

Ehd2 Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

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Project Overview

Project Name

Ehd2

Project type

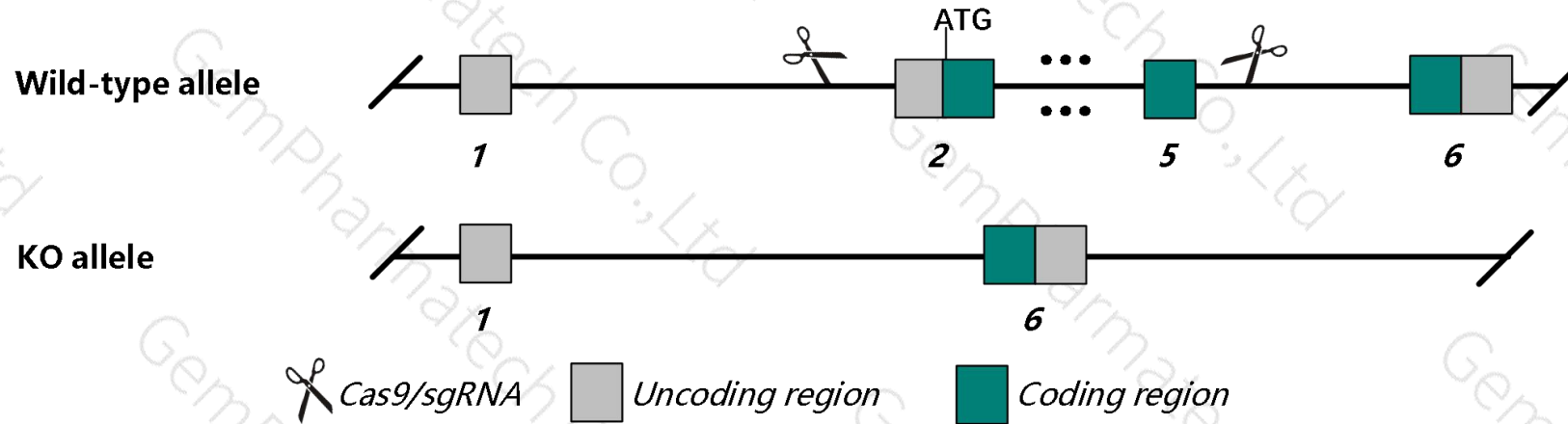
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ehd2* gene. The schematic diagram is as follows:



- The *Ehd2* gene has 2 transcripts. According to the structure of *Ehd2* gene, exon2-exon5 of *Ehd2-201* (ENSMUST00000098799.4) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ehd2* gene. The brief process is as follows: CRISPR/Cas9 system v

- The knockout region is near to the N-terminal of *Nop53* gene and *Gm28948* gene, this strategy may influence the regulatory function of the N-terminal of these genes.
- The *Ehd2* gene is located on the Chr7. 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)

Ehd2 EH-domain containing 2 [*Mus musculus* (house mouse)]

Gene ID: 259300, updated on 17-Dec-2019

Summary

Official Symbol	Ehd2 provided by MGI
Official Full Name	EH-domain containing 2 provided by MGI
Primary source	MGI:MGI:2154274
See related	Ensembl:ENSMUSG00000074364
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BC027084; C130052H20Rik
Expression	Biased expression in subcutaneous fat pad adult (RPKM 159.7), genital fat pad adult (RPKM 103.2) and 13 other tissues See more
Orthologs	human all

Genomic context

Location: 7 A2; 7 8.65 cM

See Ehd2 in [Genome Data Viewer](#)

Exon count: 6

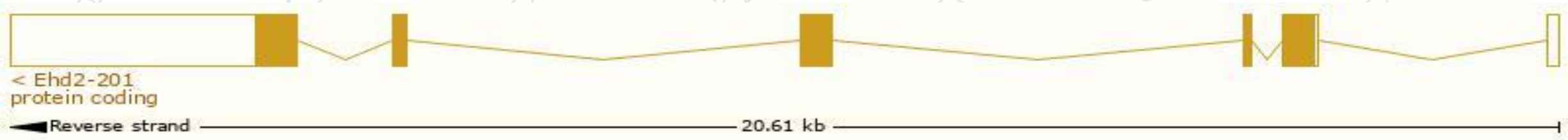
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (15946963..15967535, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (16534336..16552884, complement)

