Abcg8 Cas9-KO Strategy

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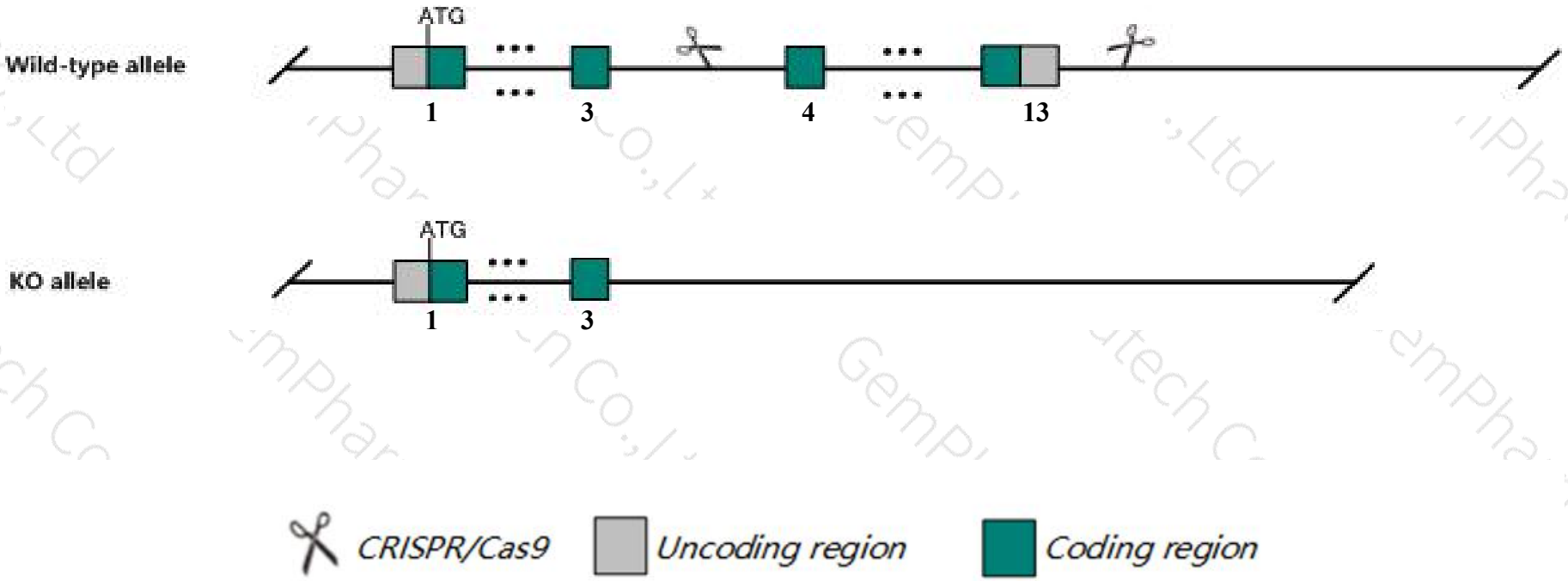
Project Overview

Project Name	***Abcg8***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abcg8* gene. The schematic diagram is as follows:



Technical routes

➢ The *Abcg8* gene has 3 transcripts. According to the structure of *Abcg8* gene, exon4-exon13 of *Abcg8-201* (ENSMUST00000045714.14) transcript is recommended as the knockout region.The region contains 1697bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Abcg8* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice

- According to the existing MGI data,Homozygous mutants fail to secrete cholesterol into bile and exhibit increased plasma and tissue plant sterol levels.

