

Abce1 Cas9-CKO Strategy

Designer:Lixin LYU

Project Overview

Project Name

Abcel

Project type

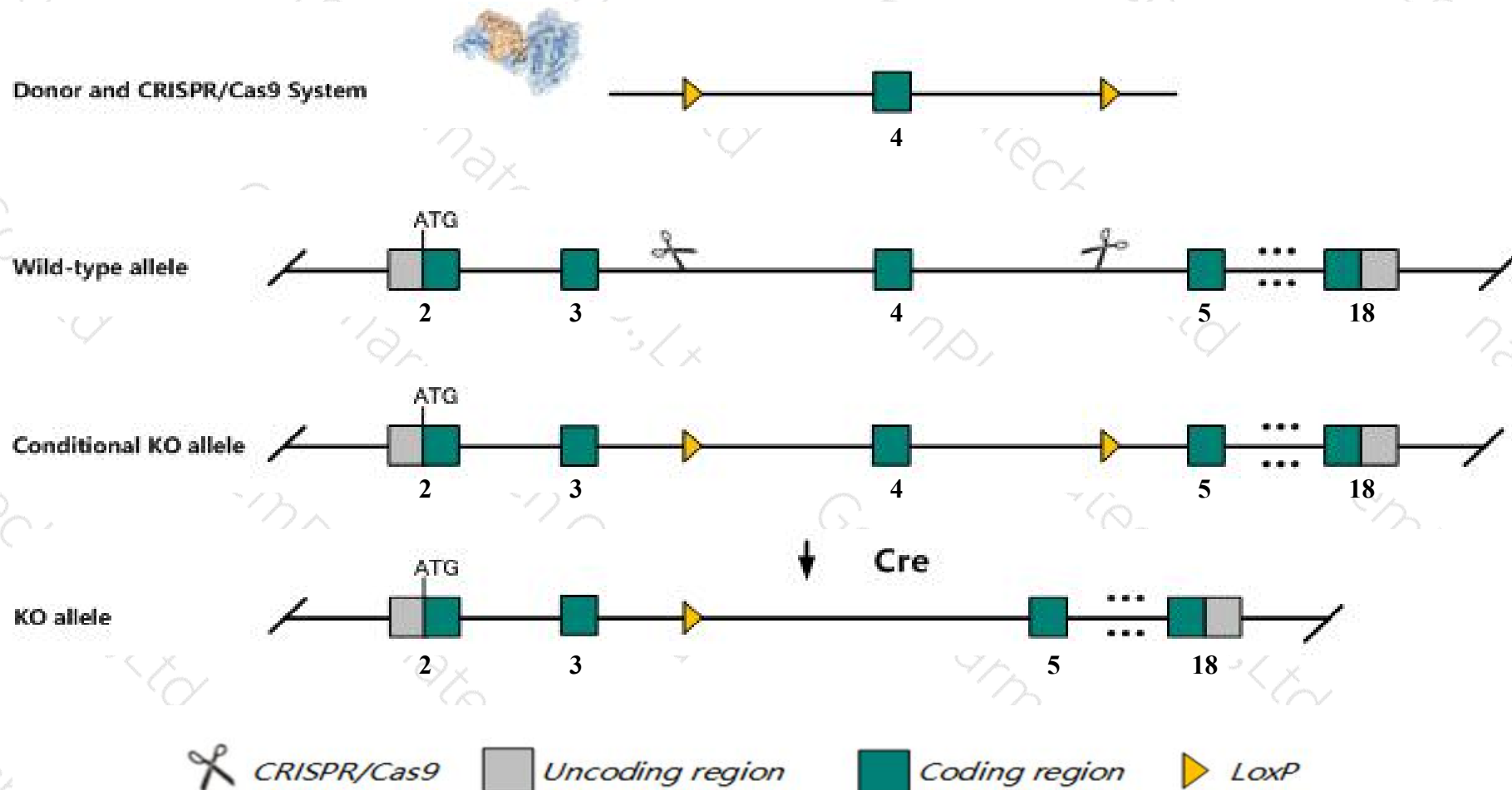
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abce1* gene. The schematic diagram is as follows:



- The *Abce1* gene has 4 transcripts. According to the structure of *Abce1* gene, exon4 of *Abce1-201* (ENSMUST00000080536.7) transcript is recommended as the knockout region. The region contains 98bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Abce1* 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, Mice homozygous for a transgenic gene disruption exhibit embryonic lethality at E7.
- The *Abce1* gene is located on the Chr8. 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)

