

Cwf19l1 Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

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Project Overview

Project Name

Cwf19l1

Project type

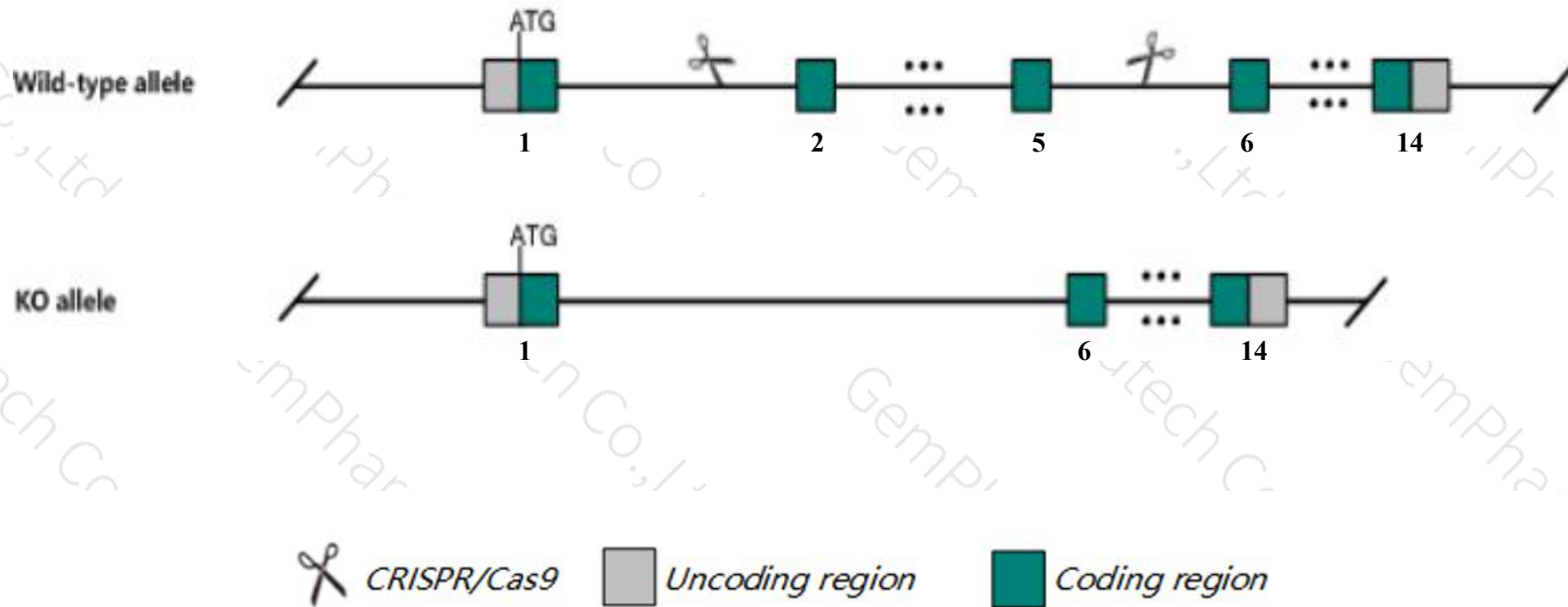
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cwf19l1* gene. The schematic diagram is as follows:



- The *Cwf1911* gene has 8 transcripts. According to the structure of *Cwf1911* gene, exon2-exon5 of *Cwf1911-201* (ENSMUST00000026218.6) transcript is recommended as the knockout region. The region contains 481bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cwf1911* gene. The brief process is as follows: CRISPR/Cas9 system

- Transcript *Cwf1911*-202&206 may not be affected.
- The *Cwf1911* gene is located on the Chr19. 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)

Cwf19l1 CWF19-like 1, cell cycle control (S. pombe) [Mus musculus (house mouse)]

Gene ID: 72502, updated on 20-Mar-2020

Summary



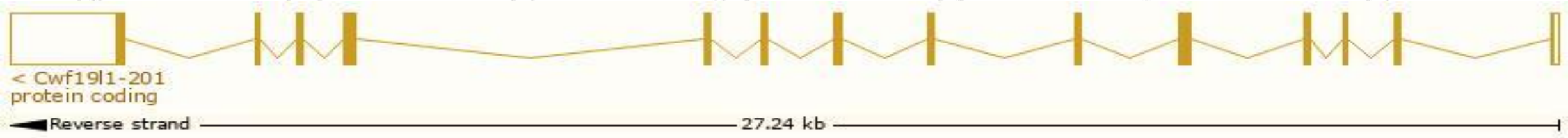
Official Symbol	Cwf19l1 provided by MGI
Official Full Name	CWF19-like 1, cell cycle control (S. pombe) provided by MGI
Primary source	MGI:MGI:1919752
See related	Ensembl:ENSMUSG000000025200
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Ubiquitous expression in CNS E14 (RPKM 3.0), CNS E18 (RPKM 3.0) and 26 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

