

Atp12a Cas9-CKO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Atp12a

Project type

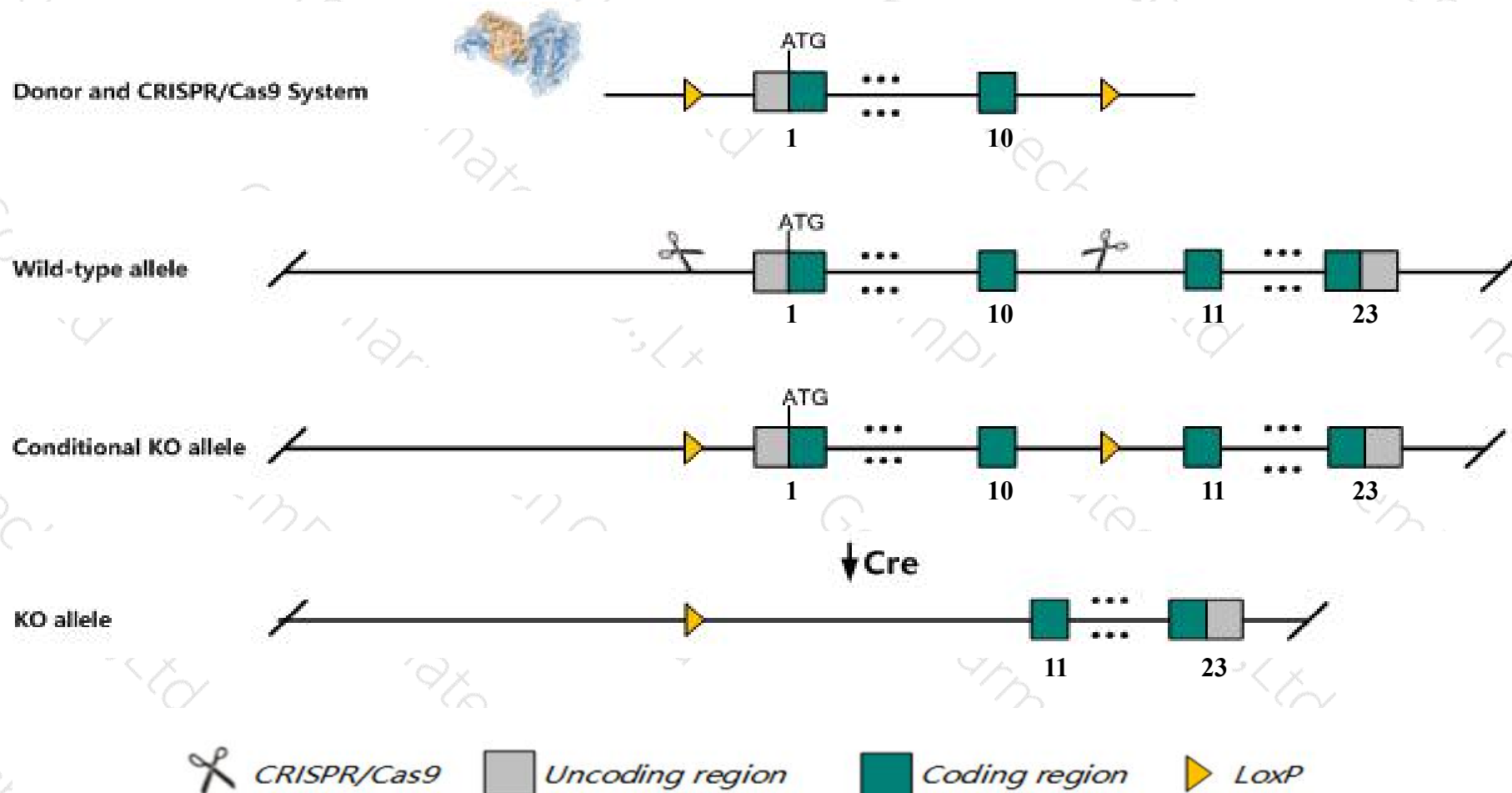
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp12a* gene. The schematic diagram is as follows:



- The *Atp12a* gene has 2 transcripts. According to the structure of *Atp12a* gene, exon1-exon10 of *Atp12a-201* (ENSMUST00000007340.3) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp12a* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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 flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Homozygous mutation of this gene results in increased potassium excretion. When placed on a potassium-free diet, mutant animals display greater weight loss and slightly increased kidney weight compared to wild-type.
- The *Atp12a* gene is located on the Chr14. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Atp12a ATPase, H⁺/K⁺ transporting, nongastric, alpha polypeptide [Mus musculus (house mouse)]

Gene ID: 192113, updated on 19-Mar-2019

Summary



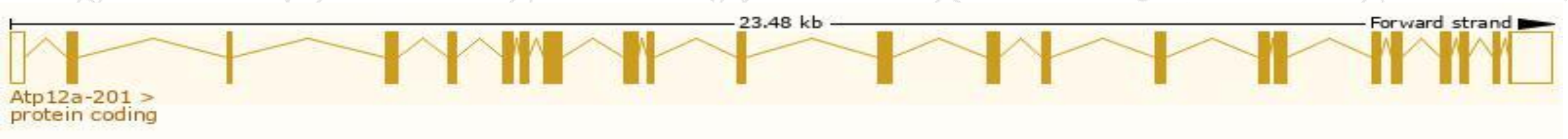
Official Symbol	Atp12a provided by MGI
Official Full Name	ATPase, H ⁺ /K ⁺ transporting, nongastric, alpha polypeptide provided by MGI
Primary source	MGI:MGI:1926943
See related	Ensembl:ENSMUSG00000022229
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Atp1a1, HKalpha2, cHKA
Expression	Restricted expression toward colon adult (RPKM 53.7) See more
Orthologs	human all

Transcript information (Ensembl)

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

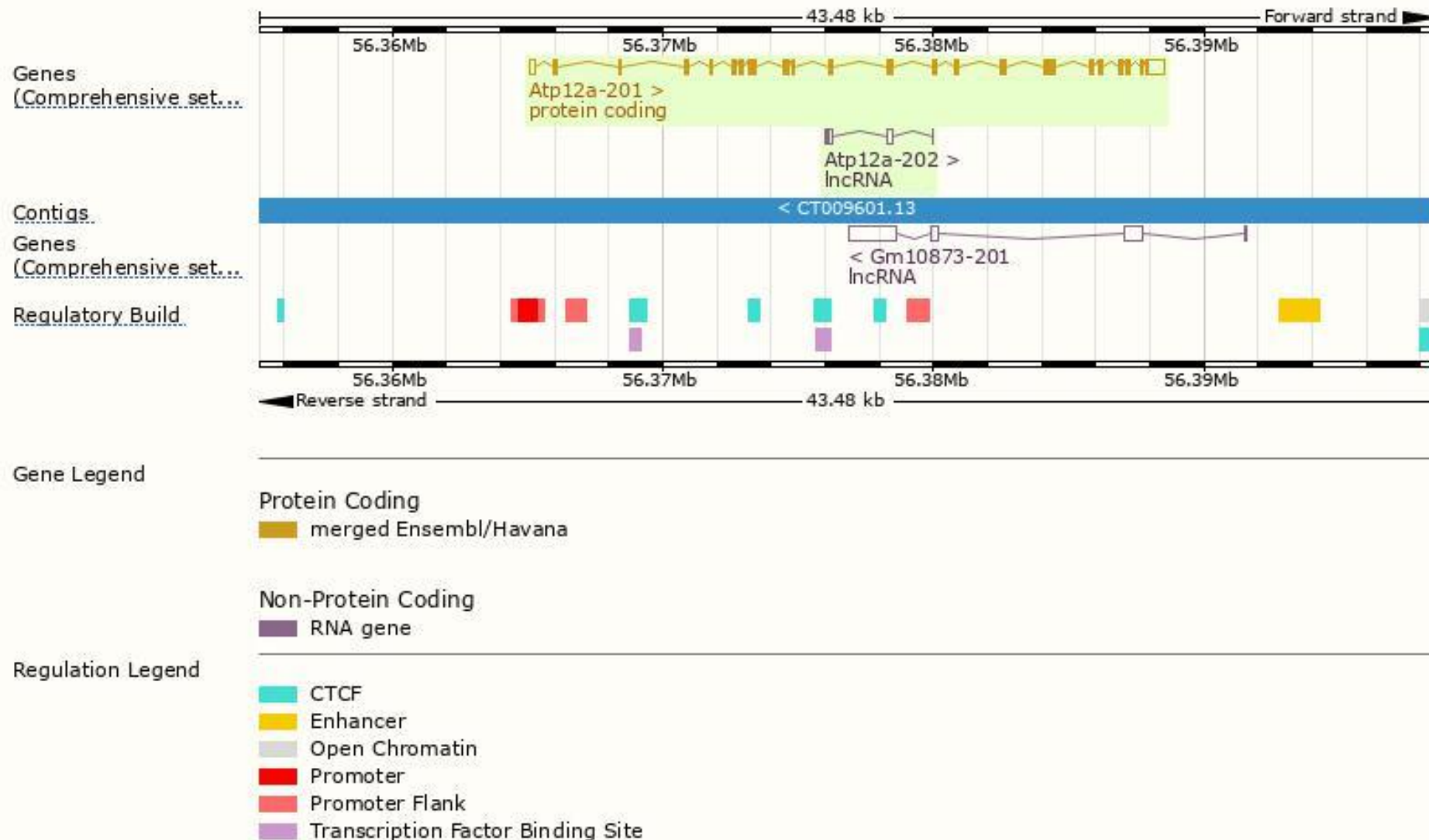
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp12a-201	ENSMUST00000007340.3	3950	1035aa	Protein coding	CCDS27148	Q9Z1W8	TSL:1 GENCODE basic APPRIS P1
Atp12a-202	ENSMUST00000225698.1	453	No protein	lncRNA	-	-	

