

Abhd2 Cas9-KO Strategy

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Project Overview

Project Name

Abhd2

Project type

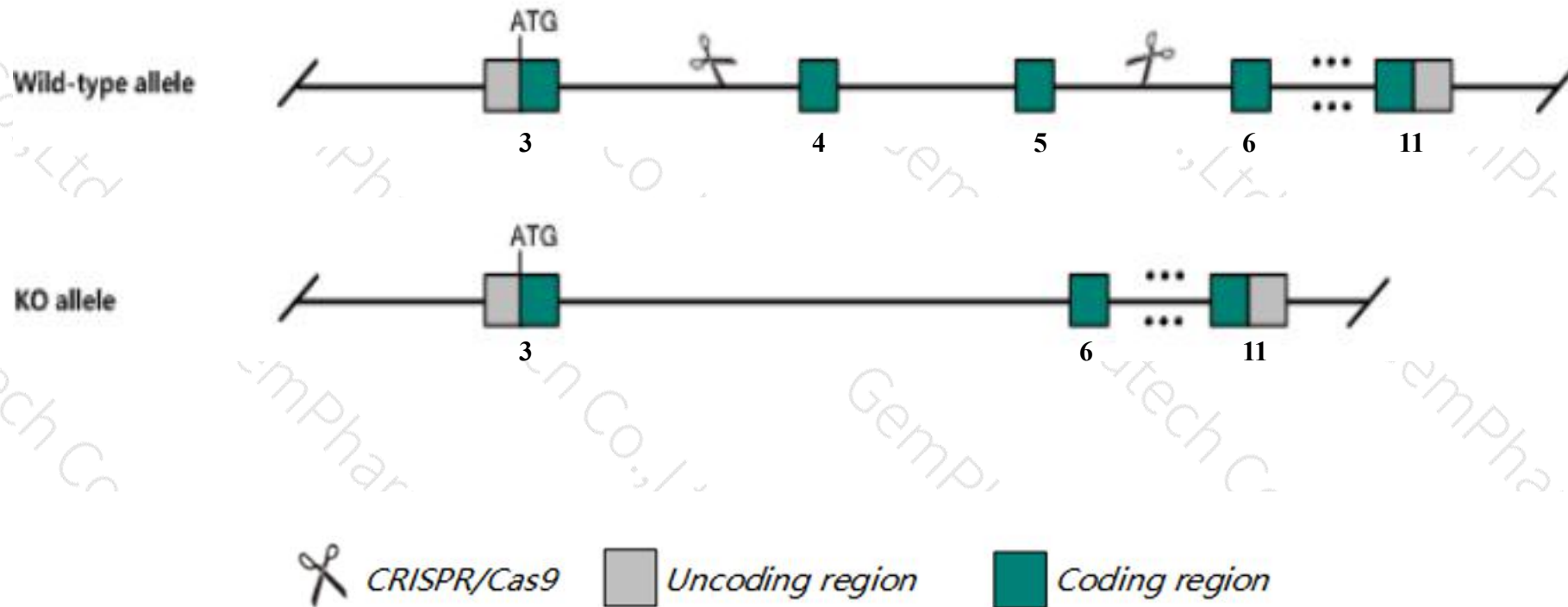
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abhd2* gene. The schematic diagram is as follows:



- The *Abhd2* gene has 2 transcripts. According to the structure of *Abhd2* gene, exon4-exon5 of *Abhd2-201* (ENSMUST00000037315.12) transcript is recommended as the knockout region. The region contains 344bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Abhd2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a gene trapped allele are overtly normal but exhibit enhanced migratory ability of cultured smooth muscle cells, and significant intimal hyperplasia after cuff placement.
- The *Abhd2* 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)

Abhd2 abhydrolase domain containing 2 [Mus musculus (house mouse)]

Gene ID: 54608, updated on 13-Mar-2020

Summary



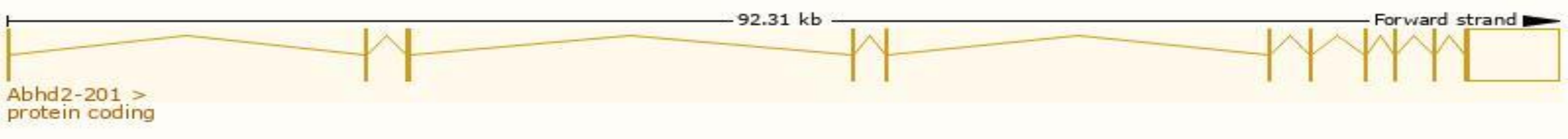
Official Symbol	Abhd2 provided by MGI
Official Full Name	abhydrolase domain containing 2 provided by MGI
Primary source	MGI:MGI:1914344
See related	Ensembl:ENSMUSG00000039202
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2210009N18Rik, LABH2, Labh-2
Expression	Broad expression in genital fat pad adult (RPKM 82.7), adrenal adult (RPKM 56.2) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

