Abcd3 Cas9-KO Strategy

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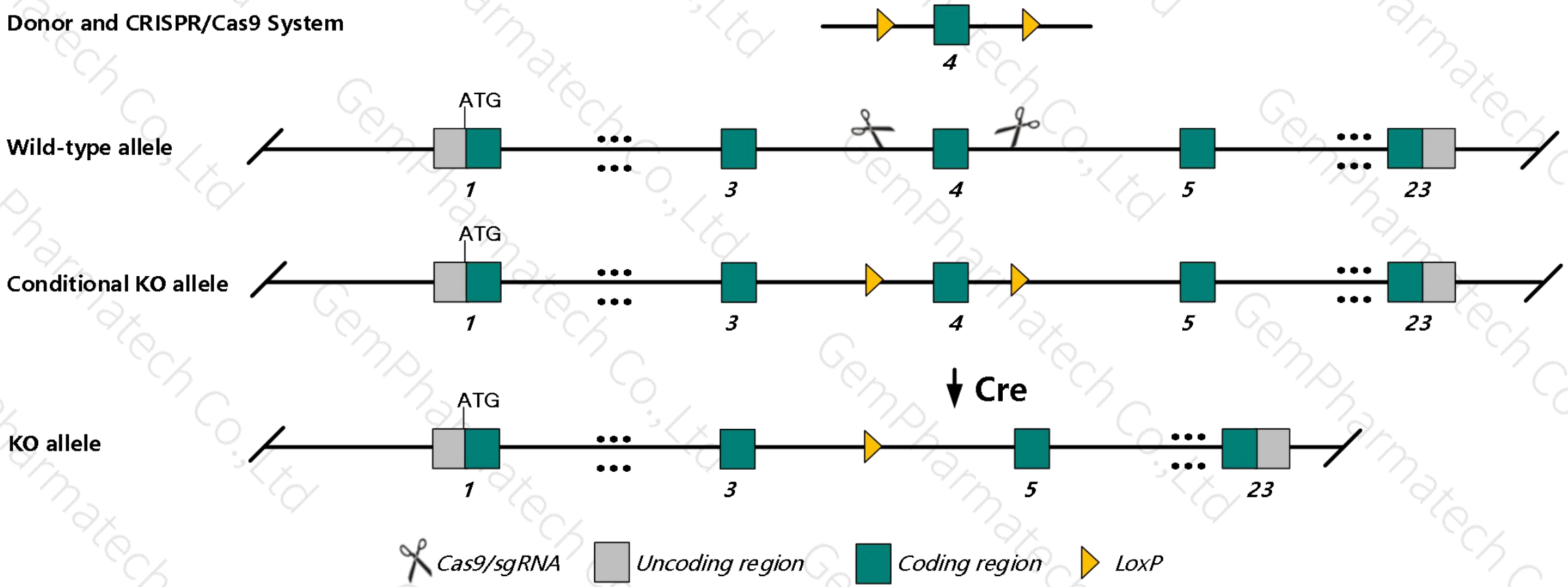
Project Overview

Project Name	***Abcd3***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abcd3* gene. The schematic diagram is as follows:



Technical routes

➢ The *Abcd3* gene has 6 transcripts. According to the structure of *Abcd3* gene, exon4 of *Abcd3-201* (ENSMUST00000029770.7) transcript is recommended as the knockout region.The region contains 89bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Abcd3* gene. The brief process is as follows: gRNA was transcribed in vitro.Cas9 and gRNA 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.

Notice

➢ According to the existing MGI data,Mice homozygous for a null mutation show enlarged livers, abnormal bile composition and peroxisome abnormalities.

