Abhd10 Cas9-KO Strategy

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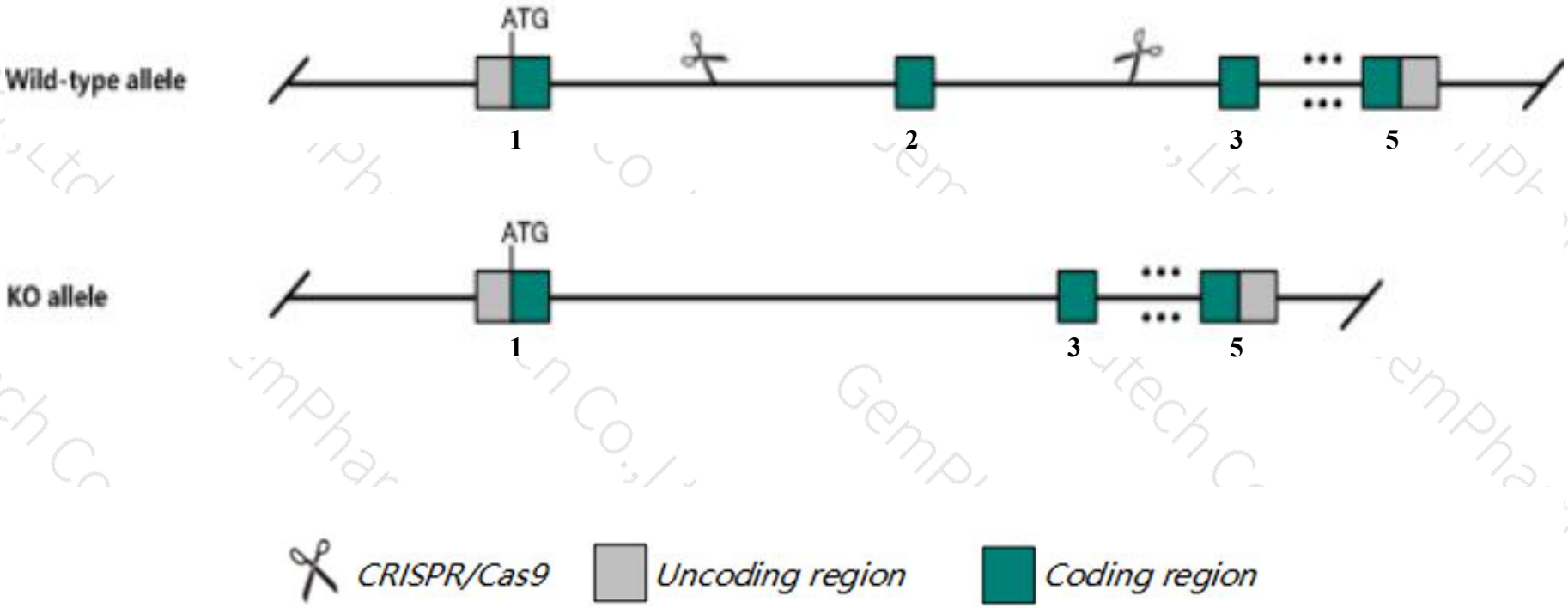
Date:2020-03-11

Project Overview

Project Name	***Abhd10***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abhd10* gene. The schematic diagram is as follows:



Technical routes

➢ The *Abhd10* gene has 5 transcripts. According to the structure of *Abhd10* gene, exon2 of *Abhd10-201* (ENSMUST00000066983.12) transcript is recommended as the knockout region.The region contains 184bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Abhd10* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ The *Abhd10* gene is located on the Chr16. 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）

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Abhd10 abhydrolase domain containing 10 [*Mus musculus* (house mouse)]

Gene ID: 213012, updated on 8-Mar-2020

Summary

Official Symbol	Abhd10 provided by MGI
Official Full Name	abhydrolase domain containing 10 provided by MGI
Primary source	MGI:MGI:2442422
See related	Ensembl:ENSMUSG00000033157
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Summary	This gene encodes a mitochondrially-localized enzyme that acts as a hydrolase. The encoded protein removes glucuronide from mycophenolic acid acyl-glucuronide. There are two pseudogenes for this gene on chromosome 8. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jan 2013]
Expression	Ubiquitous expression in cerebellum adult (RPKM 7.3), CNS E18 (RPKM 7.3) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 16; 16 B5

See Abhd10 in Genome Data Viewer

Exon count: 7

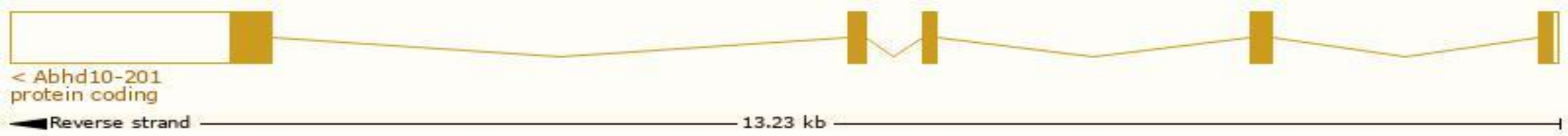
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	16	NC_000082.6 (45729720..45746137, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	16	NC_000082.5 (45730510..45743019, complement)

