

Otol1 otolin 1 [Mus musculus (house mouse)]

Gene ID: 229389, updated on 13-Mar-2020

Summary



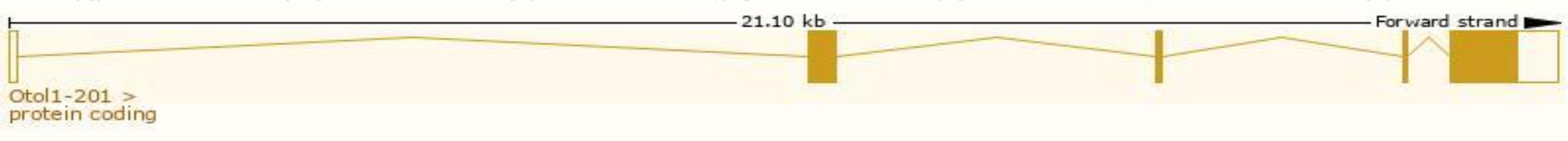
Official Symbol	Otol1 provided by MGI
Official Full Name	otolin 1 provided by MGI
Primary source	MGI:MGI:2685260
See related	Ensembl:ENSMUSG00000027788
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Gm414
Expression	Low expression observed in reference dataset See more
Orthologs	human all

Transcript information (Ensembl)

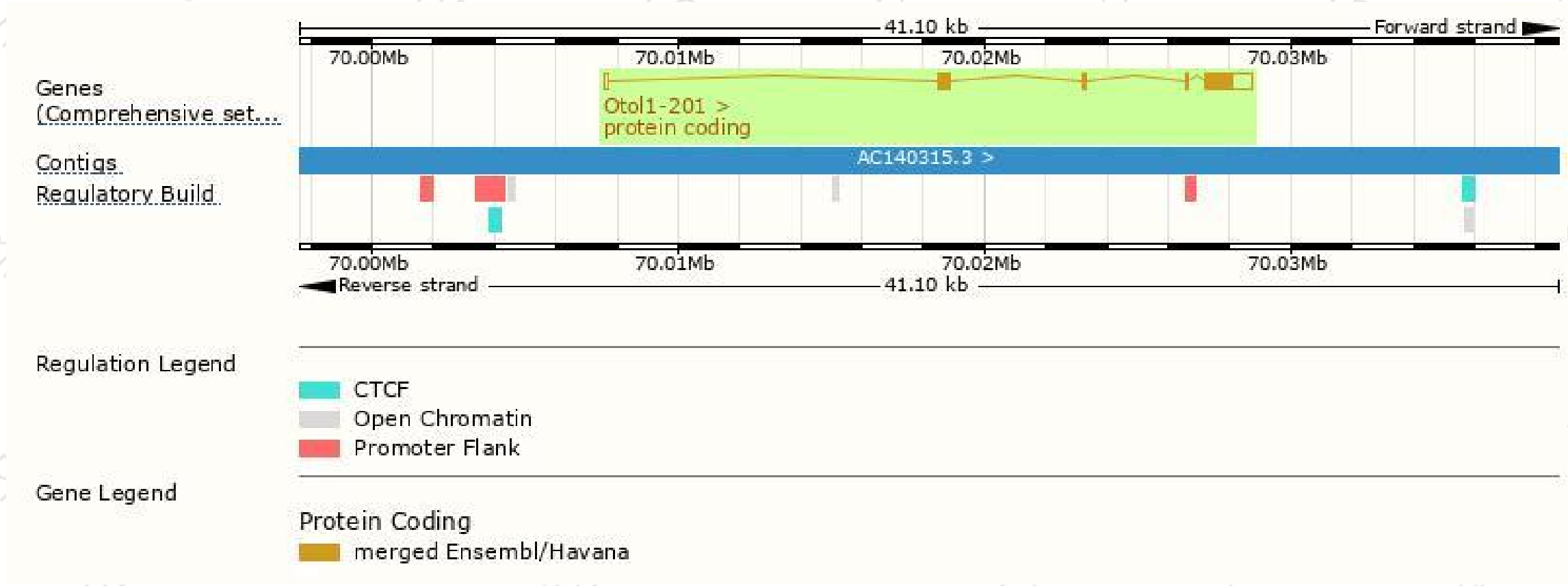
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Otol1-201	ENSMUST00000053013.5	2161	482aa	Protein coding	CCDS17409	Q4ZJM7	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

