Abcb6 Cas9-KO Strategy

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Project Overview

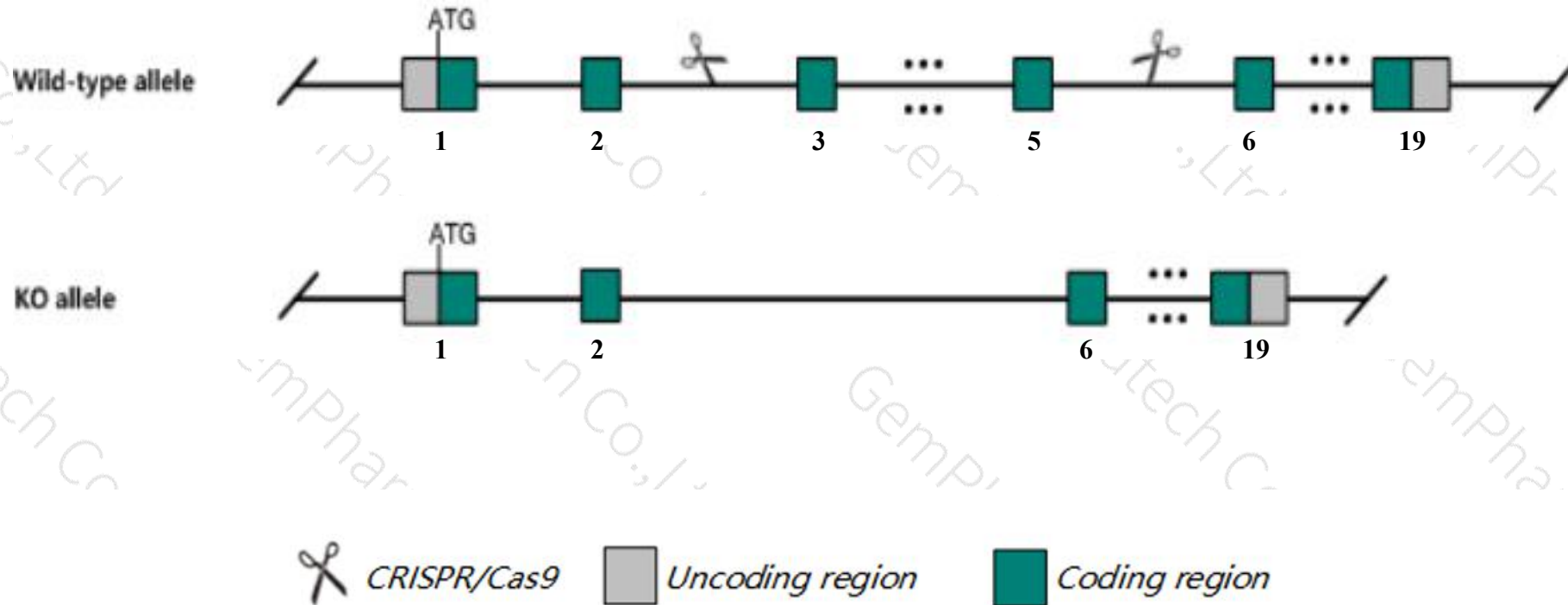|	
Project Name	***Abcb6***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abcb6* gene. The schematic diagram is as follows:

Technical routes

➢ The *Abcb6* gene has 6 transcripts. According to the structure of *Abcb6* gene, exon3-exon5 of *Abcb6-201* (ENSMUST00000027396.14) transcript is recommended as the knockout region.The region contains 467bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Abcb6* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➤ According to the existing MGI data,Mice homozygous for a null mutation display partial lethality, impaired stress erythropoiesis, and absence of ATP-dependent transport of Coproporphyrin III in mitochondria.

➤ The N-terminal of *Abcb6* gene will remain several amino acids ,it may remain the partial function of *Abcb6* gene.

➤ The effect on transcript *Abcb6*-206 is unknown.