- The *Abcg8* gene is located on the Chr17. 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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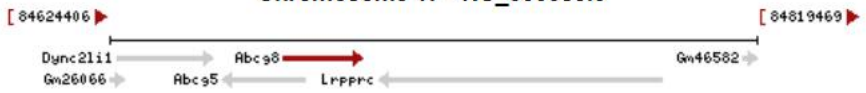
Abcg8 ATP binding cassette subfamily G member 8 [*Mus musculus* (house mouse)]

Gene ID: 67470, updated on 10-Oct-2019

Summary

Official Symbol	Abcg8 provided by MGI
Official Full Name	ATP binding cassette subfamily G member 8 provided by MGI
Primary source	MGI:MGI:1914720
See related	Ensembl:ENSMUSG00000024254
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	AI114946; sterolin-2; 1300003C16Rik
Expression	Biased expression in duodenum adult (RPKM 61.1), small intestine adult (RPKM 52.2) and 2 other tissues See more
Orthologs	human all

Chromosome 17 - NC_000083.6

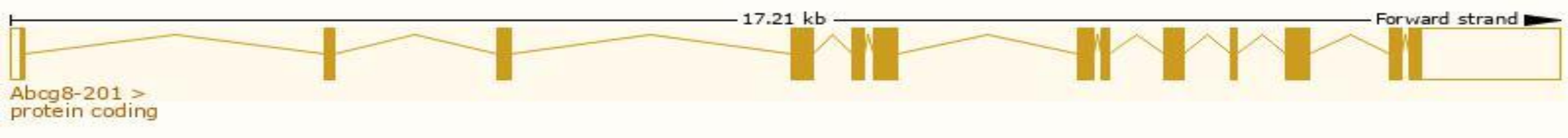


Transcript information（Ensembl）

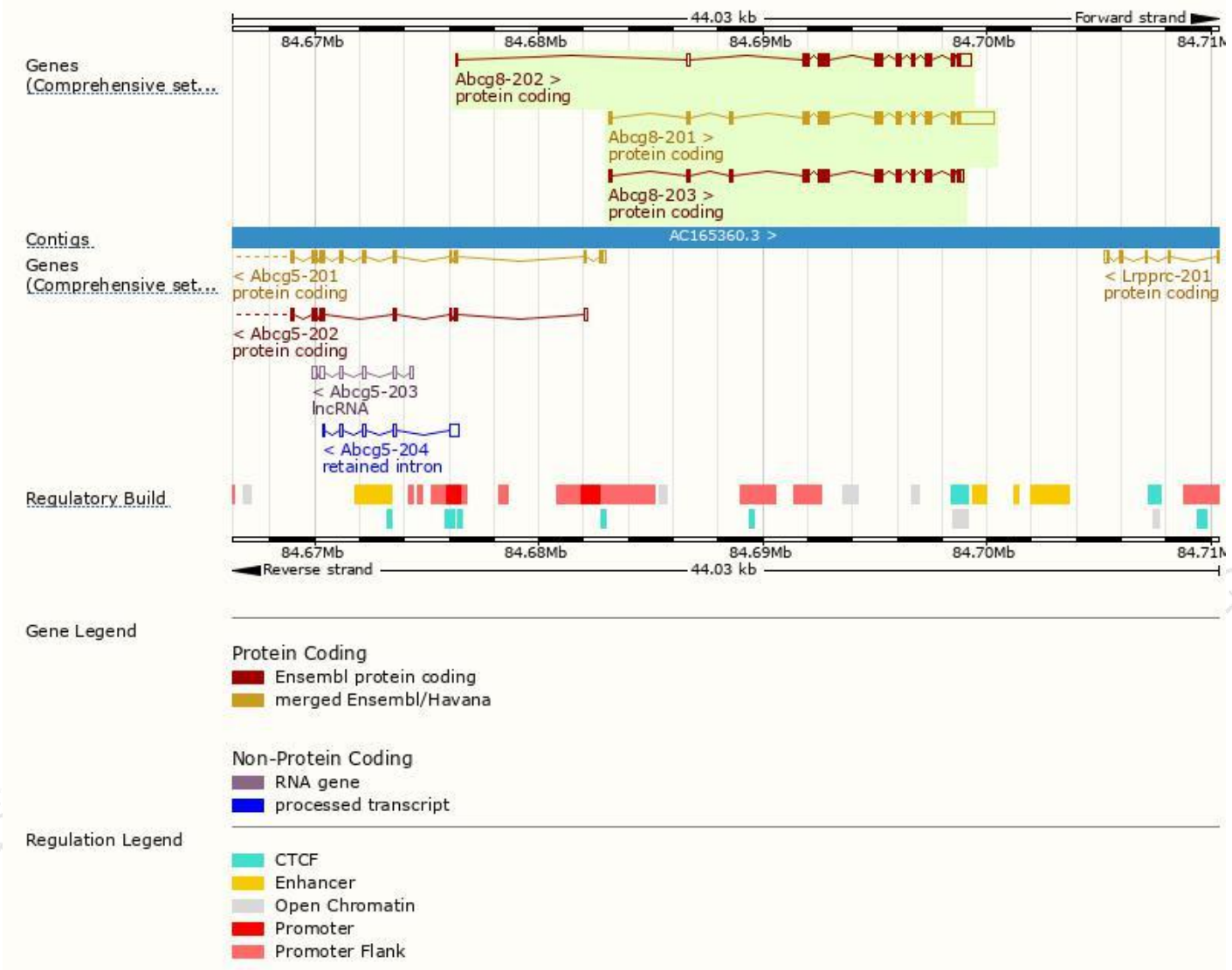
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abcg8-201	ENSMUST00000045714.14	3667	673aa	Protein coding	CCDS29002	Q9DBM0	TSL:1 GENCODE basic APPRIS P3
Abcg8-202	ENSMUST00000170725.7	2415	546aa	Protein coding	CCDS70849	E9Q0P2	TSL:1 GENCODE basic
Abcg8-203	ENSMUST00000171915.1	2284	672aa	Protein coding	CCDS84337	Q7TSR6	TSL:1 GENCODE basic APPRIS ALT2