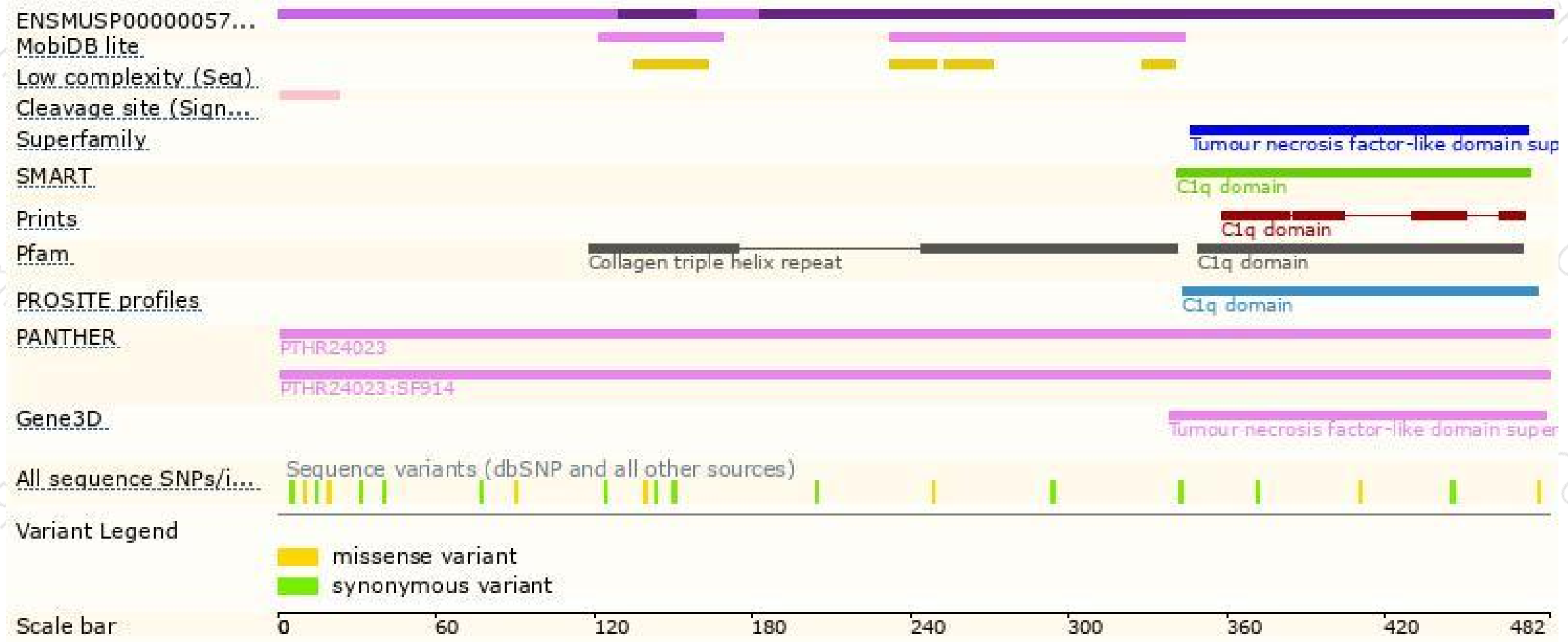
The strategy is based on the design of *Otol1-201* transcript, the transcription is shown below:



Genomic location distribution



Protein domain



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

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