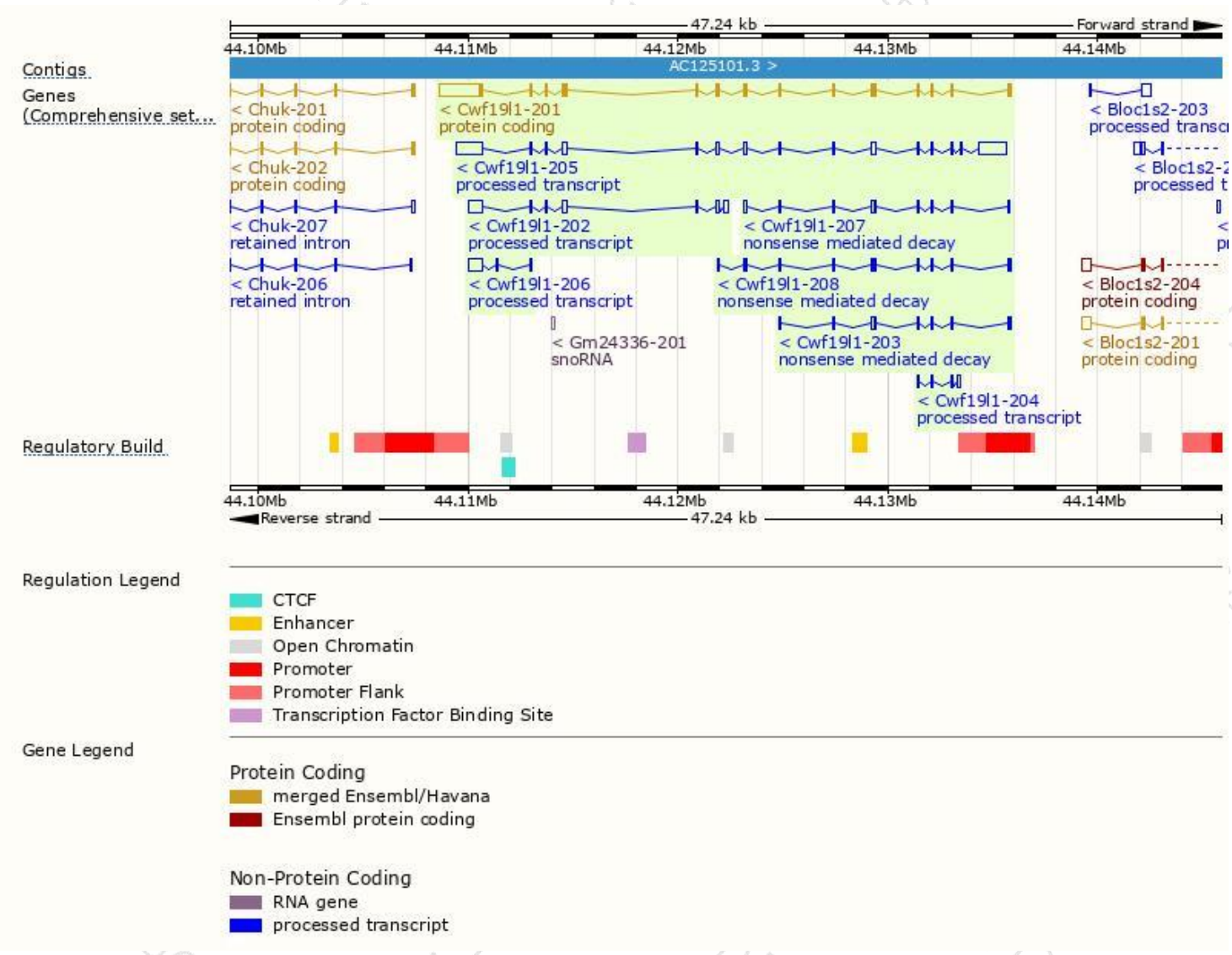
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cwf19l1-201	ENSMUST00000026218.6	3581	537aa	Protein coding	CCDS37995	Q8CI33	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
Cwf19l1-208	ENSMUST00000237939.1	963	296aa	Nonsense mediated decay	-	A0A494B9Q5	CDS 3' incomplete
Cwf19l1-207	ENSMUST00000237415.1	794	113aa	Nonsense mediated decay	-	A0A494BBD4	
Cwf19l1-203	ENSMUST00000236156.1	764	113aa	Nonsense mediated decay	-	A0A494BBD4	
Cwf19l1-205	ENSMUST00000237067.1	4068	No protein	Processed transcript	-	-	
Cwf19l1-202	ENSMUST00000235288.1	1470	No protein	Processed transcript	-	-	
Cwf19l1-206	ENSMUST00000237250.1	771	No protein	Processed transcript	-	-	
Cwf19l1-204	ENSMUST00000236626.1	467	No protein	Processed transcript	-	-	