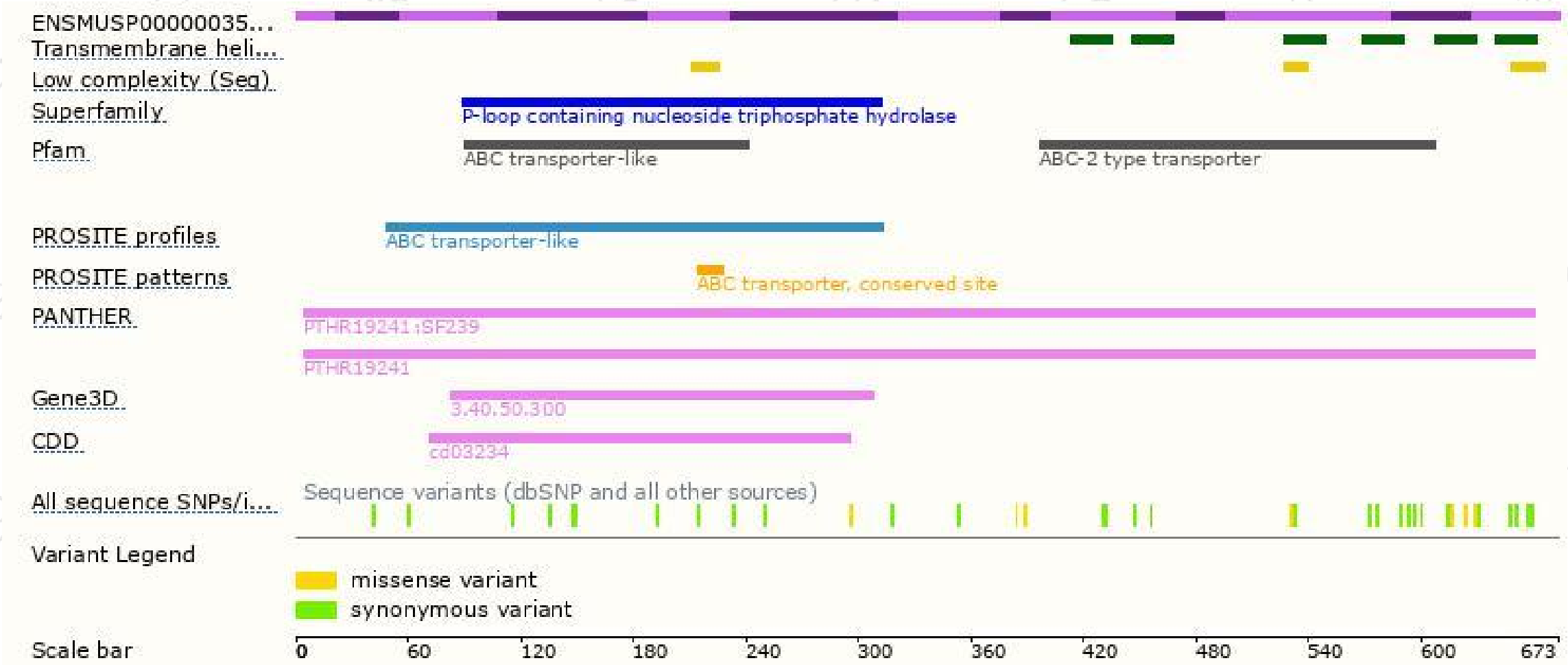
The strategy is based on the design of *Abcg8-201* transcript,The transcription is shown below