Abce1 ATP-binding cassette, sub-family E (OABP), member 1 [Mus musculus (house mouse)]

Gene ID: 24015, updated on 31-Jan-2019

Summary



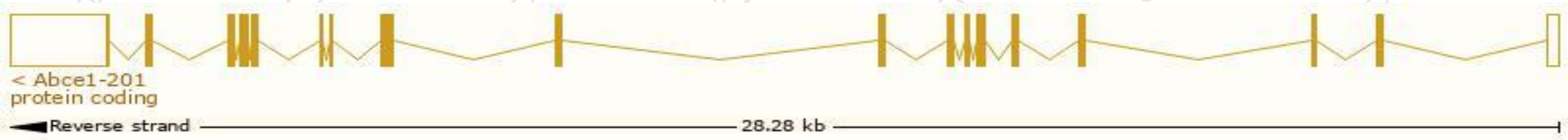
Official Symbol	Abce1 provided by MGI
Official Full Name	ATP-binding cassette, sub-family E (OABP), member 1 provided by MGI
Primary source	MGI:MGI:1195458
See related	Ensembl:ENSMUSG00000058355
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	C79080, Oabp, RLI, RNS41, RNS4I, Rnaseli
Summary	The membrane-associated protein encoded by this gene is a member of the superfamily of ATP-binding cassette (ABC) transporters. ABC proteins transport various molecules across extra- and intra-cellular membranes. ABC genes are divided into seven distinct subfamilies (ABC1, MDR/TAP, MRP, ALD, OABP, GCN20, White). This protein is a member of the OABP subfamily. Alternatively referred to as the RNase L inhibitor, this protein functions to block the activity of ribonuclease L. Activation of ribonuclease L leads to inhibition of protein synthesis in the 2-5A/RNase L system, the central pathway for viral interferon action. [provided by RefSeq, Jul 2008]
Expression	Ubiquitous expression in liver E14 (RPKM 27.7), CNS E11.5 (RPKM 26.2) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

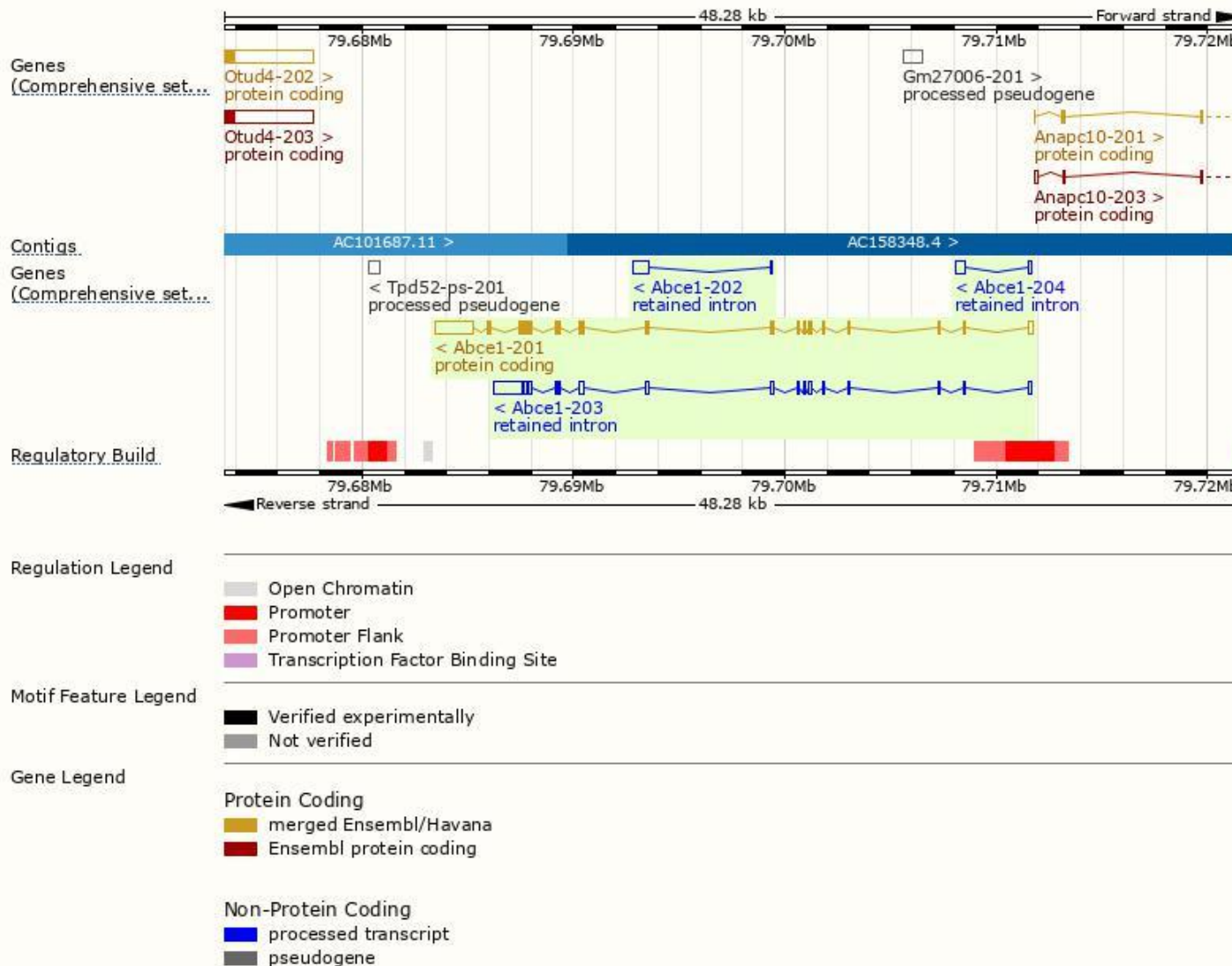
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abce1-201	ENSMUST00000080536.7	3793	599aa	Protein coding	CCDS22438	P61222 Q3UHY8	TSL:1 GENCODE basic APPRIS P1
Abce1-203	ENSMUST00000211509.1	3030	No protein	Retained intron	-	-	TSL:1
Abce1-202	ENSMUST00000209354.1	814	No protein	Retained intron	-	-	TSL:3
Abce1-204	ENSMUST00000213842.1	589	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Abce1-201* transcript,The transcription is shown below