Transcript information (Ensembl)

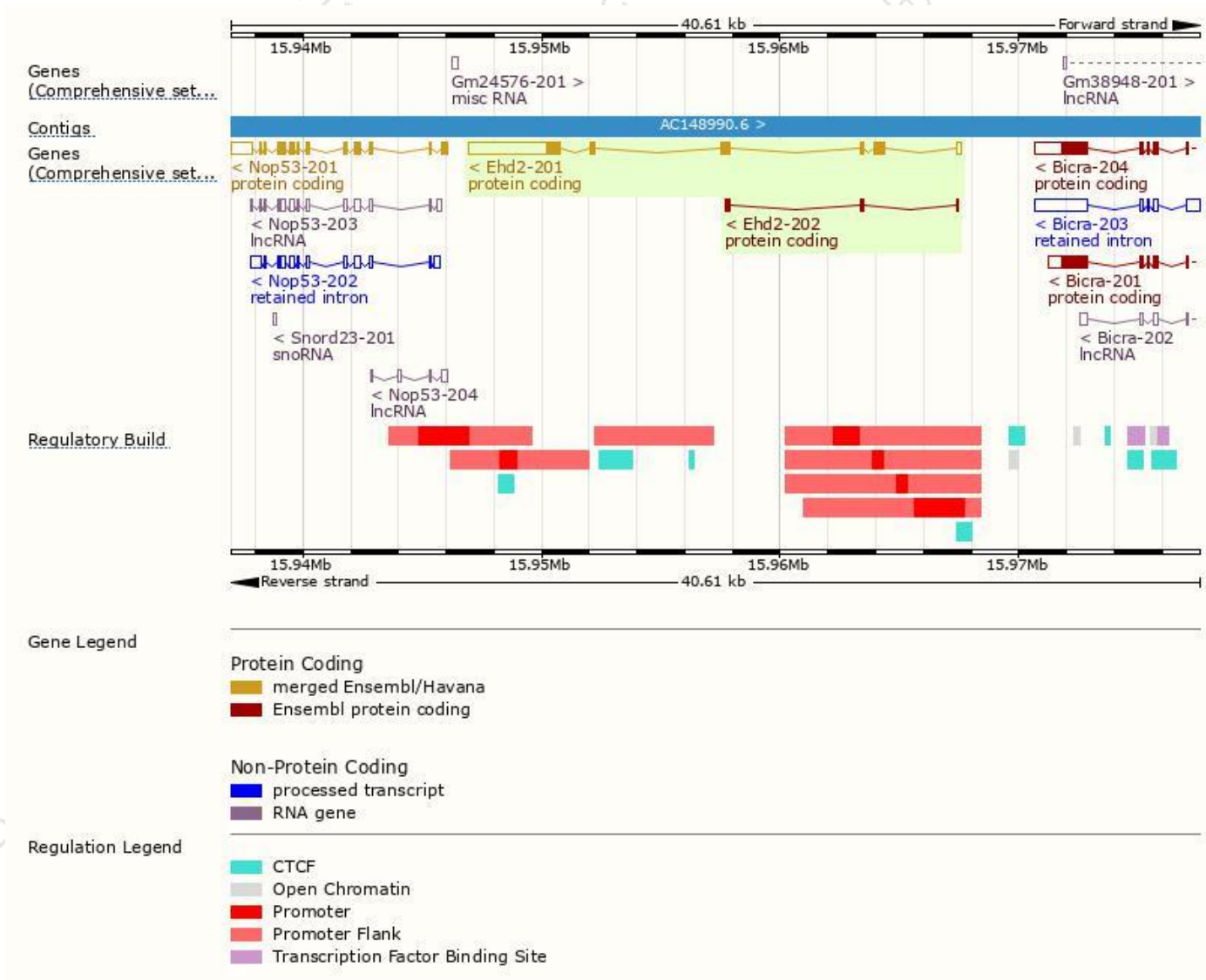
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ehd2-201	ENSMUST00000098799.4	5119	543aa	Protein coding	CCDS20842	Q8BH64	TSL:1 GENCODE basic APPRIS P1
Ehd2-202	ENSMUST00000144956.1	375	105aa	Protein coding	-	D3Z7U7	CDS 3' incomplete TSL:2

