

Ap4b1 Cas9-KO Strategy

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Reviewer:

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Design Date:

2020-4-8

Project Overview

Project Name

Ap4b1

Project type

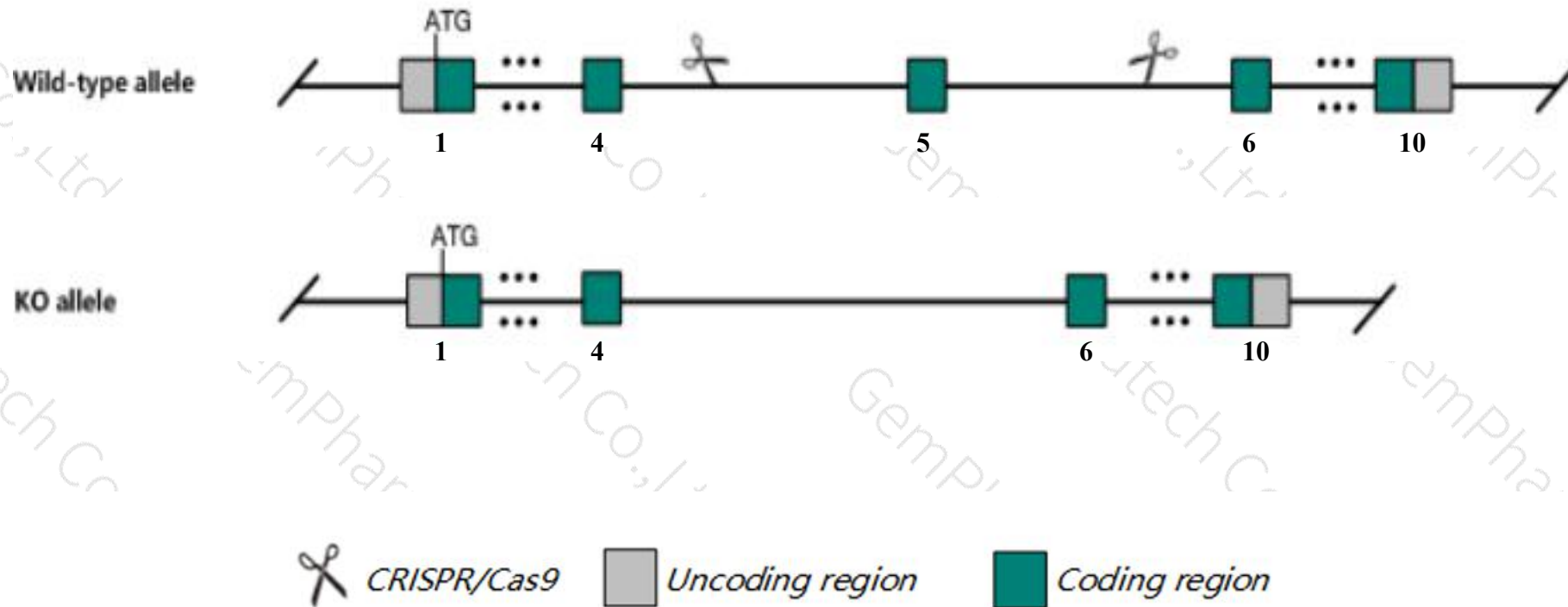
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ap4b1* gene. The schematic diagram is as follows:



- The *Ap4b1* gene has 7 transcripts. According to the structure of *Ap4b1* gene, exon5 of *Ap4b1-201* (ENSMUST00000047285.6) transcript is recommended as the knockout region. The region contains 497bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ap4b1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a null allele exhibit poor rotarod performance.
- The *Ap4b1* 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)

Ap4b1 adaptor-related protein complex AP-4, beta 1 [*Mus musculus* (house mouse)]

Gene ID: 67489, updated on 31-Mar-2020

Summary

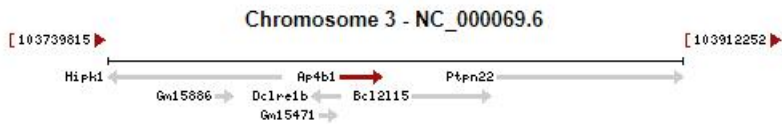
- Official Symbol** Ap4b1 provided by [MGI](#)
- Official Full Name** adaptor-related protein complex AP-4, beta 1 provided by [MGI](#)
- Primary source** [MGI:MGI:1337130](#)
- See related** [Ensembl:ENSMUSG00000032952](#)
- Gene type** protein coding
- RefSeq status** VALIDATED
- Organism** [Mus musculus](#)
- Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
- Also known as** Ap4b4; AV004952; 1810038H16Rik
- Expression** Ubiquitous expression in testis adult (RPKM 13.7), limb E14.5 (RPKM 8.1) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 3; 3 F2.2 [See Ap4b1 in Genome Data Viewer](#)