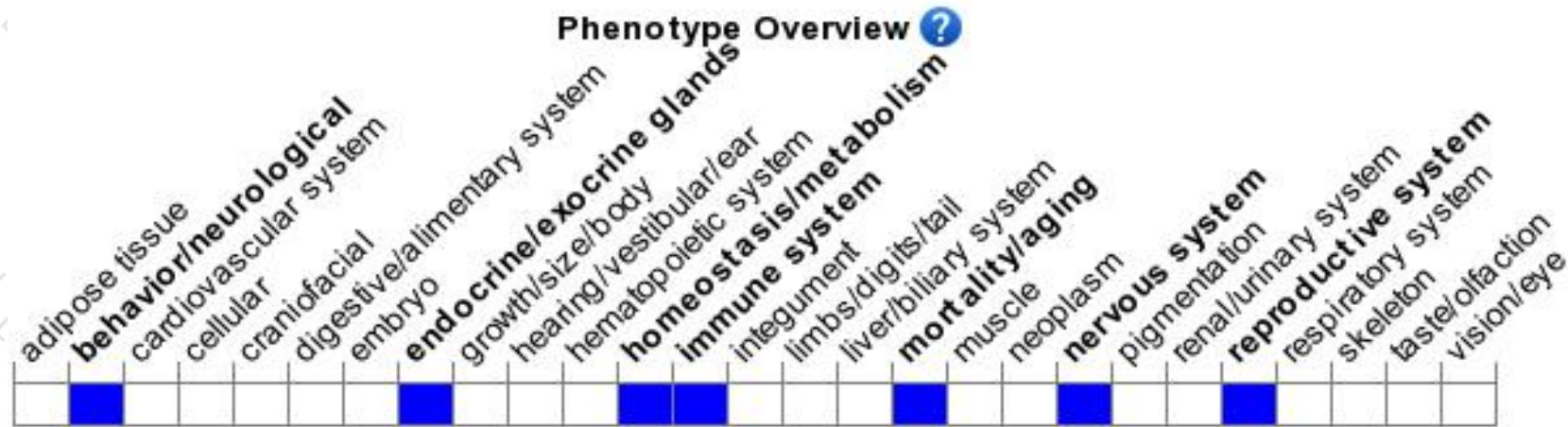
Genomic location distribution



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, Mice homozygous for a transgenic gene disruption exhibit embryonic lethality at E7.

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

Tel: 400-9660890

