

Atp2b4 Cas9-KO Strategy

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Project Overview

Project Name

Atp2b4

Project type

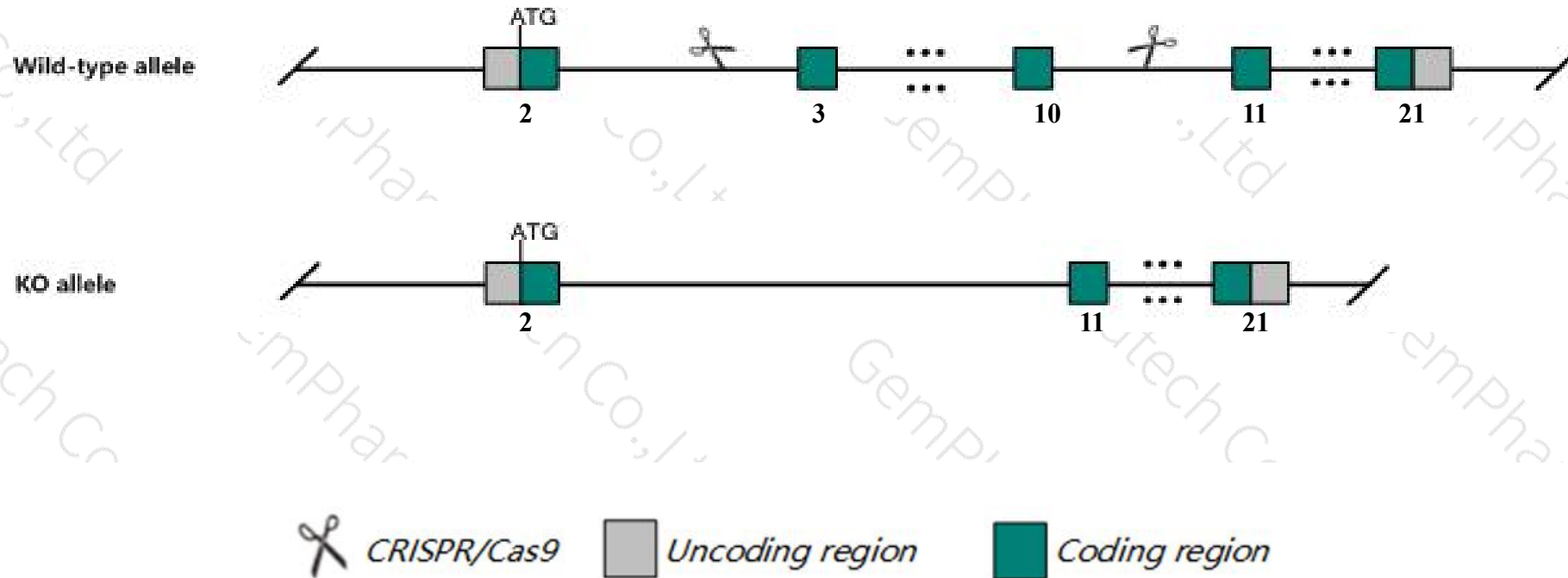
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp2b4* gene. The schematic diagram is as follows:



- The *Atp2b4* gene has 8 transcripts. According to the structure of *Atp2b4* gene, exon3-exon10 of *Atp2b4-206* (ENSMUST00000143567.7) transcript is recommended as the knockout region. The region contains 1367bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp2b4* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice display male infertility with impaired sperm motility.
- The *Atp2b4* gene is located on the Chr1. 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)

Atp2b4 ATPase, Ca⁺⁺ transporting, plasma membrane 4 [Mus musculus (house mouse)]