Exon count: 11

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	3	NC_000069.6 (103809511..103822025)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	3	NC_000069.5 (103613440..103625948)

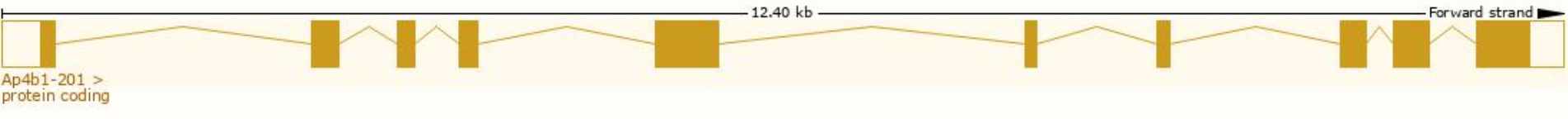


Transcript information (Ensembl)

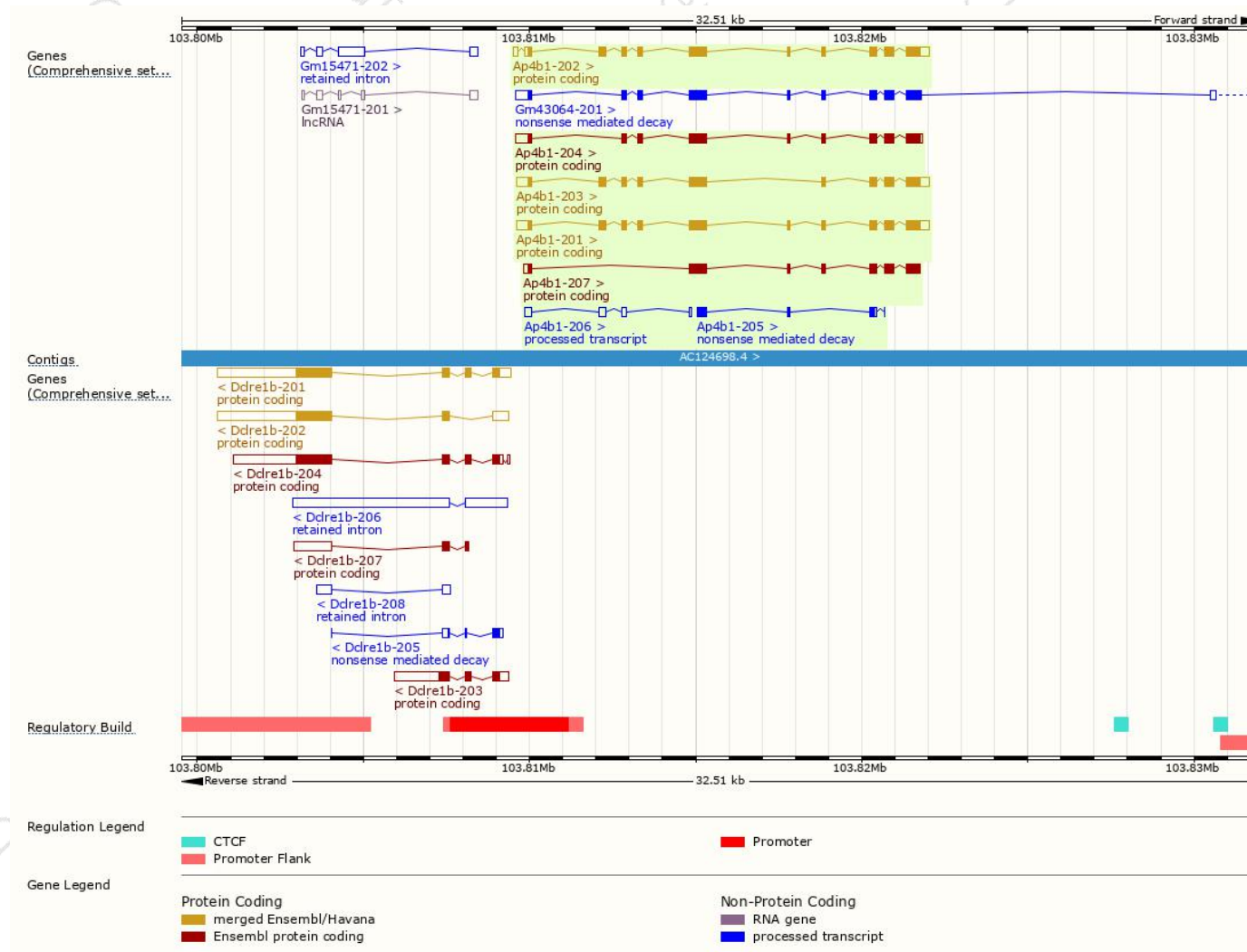
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ap4b1-201	ENSMUST00000047285.6	2799	738aa	Protein coding	CCDS17696	Q9WV76	TSL:1 GENCODE basic APPRIS P1
Ap4b1-203	ENSMUST00000106823.7	2741	710aa	Protein coding	CCDS51026	B0V3P4	TSL:1 GENCODE basic
Ap4b1-202	ENSMUST00000076599.7	2692	738aa	Protein coding	CCDS17696	Q9WV76	TSL:1 GENCODE basic APPRIS P1
Ap4b1-204	ENSMUST00000106824.7	2412	663aa	Protein coding	-	B0V3P3	TSL:5 GENCODE basic
Ap4b1-207	ENSMUST00000200377.4	1823	570aa	Protein coding	-	A0A0G2JFY6	TSL:5 GENCODE basic
Ap4b1-205	ENSMUST00000199686.1	563	154aa	Nonsense mediated decay	-	A0A0G2JDQ2	CDS 5' incomplete TSL:3
Ap4b1-206	ENSMUST00000199723.1	594	No protein	Processed transcript	-	-	TSL:5