➤ The *Abcb6* 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）

Abcb6 ATP-binding cassette, sub-family B (MDR/TAP), member 6 [*Mus musculus* (house mouse)]

Gene ID: 74104, updated on 27-Feb-2020

▲ Summary

Official Symbol	Abcb6 provided by MGI
Official Full Name	ATP-binding cassette, sub-family B (MDR/TAP), member 6 provided by MGI
Primary source	MGI:MGI:1921354
See related	Ensembl:ENSMUSG00000026198
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	1200005B17Rik
Expression	Ubiquitous expression in liver adult (RPKM 38.1), colon adult (RPKM 25.7) and 28 other tissues See more
Orthologs	human all

▲ Genomic context

Location: 1; 1 C4

See Abcb6 in Genome Data Viewer

Exon count: 19

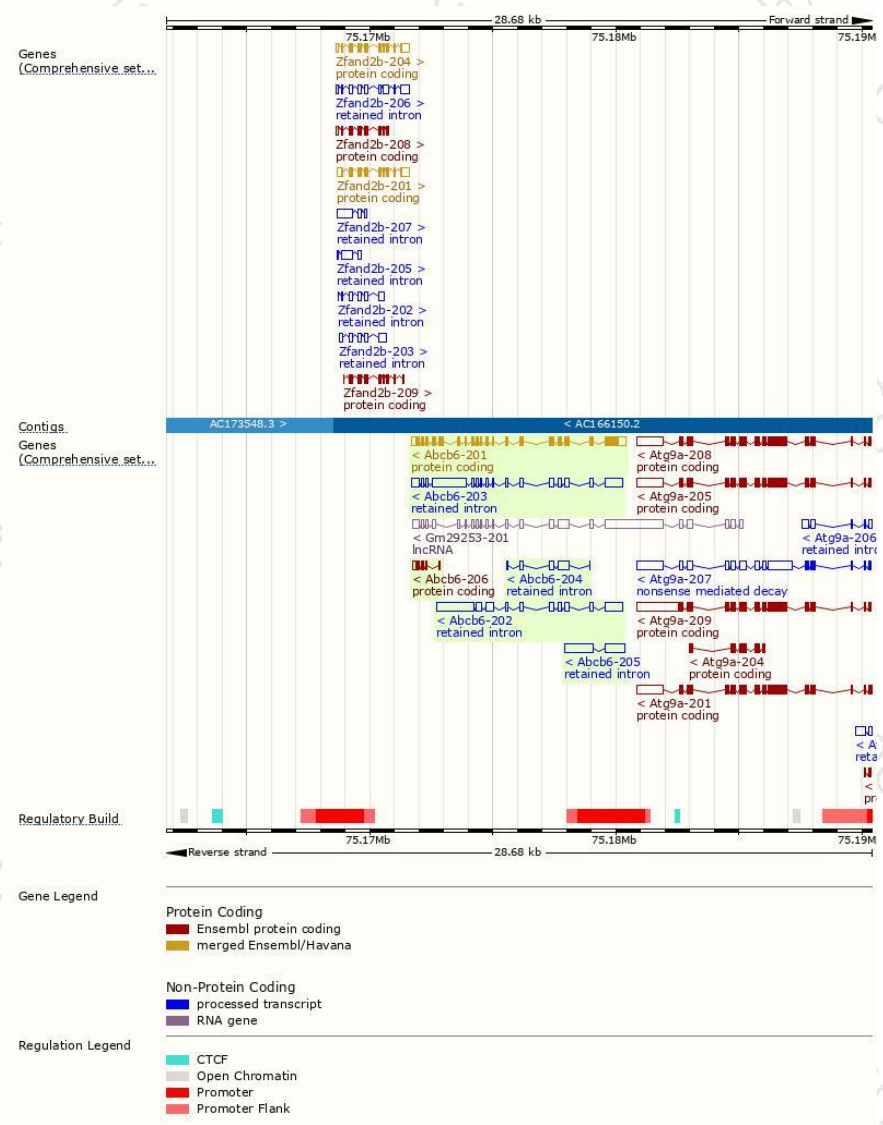| Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	1	NC_000067.6 (75171640..75180392, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	1	NC_000067.5 (75168214..75176857, complement)

Transcript information（Ensembl）

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abcb6-201	ENSMUST00000027396.14	2966	842aa	Protein coding	CCDS15065	Q9DC29	TSL:1 GENCODE basic APPRIS P1
Abcb6-206	ENSMUST00000161215.1	416	97aa	Protein coding	-	F6SGP4	CDS 5' incomplete TSL:5
Abcb6-203	ENSMUST00000160081.7	3772	No protein	Retained intron	-	-	TSL:2
Abcb6-202	ENSMUST00000159219.7	3625	No protein	Retained intron	-	-	TSL:2
Abcb6-205	ENSMUST00000161103.1	1966	No protein	Retained intron	-	-	TSL:1
Abcb6-204	ENSMUST00000160757.1	829	No protein	Retained intron	-	-	TSL:5

