Fabp6 Cas9-KO Strategy

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Design Date: 2019-11-1

Project Overview

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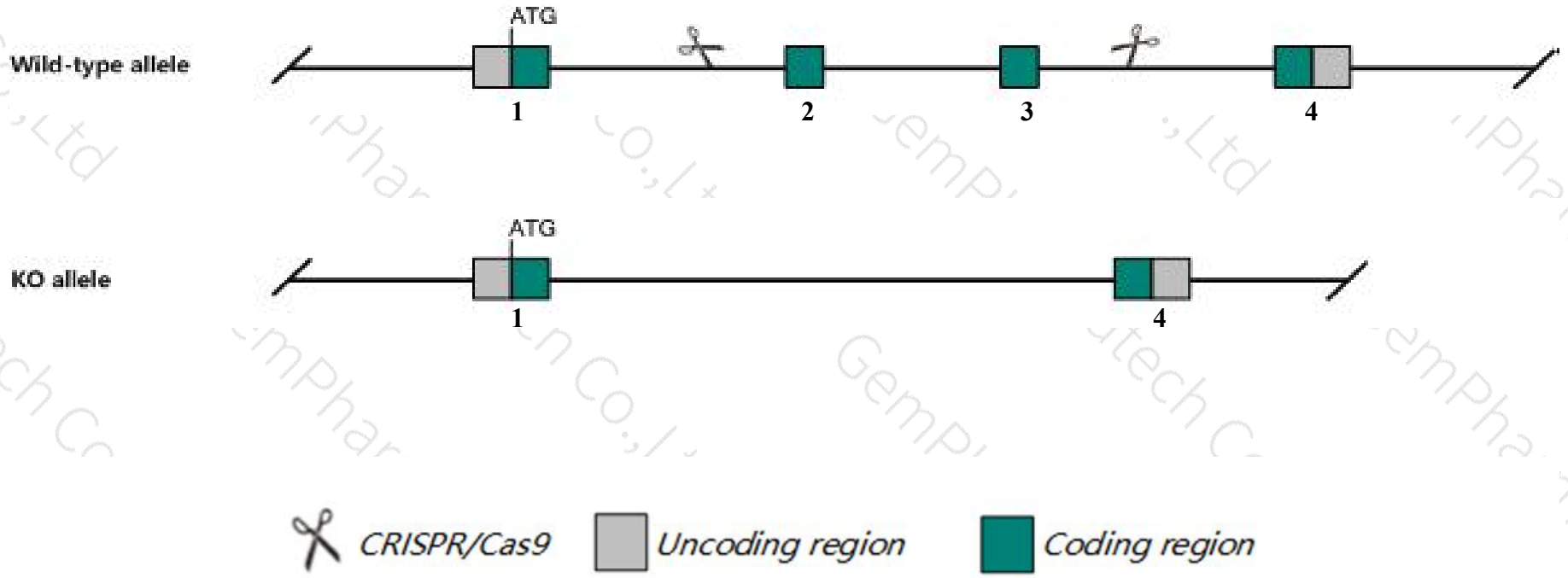
Project Name	***Fabp6***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fabp6* gene. The schematic diagram is as follows:



Technical routes

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- The *Fabp6* gene has 1 transcript. According to the structure of *Fabp6* gene, exon2-exon3 of *Fabp6-201* (ENSMUST00000020672.4) transcript is recommended as the knockout region.The region contains 266bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Fabp6* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a knock-out allele exhibit sex-specific altered bile acid absorption and transport.

- The *Fabp6* gene is located on the Chr11. 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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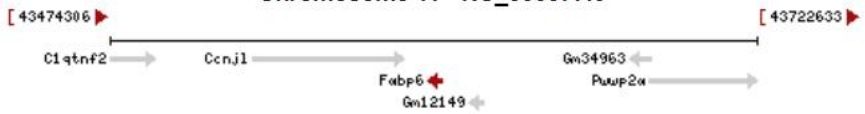
Fabp6 fatty acid binding protein 6 [*Mus musculus* (house mouse)]