The strategy is based on the design of *Ap4b1-201* transcript, the transcription is shown below



Genomic location distribution

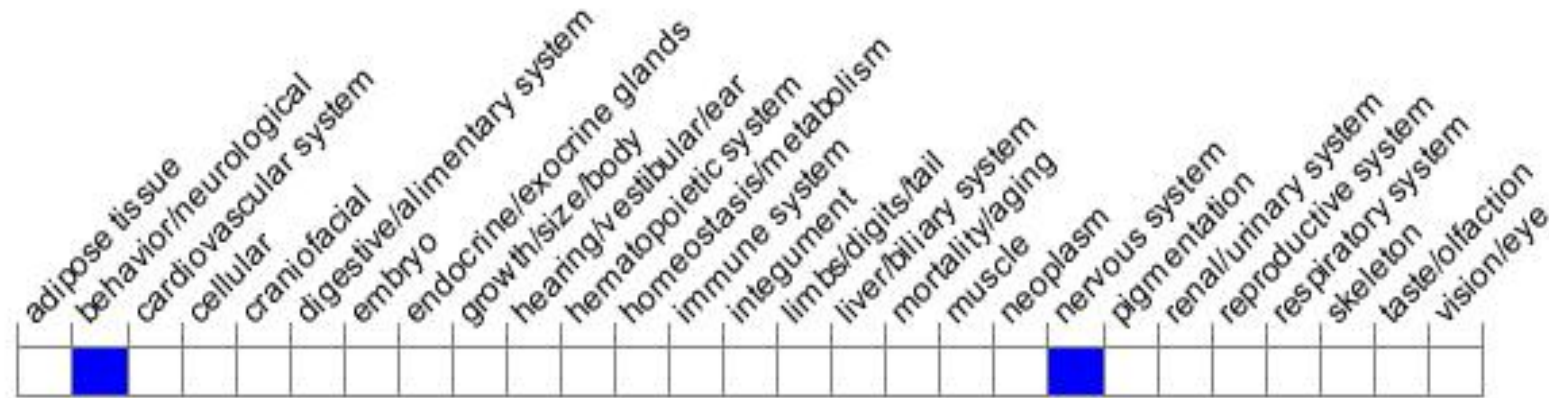


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



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 null allele exhibit poor rotarod performance.

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

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