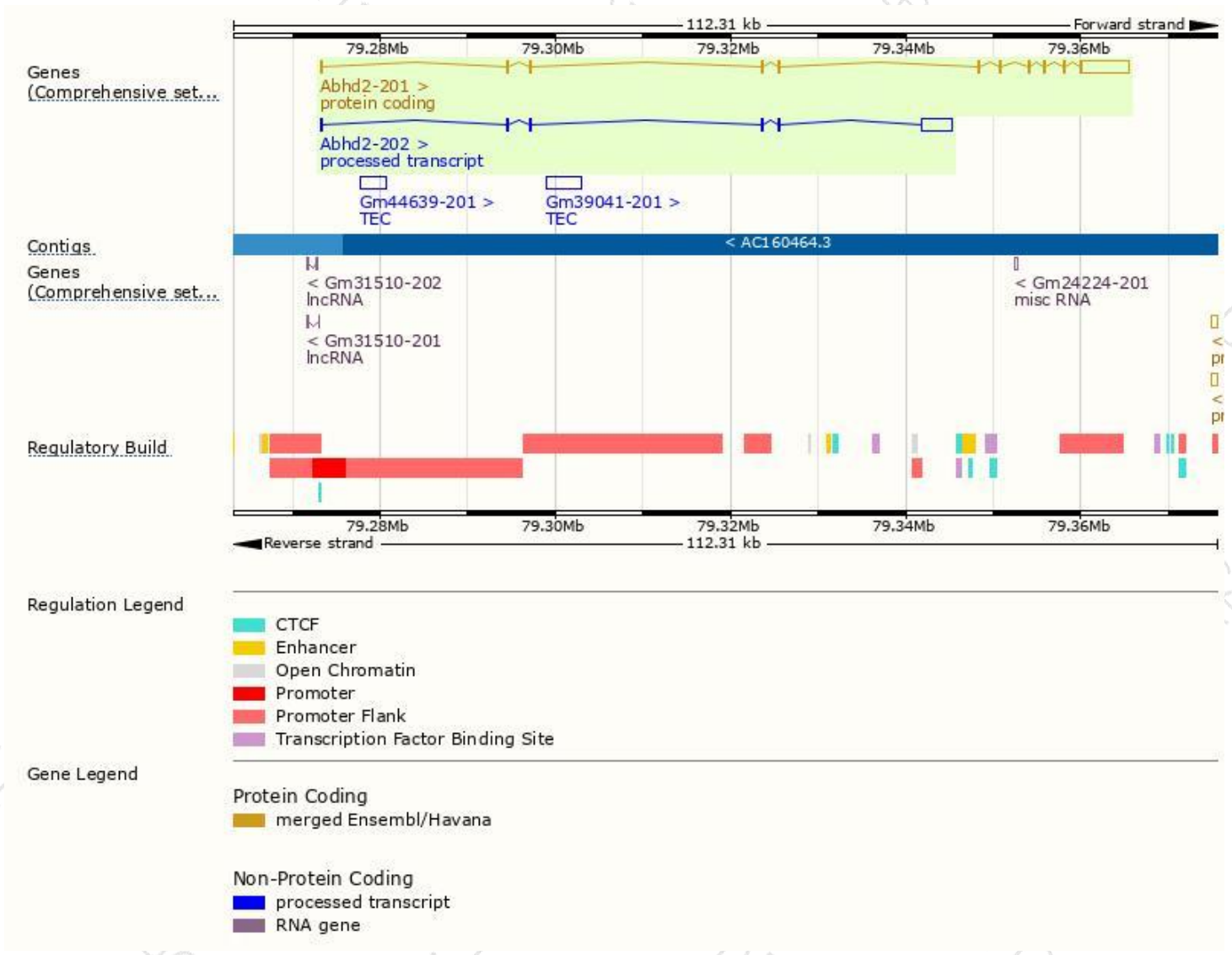
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abhd2-201	ENSMUST00000037315.12	6877	425aa	Protein coding	CCDS21380	Q9QXM0	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
Abhd2-202	ENSMUST00000135333.2	4426	No protein	Processed transcript	-	-	TSL:1