Gene ID: 16204, updated on 12-Aug-2019

Summary

Official Symbol	Fabp6 provided by MGI
Official Full Name	fatty acid binding protein 6 provided by MGI
Primary source	MGI:MGI:96565
See related	Ensembl:ENSMUSG00000020405
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	GT; ILBP; I-15P; ILBP3; Illbp; I-BABP
Summary	The protein encoded by this gene is part of the fatty acid binding protein family (FABP). FABPs are a family of small, highly conserved, cytoplasmic proteins that bind long-chain fatty acids and other hydrophobic ligands and participate in fatty acid uptake, transport, and metabolism. This protein functions within the ileum, the distal 25-30% of the small intestine, and plays a role in enterohepatic circulation of bile acids and cholesterol homeostasis. In humans, it has been reported that polymorphisms in FABP6 confer a protective effect in obese individuals from developing type 2 diabetes. In mice deficiency of this gene affects bile acid metabolism in a gender-specific manner and was reported to be required for efficient apical to basolateral transport of conjugated bile acids. [provided by RefSeq, Jan 2013]
Expression	Restricted expression toward large intestine adult (RPKM 1460.5) See more
Orthologs	human all

Chromosome 11 - NC_000077.6

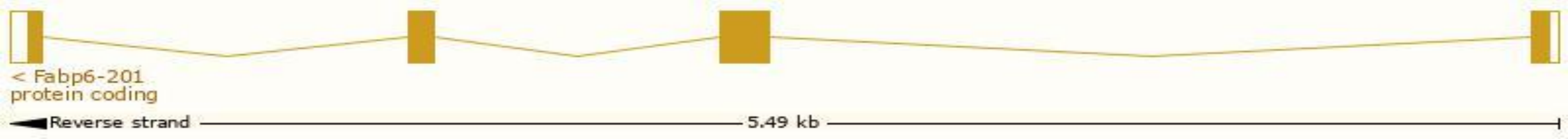


Transcript information（Ensembl）

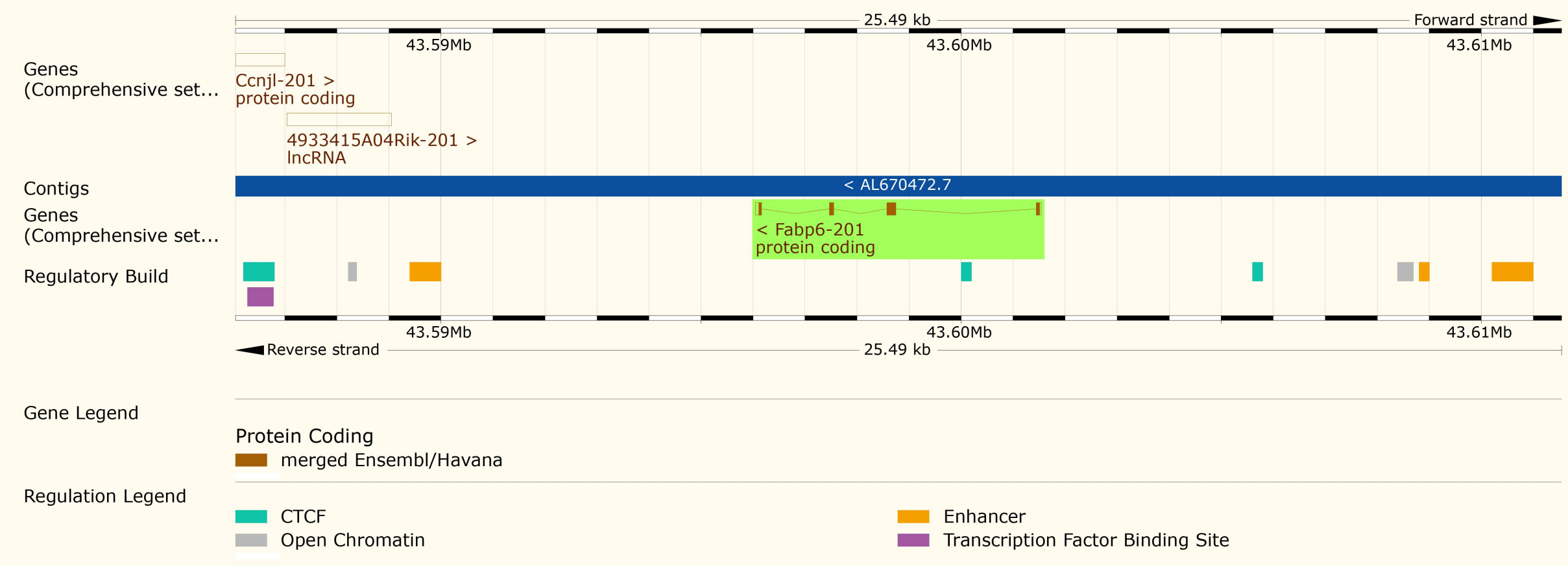
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags		
Fabp6-201	ENSMUST00000020672.4	479	128aa	ENSMUSP00000020672.4	Protein coding	CCDS24560	P51162	TSL:1	GENCODE basic	APPRIS P1