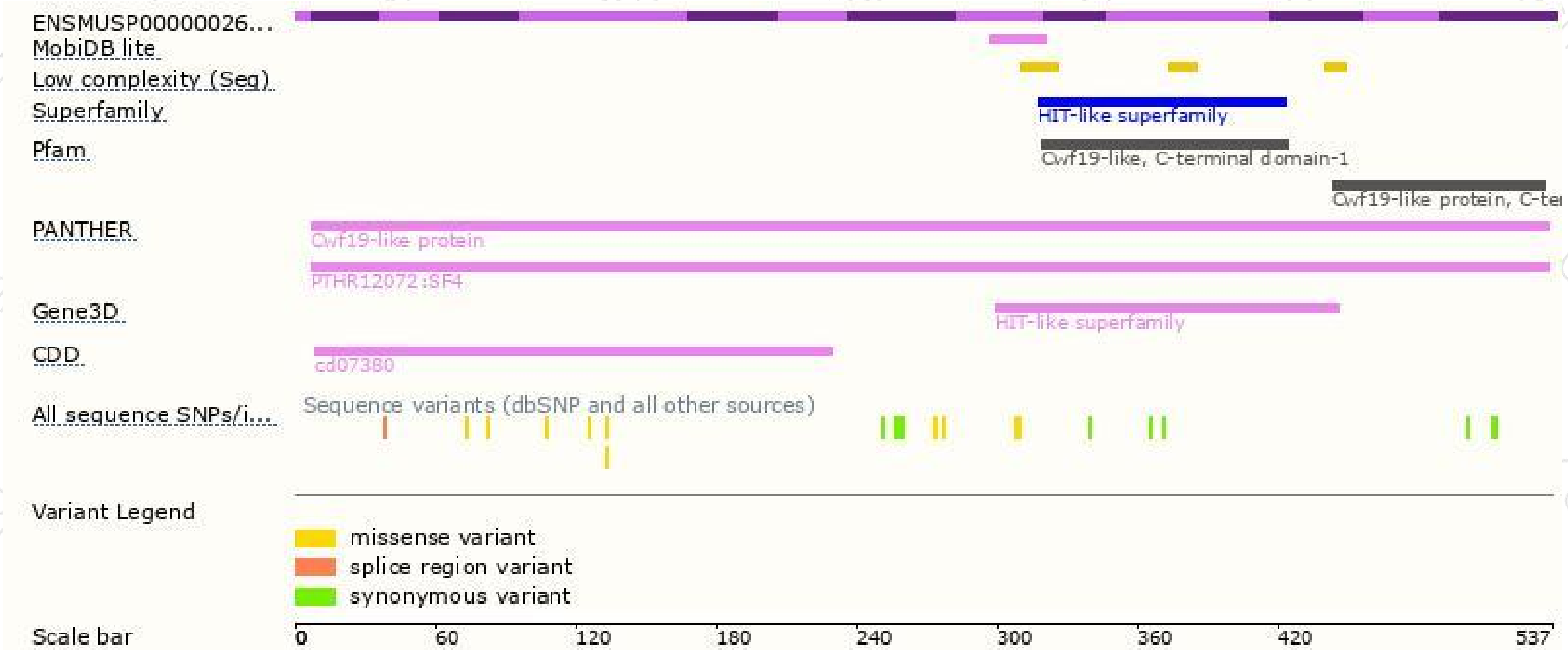
The strategy is based on the design of *Cwf19l1-201* transcript,the transcription is shown below



Genomic location distribution



Protein domain



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

Tel: 400-9660890

