Atp8b1 Cas9-KO Strategy

Designer: JiaYu

Reviewer: Xiaojing Li

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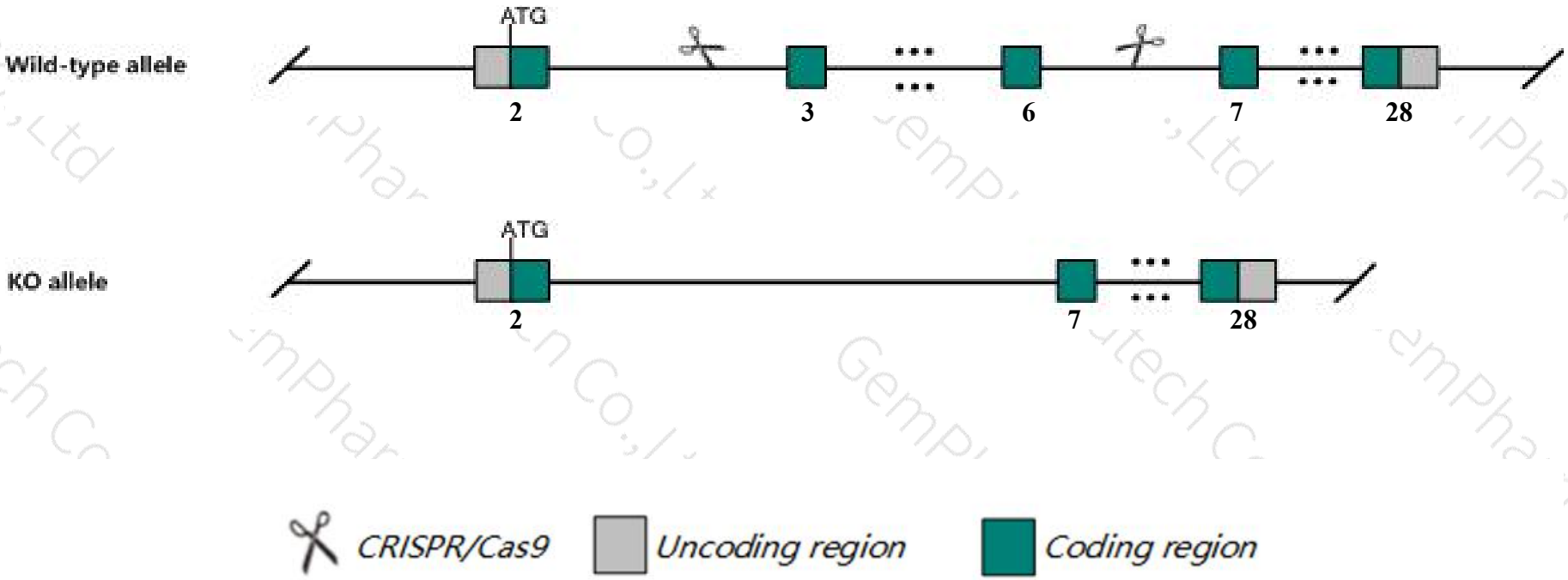
Project Overview

Project Name	***Atp8b1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp8b1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Atp8b1* gene has 3 transcripts. According to the structure of *Atp8b1* gene, exon3-exon6 of *Atp8b1-201* (ENSMUST00000025482.9) transcript is recommended as the knockout region.The region contains 373bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Atp8b1* gene. The brief process is as follows: CRISPR/Cas9 systen

Notice

➢ According to the existing MGI data,Homozygous mice display abnormal bile salt homeostasis, normal bile secretion, and an impaired ability to handle increased bile salt loading resulting in liver damage and weight loss on a bile salt supplemented diet.

➢Transcript 202 CDS 5' and 3' incomplete the influences is unknown.