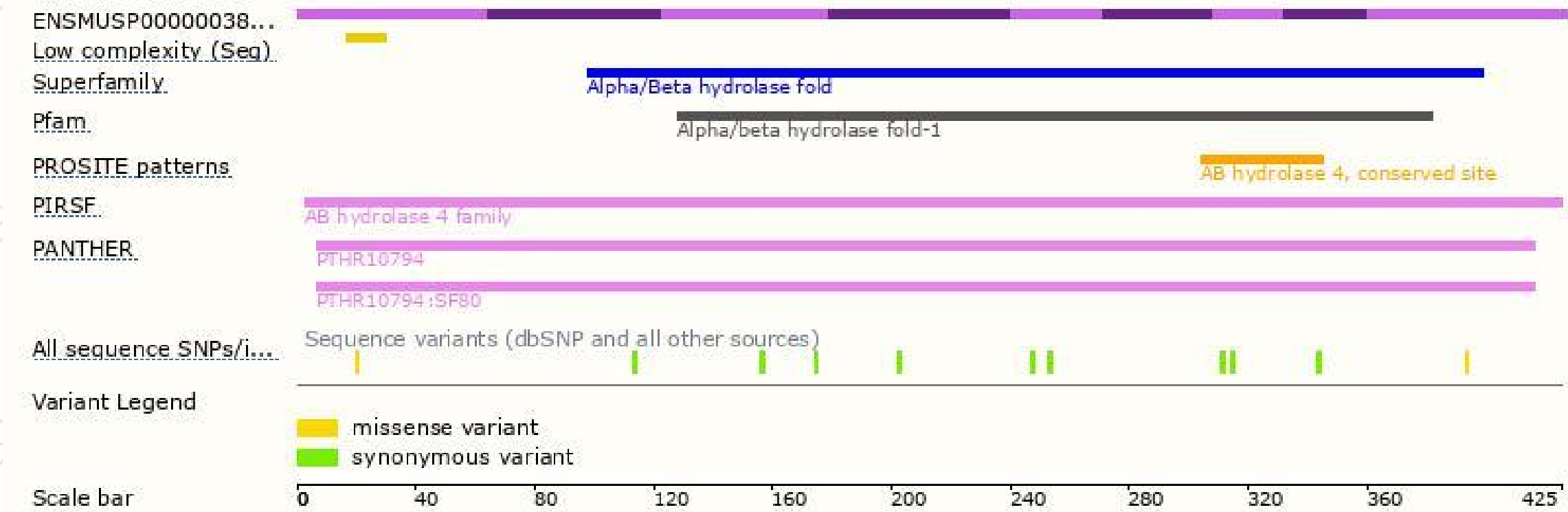
The strategy is based on the design of *Abhd2-201* transcript,the transcription is shown below:



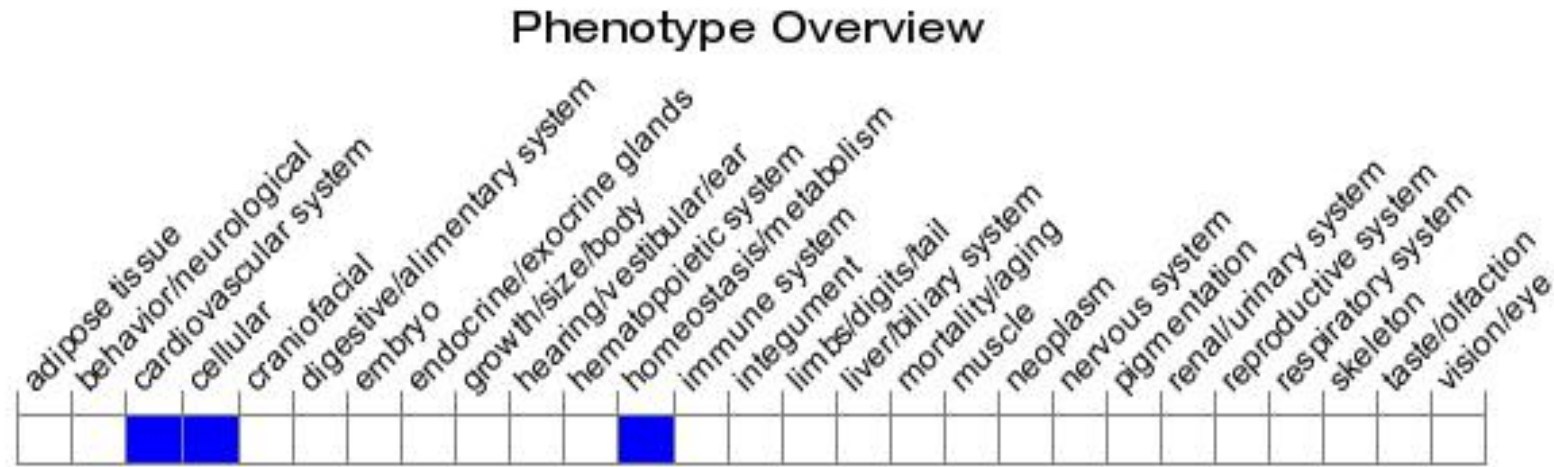
Genomic location distribution



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/>).

According to the existing MGI data, mice homozygous for a gene trapped allele are overtly normal but exhibit enhanced migratory ability of cultured smooth muscle cells, and significant intimal hyperplasia after cuff placement.

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

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