Transcript information（Ensembl）

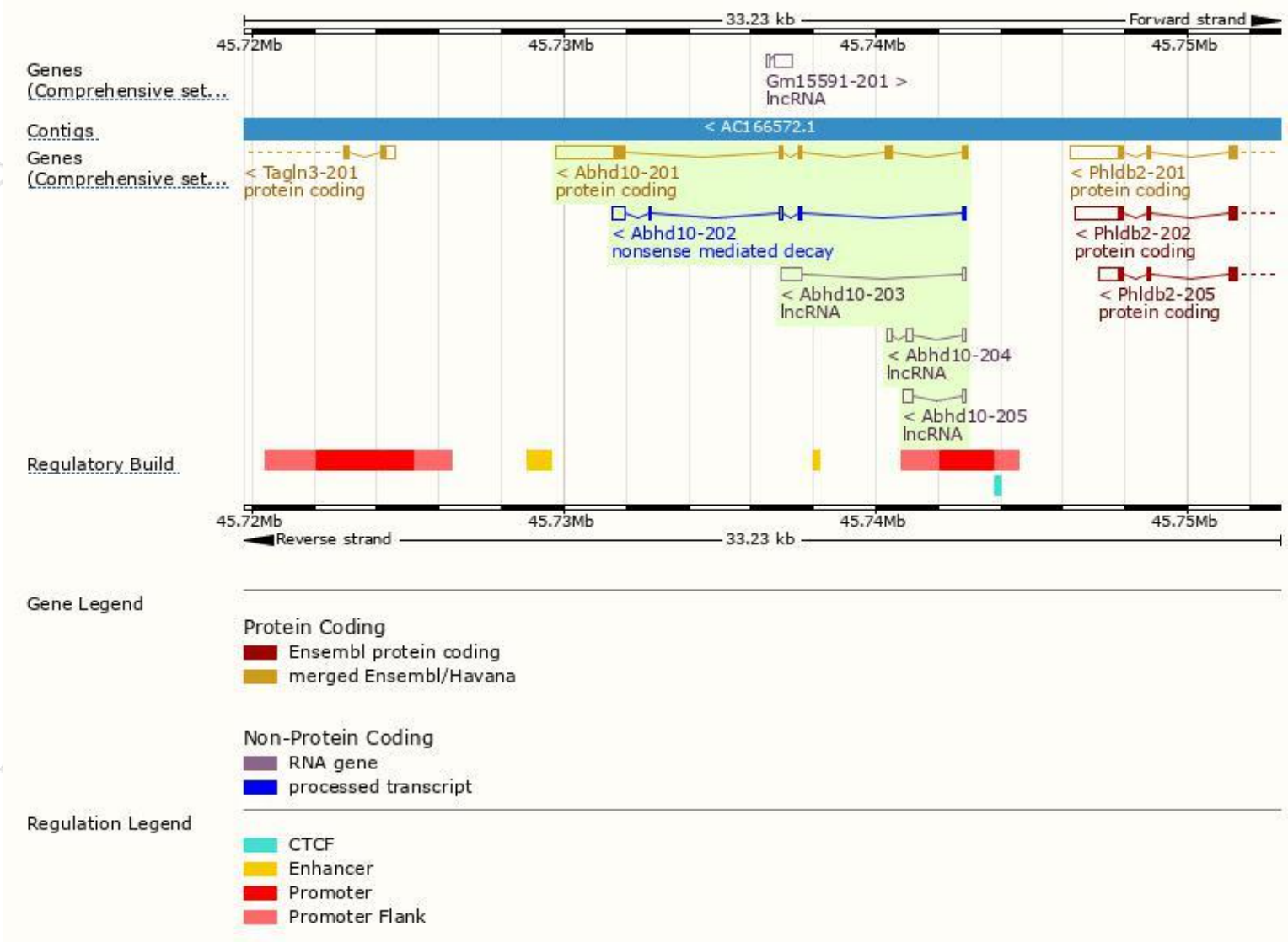
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abhd10-201	ENSMUST00000066983.12	2848	297aa	Protein coding	CCDS28201	Q6PE15	TSL:1 GENCODE basic APPRIS P1
Abhd10-202	ENSMUST00000128348.2	827	51aa	Nonsense mediated decay	-	F6X5P5	TSL:2
Abhd10-203	ENSMUST00000138517.1	771	No protein	lncRNA	-	-	TSL:3
Abhd10-204	ENSMUST00000143731.1	484	No protein	lncRNA	-	-	TSL:3
Abhd10-205	ENSMUST00000155741.1	451	No protein	lncRNA	-	-	TSL:2