➢ The *Atp8b1* gene is located on the Chr18. 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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Atp8b1 ATPase, class I, type 8B, member 1 [Mus musculus (house mouse)]

Gene ID: 54670, updated on 31-Jan-2019

Summary

Official Symbol	Atp8b1 provided by MGI
Official Full Name	ATPase, class I, type 8B, member 1 provided by MGI
Primary source	MGI:MGI:1859665
See related	Ensembl:ENSMUSG00000039529
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	AI451886, FIC1, Ic
Expression	Biased expression in large intestine adult (RPKM 22.0), colon adult (RPKM 19.6) and 11 other tissues See more
Orthologs	human all

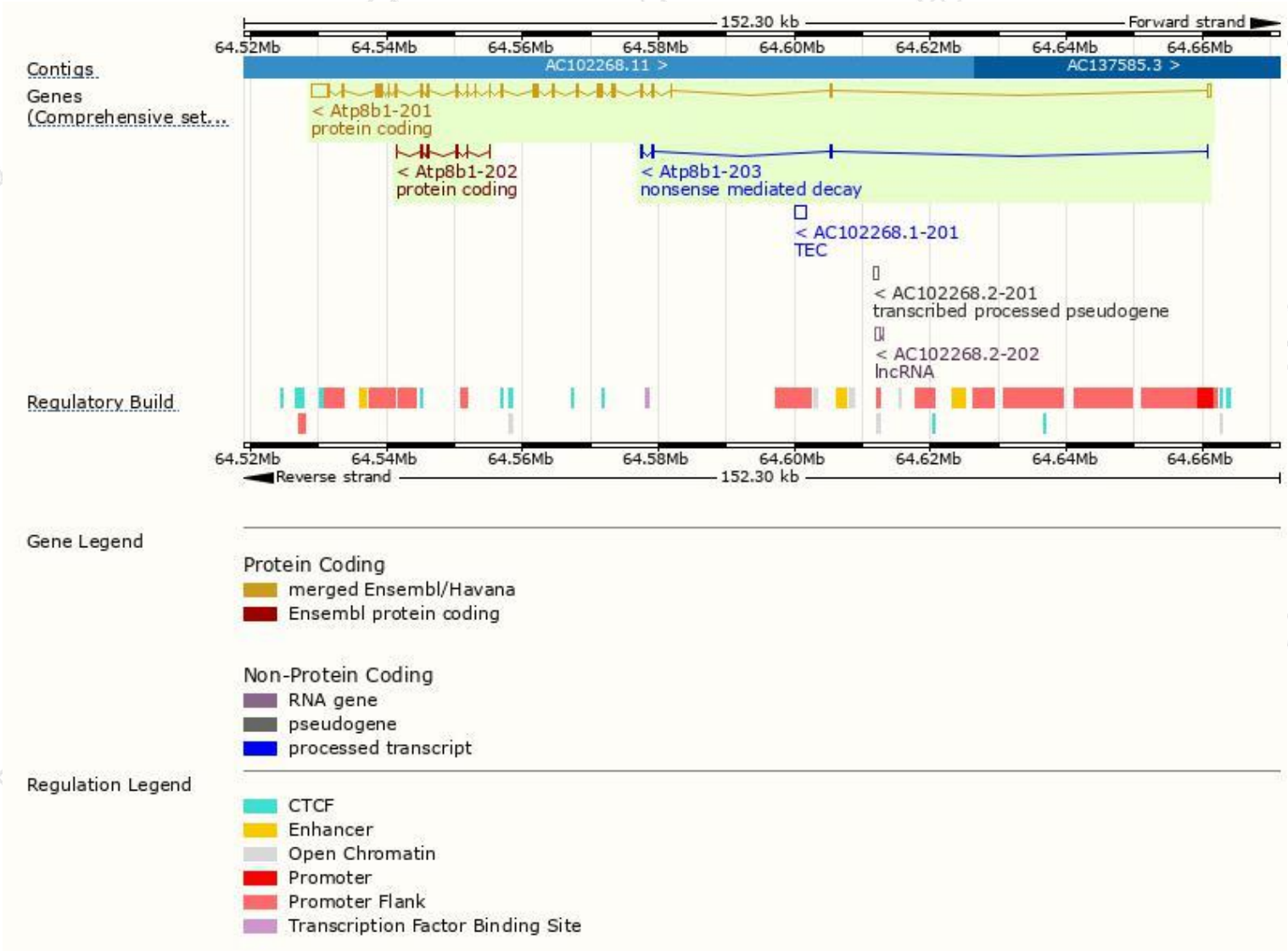
Transcript information（Ensembl）

The gene has 3 transcripts,all transcripts are shown below:

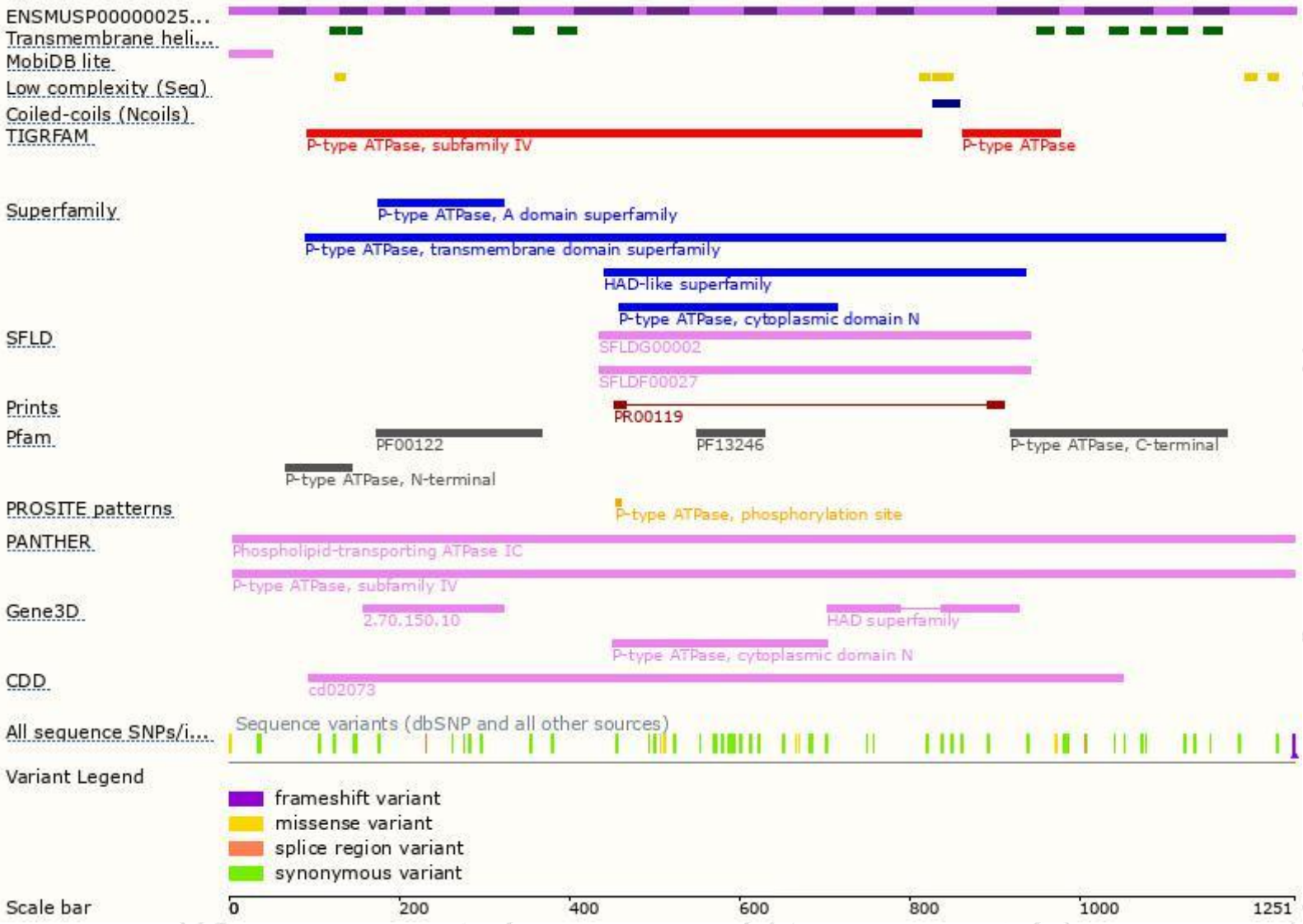
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp8b1-201	ENSMUST00000025482.9	6719	1251aa	Protein coding	CCDS29304	Q148W0	TSL:1 GENCODE basic APPRIS P1
Atp8b1-202	ENSMUST00000235459.1	737	245aa	Protein coding	-	-	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
Atp8b1-203	ENSMUST00000237686.1	531	61aa	Nonsense mediated decay	-	-	

