

Atp13a4 Cas9-KO Strategy

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Project Overview

Project Name

Atp13a4

Project type

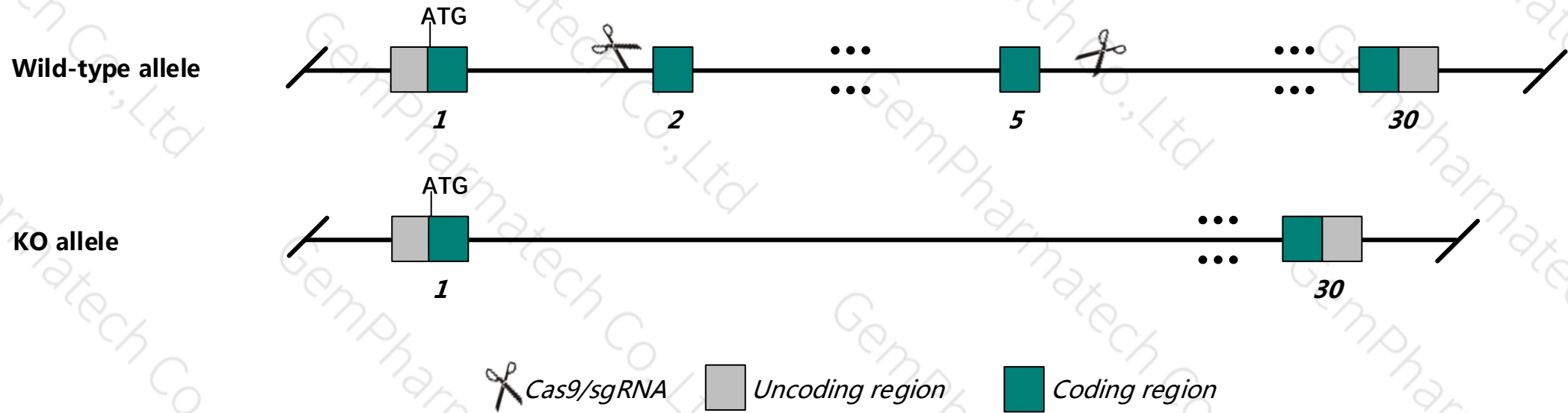
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp13a4* gene. The schematic diagram is as follows:



Technical routes

- The *Atp13a4* gene has 11 transcripts. According to the structure of *Atp13a4* gene, exon2-exon5 of *Atp13a4*-208 (ENSMUST00000182627.7) transcript is recommended as the knockout region. The region contains 473bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp13a4* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9, sgRNA were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- The *Atp13a4* 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)

Atp13a4 ATPase type 13A4 [*Mus musculus* (house mouse)]

Gene ID: 224079, updated on 20-Mar-2020

Summary

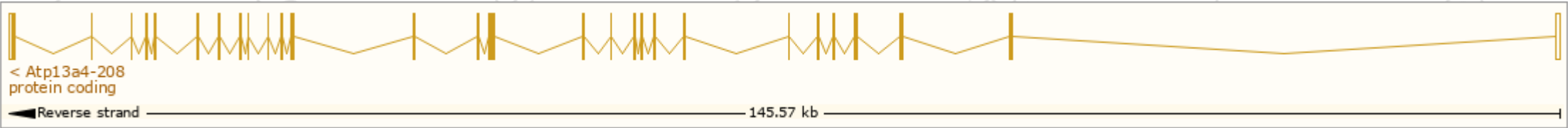
Official Symbol	Atp13a4 provided by MGI
Official Full Name	ATPase type 13A4 provided by MGI
Primary source	MGI:MGI:1924456
See related	Ensembl:ENSMUSG00000038094
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4832416L12; 4631413J11Rik; 9330174J19Rik
Expression	Biased expression in genital fat pad adult (RPKM 4.5), cerebellum adult (RPKM 2.4) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