The strategy is based on the design of *Atp12a-201* transcript,The transcription is shown below





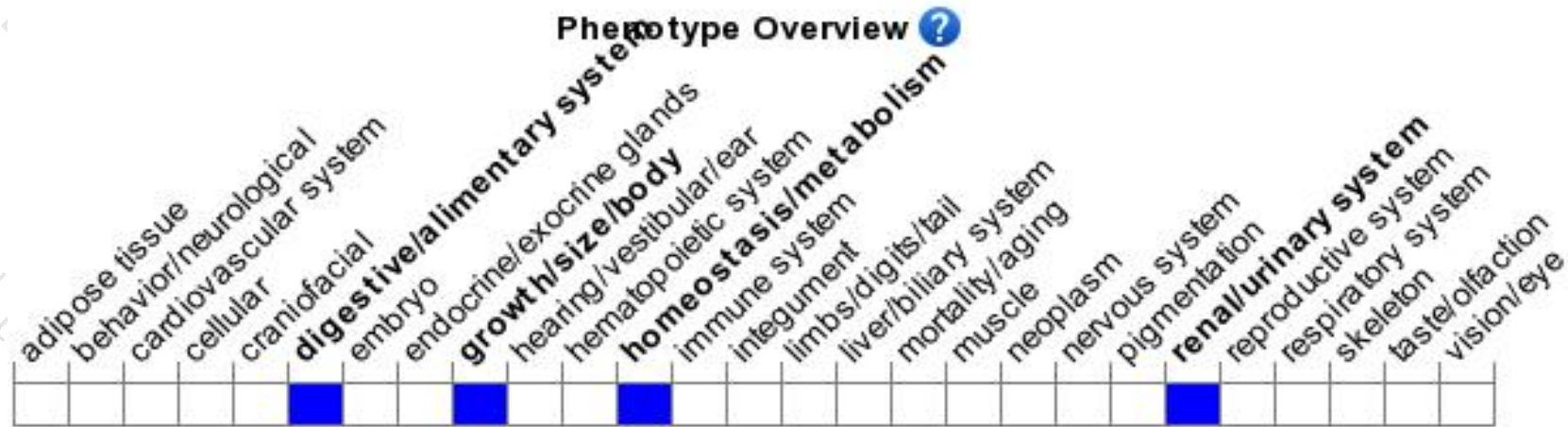
Genomic location distribution



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, Homozygous mutation of this gene results in increased potassium excretion. When placed on a potassium-free diet, mutant animals display greater weight loss and slightly increased kidney weight compared to wild-type.

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

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