The strategy is based on the design of *Atp8b1-201* transcript,The transcription is shown below

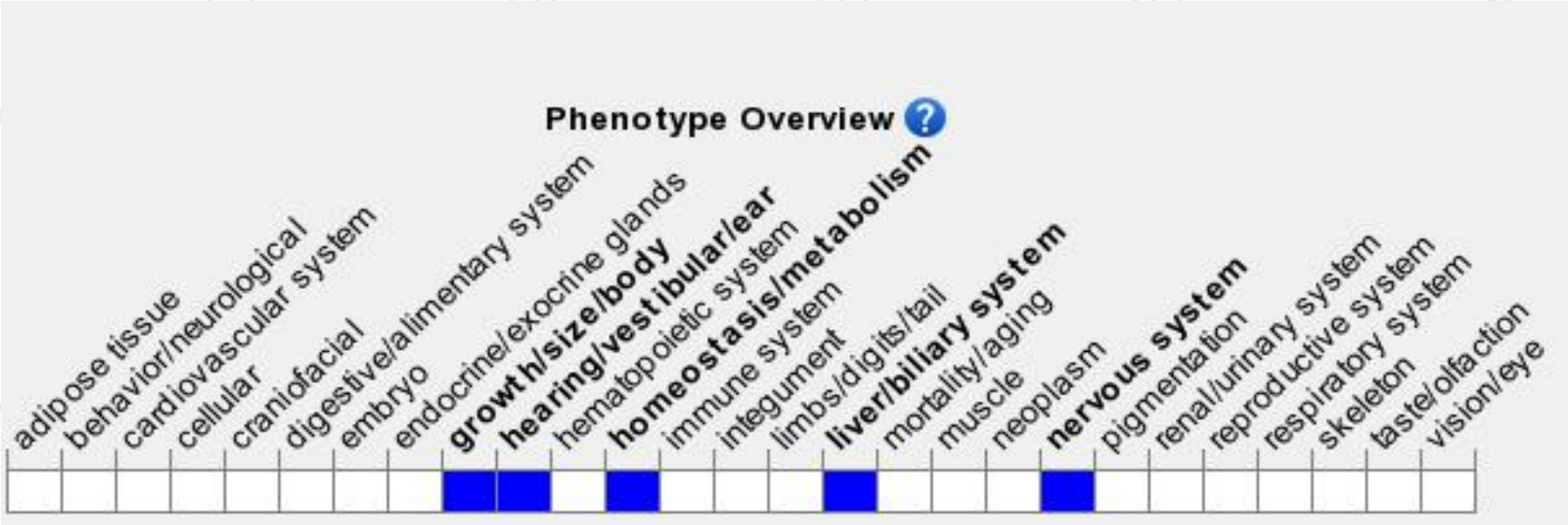
Genomic location distribution



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 mice display abnormal bile salt homeostasis, normal bile secretion, and an impaired ability to handle increased bile salt loading resulting in liver damage and weight loss on a bile salt supplemented diet.

集萃药康
GemPharmatech

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

Tel: 400-9660890

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GemPharmatech Co.,Ltd