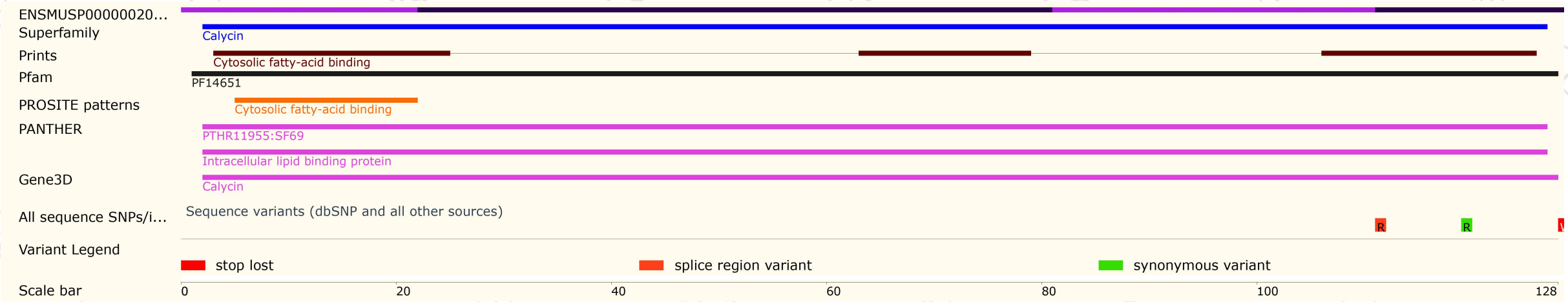
The strategy is based on the design of *Fabp6-201* transcript,The transcription is shown below



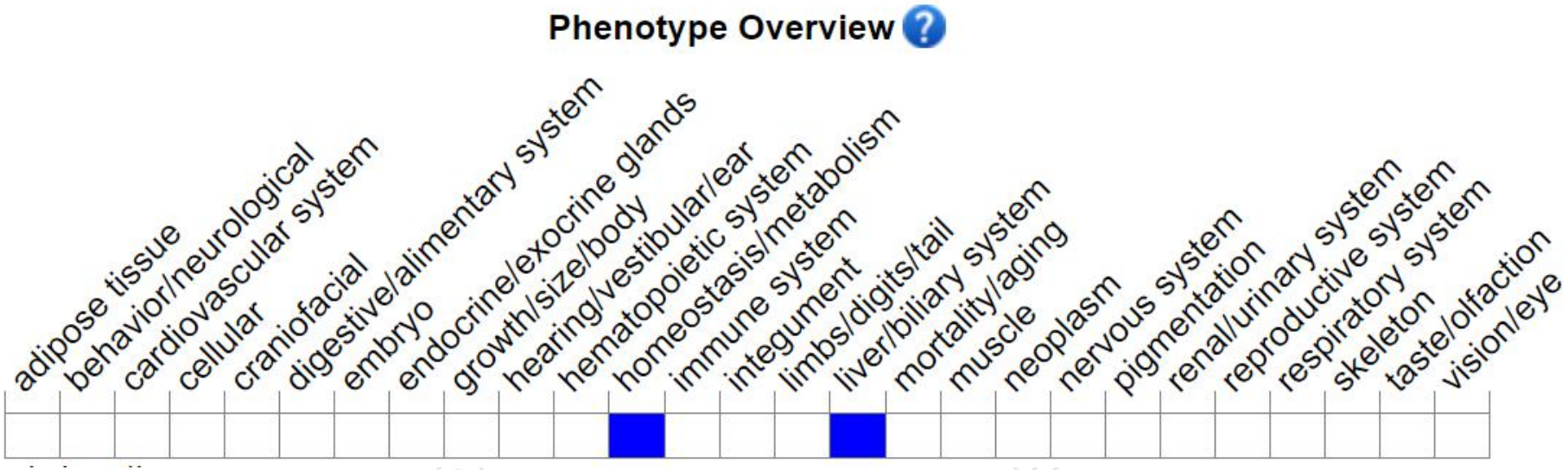
Genomic location distribution



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 knock-out allele exhibit sex-specific altered bile acid absorption and transport.

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