Gene ID: 381290, updated on 7-Apr-2019

Summary



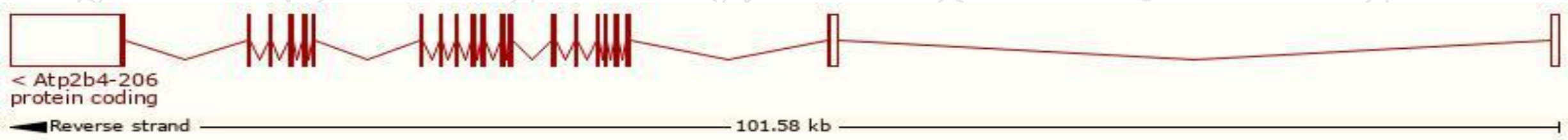
Official Symbol	Atp2b4 provided by MGI
Official Full Name	ATPase, Ca ⁺⁺ transporting, plasma membrane 4 provided by MGI
Primary source	MGI:MGI:88111
See related	Ensembl:ENSMUSG00000026463
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Pmca4
Expression	Broad expression in bladder adult (RPKM 55.6), genital fat pad adult (RPKM 33.8) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

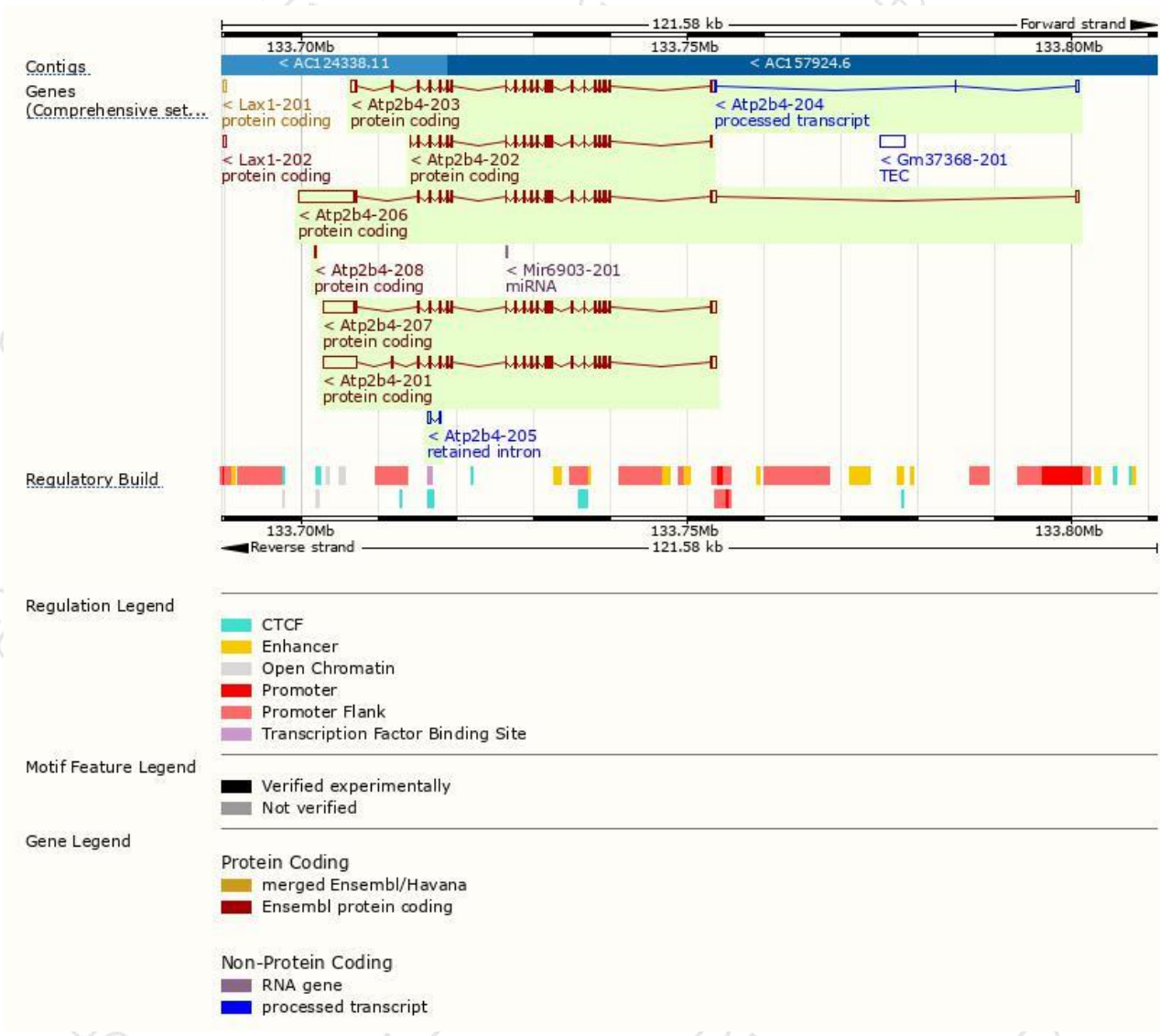
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp2b4-206	ENSMUST00000143567.7	11725	1205aa	Protein coding	CCDS15298	Q6Q477	TSL:5 GENCODE basic APPRIS P3
Atp2b4-201	ENSMUST00000048953.13	8292	1166aa	Protein coding	CCDS48365	F7AAP4	TSL:1 GENCODE basic APPRIS ALT2
Atp2b4-207	ENSMUST00000165602.8	8101	1205aa	Protein coding	CCDS15298	Q6Q477	TSL:1 GENCODE basic APPRIS P3
Atp2b4-203	ENSMUST00000125659.7	4579	1172aa	Protein coding	-	E9Q828	TSL:1 GENCODE basic APPRIS ALT2
Atp2b4-202	ENSMUST00000112264.1	3324	1107aa	Protein coding	-	Q6Q477	TSL:1 GENCODE basic APPRIS ALT2
Atp2b4-208	ENSMUST00000167348.1	243	80aa	Protein coding	-	F6V4K0	TSL:NA GENCODE basic
Atp2b4-204	ENSMUST00000128692.1	588	No protein	Processed transcript	-	-	TSL:5
Atp2b4-205	ENSMUST00000140810.1	432	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Atp2b4-206* transcript,The transcription is shown below