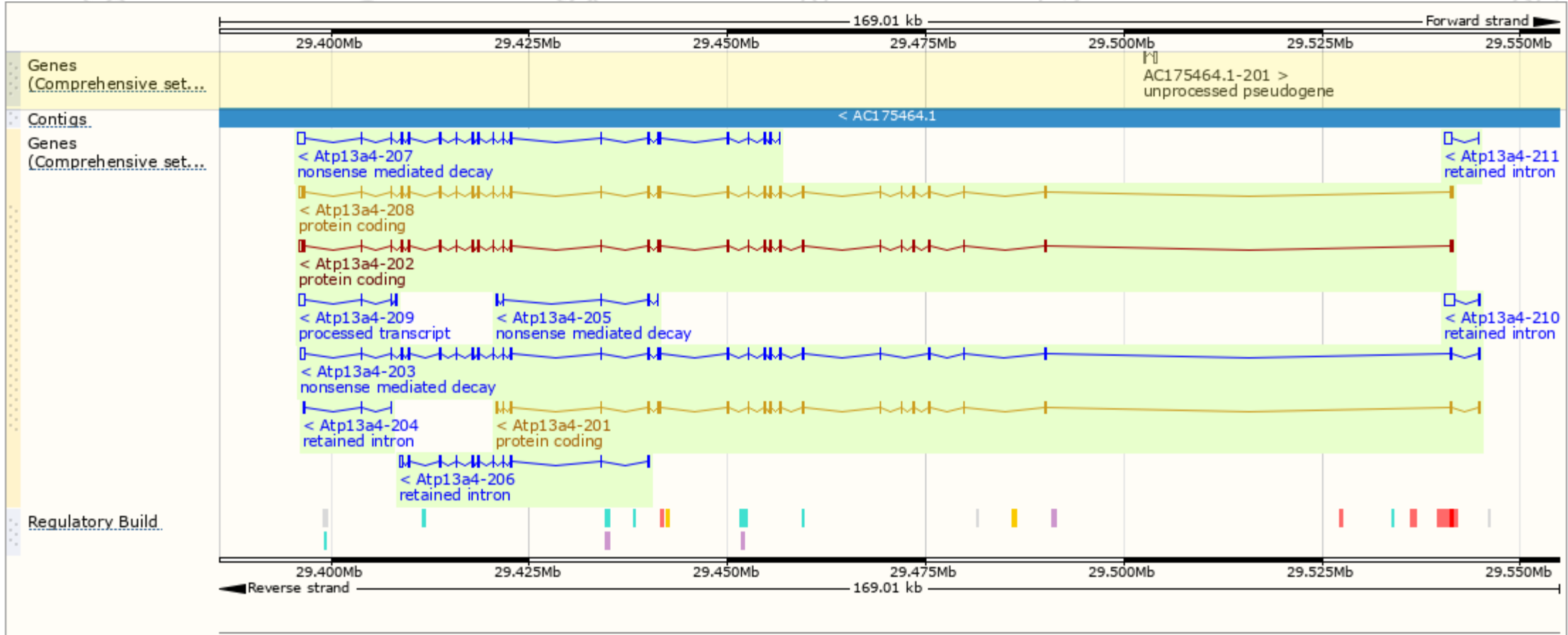
The gene has 11 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp13a4-208	ENSMUST00000182627.7	4238	1193aa	Protein coding	CCDS49816	S4R234	TSL:5 GENCODE basic APPRIS P3
Atp13a4-202	ENSMUST00000057018.14	4054	1174aa	Protein coding	CCDS59623	E9QPP7	TSL:1 GENCODE basic APPRIS ALT2
Atp13a4-201	ENSMUST00000039090.8	2878	878aa	Protein coding	CCDS49817	A0A0R4J0M2	TSL:1 GENCODE basic
Atp13a4-203	ENSMUST00000182013.7	3809	84aa	Nonsense mediated decay	-	S4R2B9	TSL:1
Atp13a4-207	ENSMUST00000182573.7	3010	576aa	Nonsense mediated decay	-	S4R2M1	CDS 5' incomplete TSL:5
Atp13a4-205	ENSMUST00000182168.7	552	87aa	Nonsense mediated decay	-	S4R262	CDS 5' incomplete TSL:5
Atp13a4-209	ENSMUST00000182676.7	958	No protein	Processed transcript	-	-	TSL:1
Atp13a4-206	ENSMUST00000182357.1	1501	No protein	Retained intron	-	-	TSL:1
Atp13a4-210	ENSMUST00000182694.1	1404	No protein	Retained intron	-	-	TSL:1
Atp13a4-211	ENSMUST00000182824.1	1045	No protein	Retained intron	-	-	TSL:1
Atp13a4-204	ENSMUST00000182094.1	356	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Atp13a4*-208 transcript,The transcription is shown below



Genomic location distribution



Protein domain



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