➢ The *Abcd3* 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）

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Abcd3 ATP-binding cassette, sub-family D (ALD), member 3 [*Mus musculus* (house mouse)]

Gene ID: 19299, updated on 13-Mar-2020

Summary

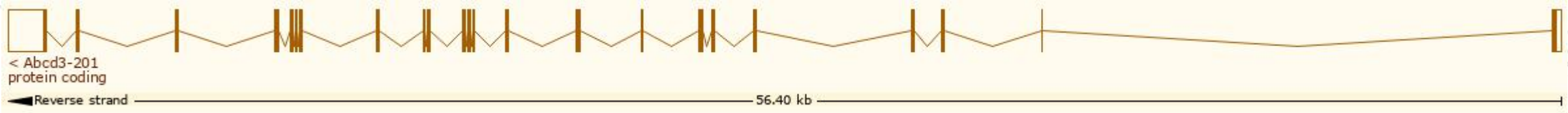
Official Symbol	Abcd3 provided by MGI
Official Full Name	ATP-binding cassette, sub-family D (ALD), member 3 provided by MGI
Primary source	MGI:MGI:1349216
See related	Ensembl:ENSMUSG00000028127
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	PMP68; PMP70; Pxmp1; AI313901; AU018866; AW146054
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 ALD subfamily, which is involved in peroxisomal import of fatty acids and/or fatty acyl-CoAs in the organelle. All known peroxisomal ABC transporters are half transporters which require a partner half transporter molecule to form a functional homodimeric or heterodimeric transporter. This peroxisomal membrane protein likely plays an important role in peroxisome biogenesis. Mutations have been associated with some forms of Zellweger syndrome, a heterogeneous group of peroxisome assembly disorders. [provided by RefSeq, Jul 2008]
Expression	Ubiquitous expression in liver adult (RPKM 16.9), bladder adult (RPKM 15.9) and 27 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

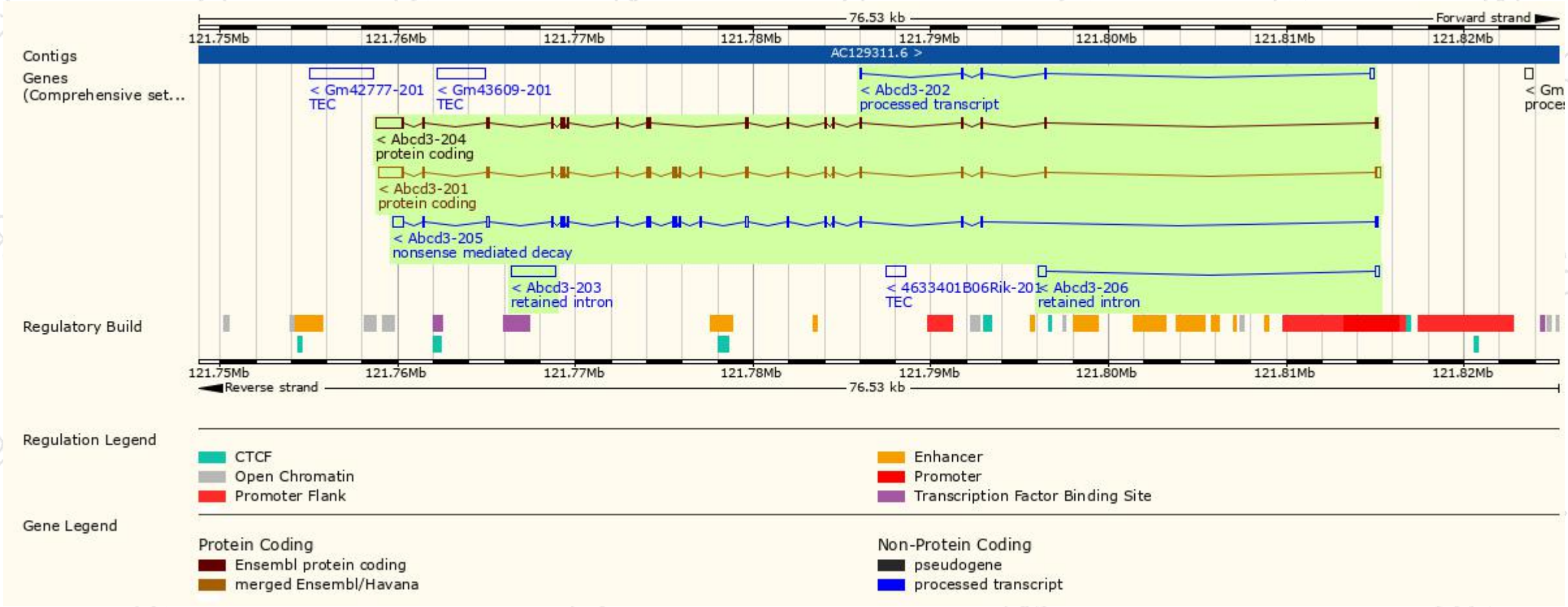
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abcd3-203	ENSMUST00000196340.1	2489	No protein	Retained intron	-	-	TSL:NA
Abcd3-206	ENSMUST00000199593.1	638	No protein	Retained intron	-	-	TSL:1
Abcd3-201	ENSMUST00000029770.7	3489	659aa	Protein coding	CCDS17806	P55096	TSL:1 GENCODE basic APPRIS P1
Abcd3-204	ENSMUST00000197383.4	3156	549aa	Protein coding	-	A0A0G2JDI9	TSL:5 GENCODE basic
Abcd3-202	ENSMUST00000195965.1	478	No protein	Processed transcript	-	-	TSL:5
Abcd3-205	ENSMUST00000197662.4	2467	58aa	Nonsense mediated decay	-	A0A0G2JGA4	TSL:5