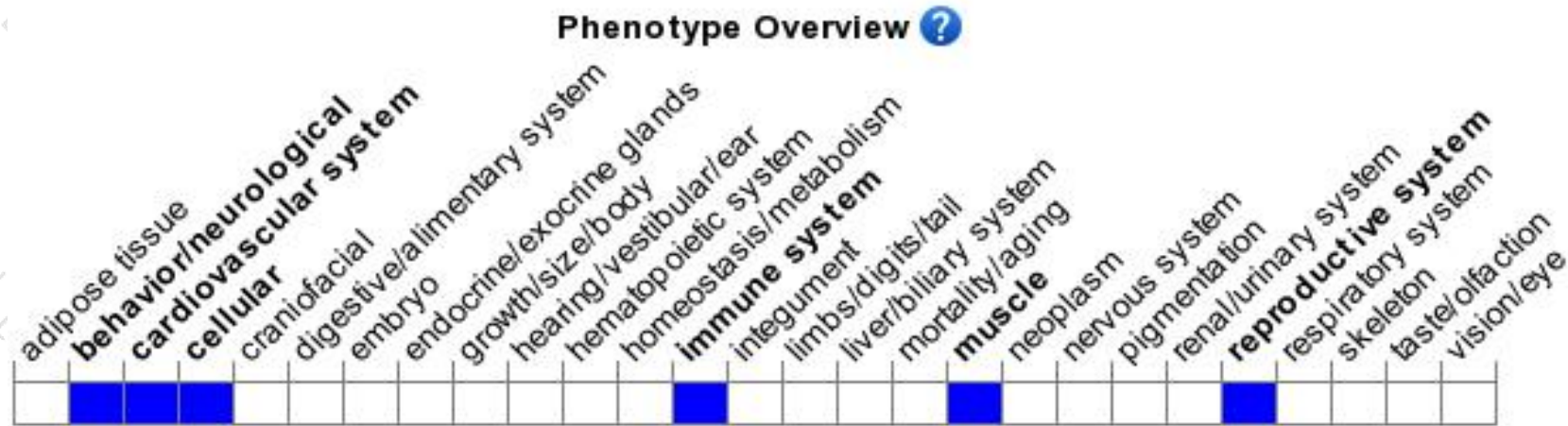
Genomic location distribution



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, Homozygous null mice display male infertility with impaired sperm motility.

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

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