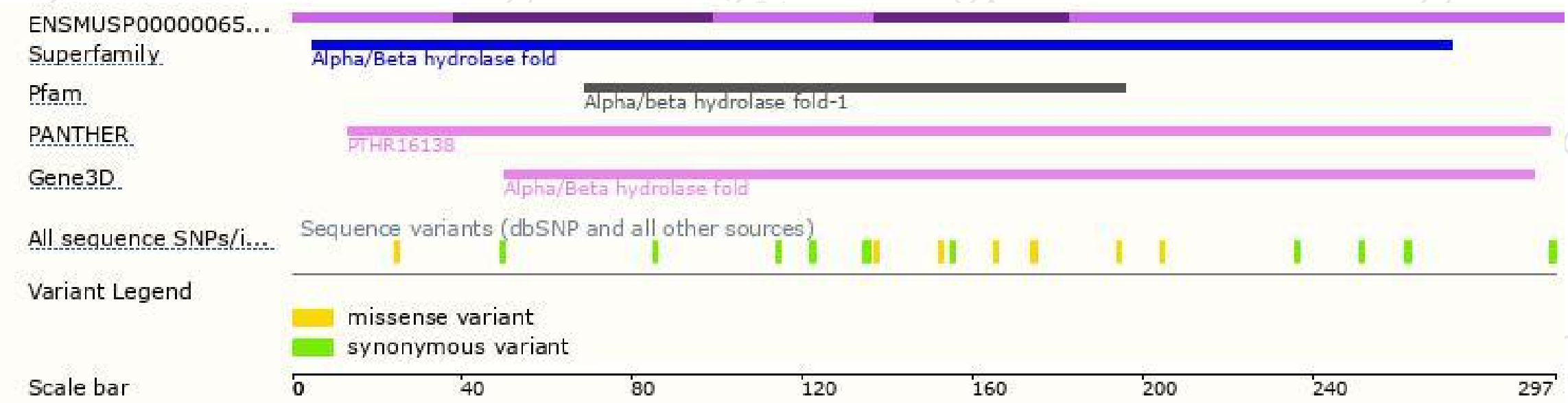
The strategy is based on the design of *Abhd10-201* transcript,The transcription is shown below



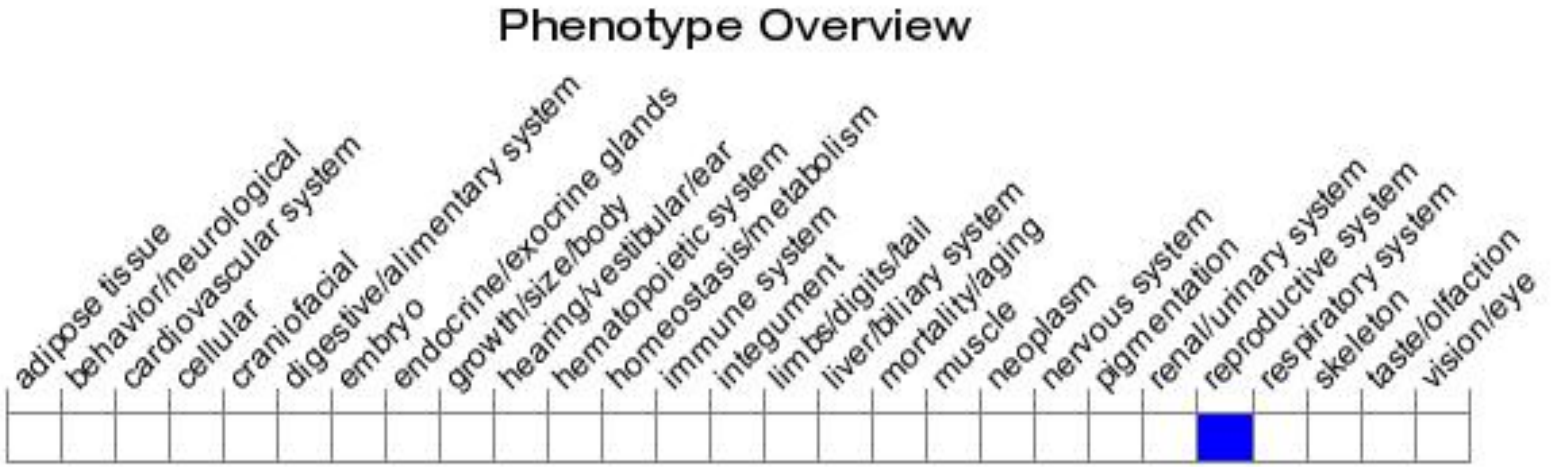
Genomic location distribution



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/).

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

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