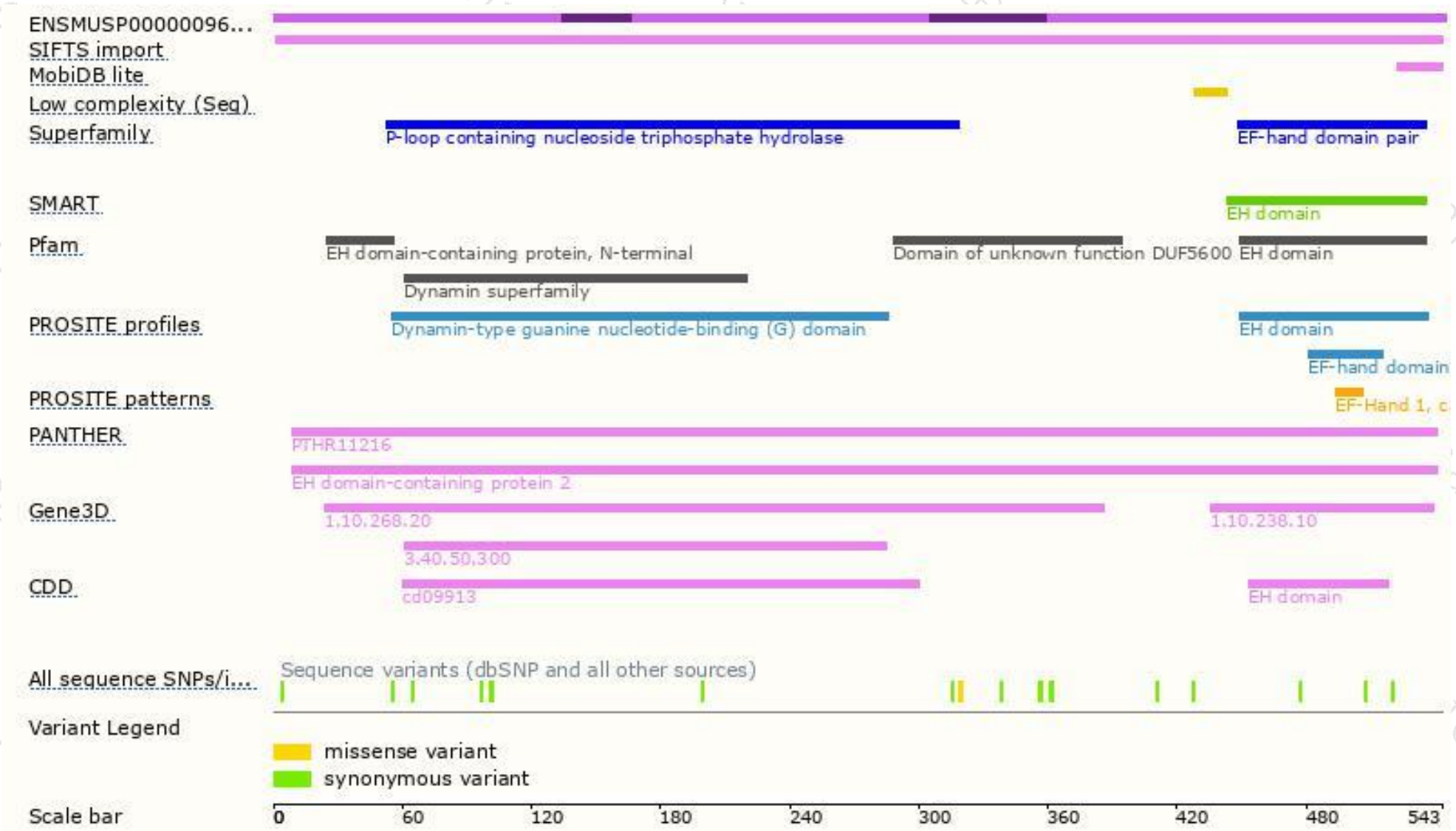
The strategy is based on the design of *Ehd2-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

Tel: 400-9660890