The strategy is based on the design of *Abcd3-201* transcript, the transcription is shown below:

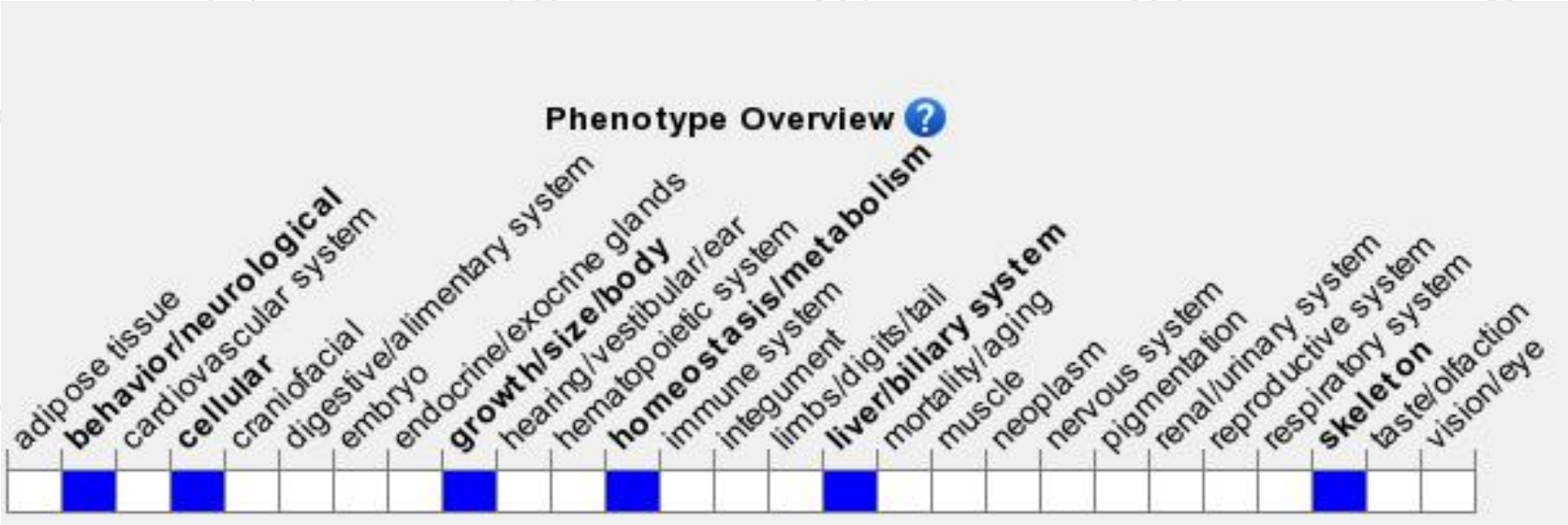


Genomic location distribution



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/).

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

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