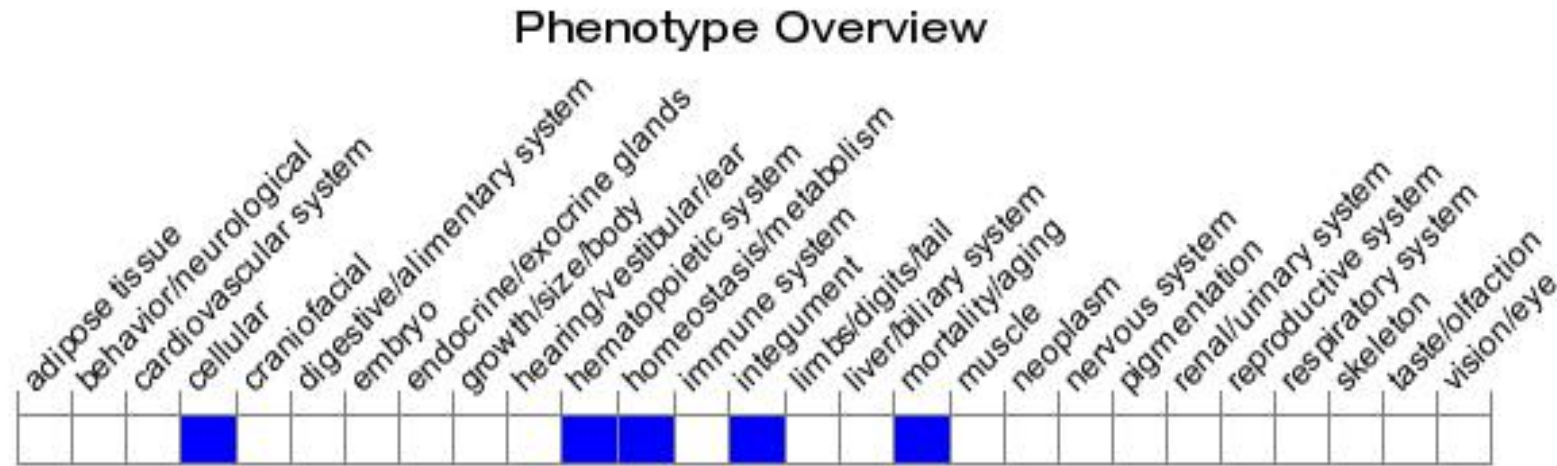The strategy is based on the design of *Abcb6-201* transcript,The transcription is shown below

< Abcb6-201
protein coding

Reverse strand 　　　　　　　　　　　　　8.68 kb
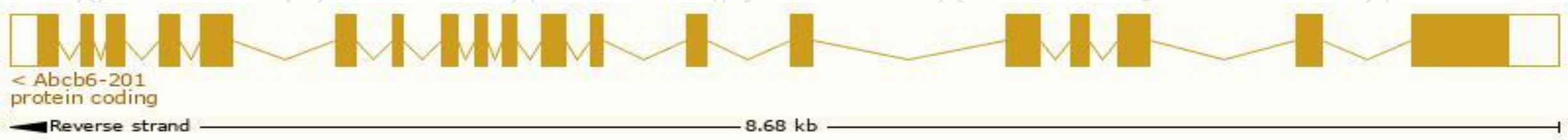
Genomic location distribution

Protein domain

ENSMUSP00000027...	
Transmembrane heli...	
Low complexity (Seg)	
Superfamily	P-loop containing nucleoside triphosphate
	ABC transporter type 1, transmembrane domain superfamily
SMART	AAA+ ATPase domain
Pfam	Mitochondrial ABC-transporter, N-terminal five TM domain / ABC transporter-like
	ABC transporter type 1, transmembrane domain
PROSITE profiles	ABC transporter type 1, transmembrane domain / ABC transporter-like
PROSITE patterns	ABC transporter, co
PANTHER	PTHR24221:SF187
	Type I protein exporter
Gene3D	3.40.50.300
	ABC transporter type 1, transmembrane domain superfamily
CDD	cd03253
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)

Variant Legend
- ▮ missense variant
- ▮ synonymous variant

Scale bar: 0   80   160   240   320   400   480   560   640   720   842

Mouse phenotype description(MGI)

Phenotype Overview

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 null mutation display partial lethality, impaired stress erythropoiesis, and absence of ATP-dependent transport of Coproporphyrin III in mitochondria.

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