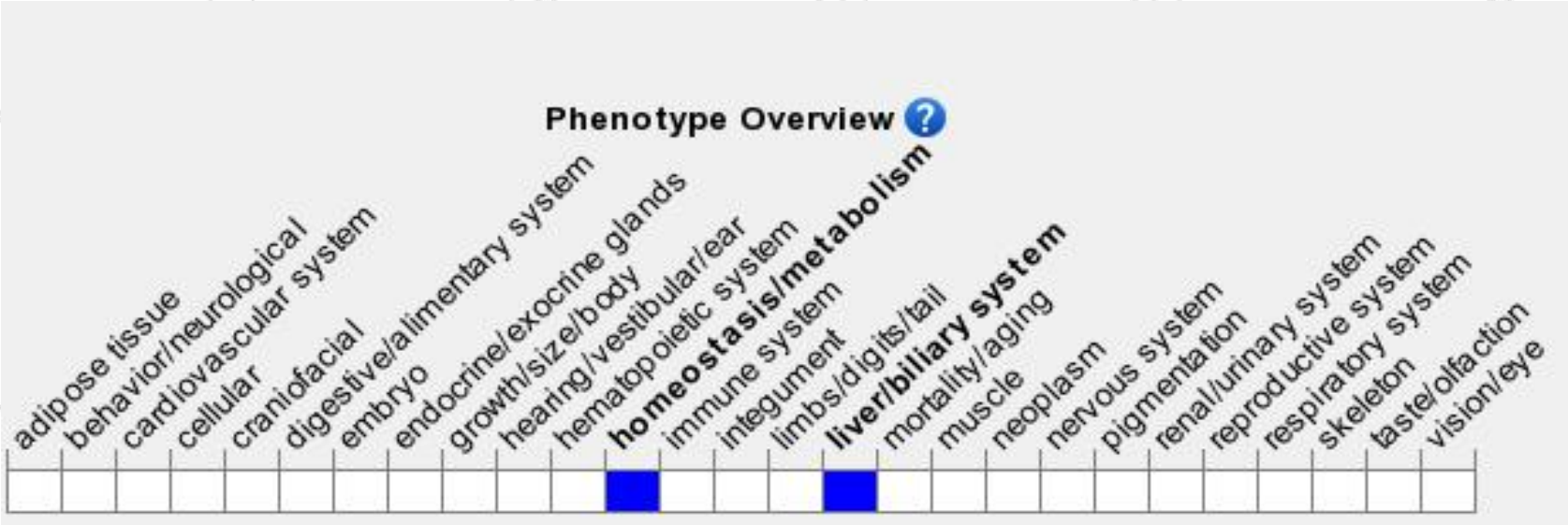
Genomic location distribution



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 mutants fail to secrete cholesterol into bile and exhibit increased plasma and tissue plant sterol levels.

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

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